
WIRE

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:31:00 1998: Master time 5.54 Seconds
Tabular output not generated. 221.678 Million cell updates/sec

Title: >US-08-844-215-14
Description: (1-106) from US08844215 pep
Perfect Score: 749
Sequence: 1 AFITQSGILSLSPGEAIL YCCQYGIPTFGGIVK 106

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 29.587 Variance 163.496: scale 0.181

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length	DR ID Description Pred. No.
1	575	90.1	106 10	P54275 Anti-HIV gp41 immunog 3.03e-41
2	575	90.1	106 10	W01320 VL of Fab, DL 41 19, 3.03e-41
3	570	89.5	106 9	P54316 Anti-HIV gp120 immuno 7.26e-41
4	570	89.5	104 10	W01278 VL region of HIV neut 7.26e-41
5	570	89.5	129 7	P38572 vK25-JV2 7.26e-41
6	566	88.9	108 10	W01265 VL region of HIV neut 1.46e-40
7	565	88.9	108 10	P54307 Anti-HIV gp120 immuno 1.46e-40
8	566	88.9	111 10	P54277 Anti-HIV gp41 immunog 1.46e-40
9	566	88.9	111 10	W01322 VL of Fab, GL 41 1, B 1.46e-40
10	563	88.5	107 10	P54311 Anti-HIV gp120 immuno 2.47e-40
11	563	88.5	107 10	W01264 VL region of HIV neut 2.47e-40
12	558	87.9	107 7	P38569 Human lambda light ch 5.86e-40
13	558	87.9	109 9	P50217 HSV glycoprotein F bi 8.35e-40
14	550	86.8	104 9	P54317 Anti-HIV gp120 immuno 2.38e-39
15	550	86.8	104 10	W01276 VL region of HIV neut 2.38e-39
16	548	86.5	129 7	P41286 P105 rearranged varia 3.37e-39
17	546	86.2	109 10	P56286 Light chain of Amb al 4.77e-39
18	542	85.7	214 19	W07615 Ulcerative colitis-as 9.59e-38
19	541	85.6	108 10	W01299 VL region of HIV neut 1.14e-38
20	541	85.6	134 20	W11155 Anti-lung tumour anti 1.14e-38

21	638	95.2	129 7	P38673	P105VP-P105VP	1.92e-38
22	634	84.6	109 10	P54263	Anti-HIV gp120 immuno	3.69e-38
23	628	83.8	107 10	P54308	Anti-HIV gp120 immuno	1.17e-37
24	628	83.8	107 10	W01266	VL region of HIV neut	1.19e-37
25	626	83.6	108 10	P54255	Anti-HIV gp120 immuno	1.58e-37
26	626	83.6	108 10	W01275	VL region of HIV neut	1.56e-37
27	625	83.4	215 19	W07616	Ulcerative colitis-as	1.85e-37
28	624	83.3	124 22	W24539	Immunoglobulin Fc12	2.20e-37
29	619	82.6	109 9	P50218	HSV glycoprotein F bi	5.26e-37
30	618	82.5	112 10	P54279	Anti-HIV gp41 immuno	5.26e-37
31	618	82.5	112 10	W01324	VL of Fab, SS 41 8, B	5.26e-37
32	616	82.2	104 9	P54315	Anti-HIV gp120 immuno	8.86e-37
33	616	82.2	104 10	W01273	VL region of HIV neut	8.86e-37
34	612	82.2	122 2	P81245	Anti-pseudomonas aer	8.86e-37
35	610	82.2	128 1	P91001	Anti-P. aeruginosa st	8.86e-37
36	612	81.7	105 10	W01272	VL region of HIV neut	1.78e-36
37	612	81.7	105 9	P54314	Anti-HIV gp120 immuno	1.78e-36
38	611	81.6	116 7	P38650	Human V-kappa fragmen	2.11e-36
39	611	81.6	116 20	W03948	DNA fragment vK65.8,	2.11e-36
40	611	81.6	116 11	P54286	Human V-kappa vK65.9	2.11e-36
41	610	81.4	108 10	W01267	VL region of HIV neut	2.55e-36
42	607	81.0	109 5	P25224	VL region of human th	4.24e-36
43	597	79.7	108 10	P54309	Anti-HIV gp120 immuno	2.41e-35
44	594	79.3	107 19	W01297	VL region of HIV neut	4.96e-35
45	594	79.3	107 19	W01295	VL region of HIV neut	4.06e-35

ALIGNMENTS

RESULT 1
ID R54275 standard: protein: 109 AA.
AC R54275:
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.
KW Human immunodeficiency virus: HIV1; glycoprotein gp41; epitope:
KW neutralisation: monoclonal antibody: light chain; variable region:
KW framework region: complementarity determining region.
OS Homo sapiens.
PH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..35
FT /label= CDR1
FT Region 36..50
FT /label= FR2
FT Region 51..57
FT /label= CDR2
FT Region 58..89
FT /label= FR3
FT Region 90..97
FT /label= CDR3
FT Region 98..109
FT /label= FR4
PR W09457922-A.
PD 14-APR-1994.
PE 30-SEP-1993: 509328.
PR 30-SEP-1993: GS-954.48.
PA (SCPI) SCRIpps RES INST.
PI Barbas CF, Burton DR, Lerner RA;
WP1: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immunotherapy
PS Claim 1: Page 215-216, 248pp, English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dielctronic vector to produce a library of fragments. Ecoli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the VAB regions of their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence P54275 neutralises HIV1
CC gp41.

FT /label= FR1 22...33

FT /Region

FT /label= CDR1 34...48

FT /Region

FT /label= FR2 49...55

FT /Region

FT /label= CDR2 56...87

FT /Region

FT /label= FR3 88...96

FT /Region

FT /label= CDR3 97...108

FT /Region

FT /label= FR4

FT /Region

FT /label= CDR4

FT /Region

FT /label= CDR5

FT /Region

FT /label= CDR6

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FT /label= CDR7

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FT /label= CDR8

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FT /label= CDR37

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FT /label= CDR38

FT /Region

FT /label= CDR39

FT /Region

FT /label= CDR40

FT /Region

FT /note= "Met encoded by AIC (sic)"

FT Misc_difference 35

FT /note= "Pro encoded by GCA (sic)"

FT Misc_difference 99

FT /note= "Leu encoded by GTG (sic)"

FT Misc_difference 113

FT /note= "Gly encoded by GAT (sic)"

FT Misc_difference 114

FT /note= "Ser encoded by AAC (sic)"

FT Misc_difference 116

FT /note= "Pro encoded by GTT (sic)"

PN WO9312232-A

PD 24-JUN-1993

PF 10-DEC-1993: 019328

PR 10-DEC-1993: US-804652

PA (DAND) DANA FARBER CANCER INST INC.

PA (NEWEL) NEW ENGLAND DEACONESS HOSPITAL CORP.

PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;

PI WPI: 93-214174/26.

DR N-PSDB: Q42706

PT DNA segments encoding monoclonal antibody - which binds to gp120

PT and neutralises HIV, for treating AIDS, and for diagnosing and

PT monitoring HIV infection

PS Disclosure, page 74-75; 109pp; English.

CC The nucleotide sequence of F105 Vx (542707 - sequence differs from

CC other F105 Vx sequences given elsewhere in the specification) was

CC compared with germline gene Hmuk325 (542705), showing 97.7%

CC similarity by nucleotide sequence analysis. F105 appears to

CC be derived from a member of the Vx III subgroup gene family.

CC Sequence 129 AA;

SQ

Query Match 89.5%; Score 670; DB 7; Length 129;

Best Local Similarity 91.4%; Pred. No. 7.26e-41;

Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Db 24 lqspstslspgeratlsragsissnylawyggkpgqgprlllygassratgipdrf 83

QY 3 LQSPSTSLSPGERATLSRAGSISLSKYLAWYGGKPGQGPRLLYGASSRATGIPDRF 62

Db 84 ssgsgtdftlsrlspclcdpavvyccqygtspytfgggtqldk 106

QY 63 SSGSGTDFTLSRLSPCLCDPAVVCQYGTPTFGGCTKVEIK 106

RESULT 6

ID W01265 standard; Protein: 108 AA.

AC W01265

DT 28-JAN-1997 (first entry)

DE VL region of HIV neutralising MAb, clone b24.

KW Heavy chain, light chain; variable region, VH, monoclonal antibody;

KW MAB, HIV, human immunodeficiency virus, glycoprotein, gp120, clone;

KW virus infectivity assay; precursor gp160; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Region 1..21

FT /label= FR1

FT Region 22..33

FT /label= CDR1

FT Region 34..48

FT /label= FR2

FT Region 49..55

FT /label= CDR2

FT Region 56..87

FT /label= FR3

FT Region 88..96

FT /label= CDR3

FT Region 97..108

FT /label= FR4

PN WO9602273-A1

PD 01-FEB-1996

PF 11-JUL-1995: U08743

PR 18-JUL-1994: US-276852

FT /label= FR1 22...33

FT /Region

FT /label= CDR1 34...48

FT /Region

FT /label= FR2 49...55

FT /Region

FT /label= CDR2 56...87

FT /Region

FT /label= FR3 88...96

FT /Region

FT /label= CDR3 97...108

FT /Region

FT /label= FR4

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FT /label= CDR4

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FT /label= CDR5

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FT /label= CDR8

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FT /label= CDR9

FT /Region

FT /label= CDR10

FT /Region

FT /label= CDR11

FT /Region

FT /label= CDR12

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PA (Scri ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18
PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example; Fig 11: 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK1
CC gene clone b24. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;

Query Match 88.9%; Score 666; DB 19; Length 108;
Best Local Similarity 89.6%; Pred. No. 1.46e-40;
Matches 95; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

Db 1 eltsqsgtltispggeratiscrasqsvsnlylawyqkpgqaprllygvsnratgipdr 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2 ELTQSPGTLSPGERATLSRASPSSSKYLAWYQKPGQAPRLFLFYDASSRATGIPDR 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 fsgsgsgtdftltisrlepedfavyscqgqtsptwfqggtkveik 106
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 FSGSGSGTDFTLSLPEDFAVYCCQYGT-PTTFGQGTKEIK 106
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
ID R54307 standard: protein; 108 AA.
AC R54307;
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region b24.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
FT W09407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U093328.
PR (Scri ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
PI WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Claim 11; Page 217; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence R54307 neutralises HIV1
CC gp41.
SQ Sequence 108 AA;

Query Match 88.9%; Score 666; DB 19; Length 111;
Best Local Similarity 89.6%; Pred. No. 1.46e-40;
Matches 95; Conservative 6; Mismatches 4; Indels 1; Gaps 0;

Db 2 aeltsgptltispggeratiscrasqsvsnlylawyqkpgqaprllygvsnratgipdr 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 AELTQSPGTLSPGERATLSRASPSSSKYLAWYQKPGQAPRLFLFYDASSRATGIPDR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 62 fsgsgsgtdftltisrlepedfavyscqgqtsptwfqggtkveik 107
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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CY 61 PFSGSGSDFTLSISRLPEFAVYVQYQYCTPTPTGQTKVEIK 106

RESULT 9
ID W01322 standard: Protein: 111 AA.
AC W01322;
DI 29-JAN-1997 (first entry)
DE VL of Fab, GL 41 L, binds to HIV gp41.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
KW MAB: HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers

FT Region 1..23
FT /label= FR1
FT Region 24..35
FT /label= CDR1
FT Region 36..50
FT /label= FR2
FT Region 51..57
FT /label= CDR2
FT Region 58..89
FT /label= FR3
FT Region 90..97
FT /label= CDR3
FT Region 98..111
FT /label= FR4
PN W09602273-A1.
PD 11-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (Scripps) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example 3, Fig 19; 36pp; English.
CC The sequences given in W01320-24 represent the light chain variable
CC regions (VH) of a series of antibody fragments (FAB's) which are
CC immunoreactive with HIV glycoprotein gp41. This sequence represents
CC the sequence of the clone, GL 41 L. These sequences represent light
CC chains which bind to the heavy light chain clones given in W01315-19. A
CC monoclonal antibody containing one of these Fab sequences may have the
CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
CC assay by 50% at a concentration of less than 700 ng of antibody/ml.
CC The MAB may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 111 AA;

Query Match 88.9%; Score 666; DB 19; Length 111;
Best Local Similarity 86.8%; Pred NO 1 45e-40;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Db 2 aeltspgtlslspgertlscrasqslsnnylawyyqkqgqaprllygssrtgtdpr 61
|||||
QY 1 AELTSPGTLSLSPGERATLSRASQSLSSKYLAWYQKQAPRFLFYDASSRATGIPDR 60
|||||
Db 62 rfsgsgsgadftlslrlepedfavyqcyqgagshftgqgkileik 107
|||||
QY 61 #FSGSGSGTDTLSISPLEPEDFAVYVQYQYCTPTPTGQTKVEIK 106
|||||

RESULT 10
ID R54311 standard: protein: 107 AA.
AC R54311;
DI 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region
OS Homo sapiens.
FH Key Location/Qualifiers

FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107
FT /label= FR4
PN W09407925-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (Scripps) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example; Page 180; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC electrostatic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54311 is from a gp120-
CC specific clone
SQ Sequence 107 AA;

Query Match 88.5%; Score 663; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.45e-40;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;
Db 1 eltsptlslspgertlscrasqslsnnylawyyqkqgqaprllygssrtgtdpr 60
|||||
QY 2 ELTSPGTLSLSPGERATLSRASQSLSSKYLAWYQKQAPRFLFYDASSRATGIPDR 61
|||||
Db 61 fsgsgsgadftlslrlepedfavyqcyqgagshftgqgkileik 106
|||||
QY 62 PFSGSGSGTDTLSISPLEPEDFAVYVQYQYCTPTPTGQTKVEIK 106
|||||

RESULT 11
ID W01269 standard: Protein: 107 AA.
AC W01269;
DI 28-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone B20.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers

FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107

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FT /label= FR4
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-275852.
PA (SRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DP, Lerner PA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example: Fig 11; 366pp; English.
CC The sequences given in WO1261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, B20. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection
SQ Sequence 107 AA:

Query Match 88.5%; Score 663; DB 19; Length 107;
Best Local Similarity 85.8%; Pred. No. 2,46e-40;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1,

Db 1 eltspgtltspgeratlsrscasqslsnnnylawyqkqgqaprllygsstrgtgipdr 60
QY 2 fltspgtltspgeratlsrscasqslsnnnylawyqkqgqaprllygsstrgtgipdr 61

Db 61 fsgsgstgdtltlsrlepedfavyycqygnsvytfgggtkleik 106
QY 62 fsgsgstgdtltlsrlepedfavyycqygnsvytfgggtkleik 106

RESULT 12
ID R38593 standard; peptide; 107 AA
AC R38593:
DE 28-OCT-1993 (first entry)
KW Human lambda light chain subgroup 3 (HL3).
KW Antibody; variable domain; light; L; heavy; H; consensus;
QS affinity; antigen; immunogenicity; humanisation; framework.
QS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 96
FT /note= "residue conserved in less than 50% of the
FT known sequences of HL3"
PN WO9311794-A.
PD 24-JUN-1993.
PF 14-DEC-1992; U10906.
PR 13-DEC-1991; US-808464
PA (XOMA ) XOMA CORP.
PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
DR WPI: 93-213827/25.
PT Antibodies prep. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Claim 2; Page 93-94; 160pp; English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (HK1 - R38590, HK3 - NGK, HK2 - GST, HL1 - R38591, HL2 -
CC R38592, HL3 - R38593, HL4 - R38594, HK4 - R38595, HL4 - R38596,
CC and HL5 - R38597) and heavy chains (HH3 - R38598, HH1 - R38599 and
CC HH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding
CC This ensures that the binding properties of the modified antibody
CC are not diminished.

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SQ Sequence 107 AA:

Query Match 87.9%; Score 658; DB 7; Length 107;
Best Local Similarity 90.5%; Pred. No. 5,89e-40;
Matches 95; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

Db 4 ltspgtltspgeratlsrscasqslsnnnylawyqkqgqaprllygsstrgtgipdr 62
QY 3 ltspgtltspgeratlsrscasqslsnnnylawyqkqgqaprllygsstrgtgipdr 63
Db 63 ssgsgstgdtltlsrlepedfavyycqygnsvytfgggtkleik 107
QY 63 ssgsgstgdtltlsrlepedfavyycqygnsvytfgggtkleik 106

RESULT 13
ID R50217 standard; protein; 109 AA.
AC R50217:
DE 31-OCT-1994 (first entry)
KW HSV glycoprotein F binding MAB clone rsv6/11/21/22L VH/VL domain.
KW Complementarily determination region, CDR3, human, bronchiolitis;
KW monoclonal antibody; epitope; glycoprotein F; influenza virus;
KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;
KW lung; pneumonia.
QS Synthetic.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT /Region 24..35
FT /label= CDP1
FT /Region 36..50
FT /label= FR2
FT /Region 51..57
FT /label= CDP2
FT /Region 58..89
FT /label= FR3
FT /Region 90..98
FT /label= CDR3
FT /Region 99..109
FT /label= FR4
PN WO9406448-A.
PD 31-MAR-1994.
PR 16-SEP-1992; US-945515.
PR 16-SEP-1992; US-945515.
PA (SRI ) SCRIPPS RES INST.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Barbas CF, Burton DP, Chanock RM, Crowe JE, Murphy BR;
DR WPI: 94-118147/14.
PT Human neutralising monoclonal antibodies to respiratory syncytial
PT virus - for treatment prophylaxis and diagnosis of RSV and other
PT diseases of the respiratory tract
PS Disclosure: Fig 4; 104pp; English.
CC The sequences given in R50215-19 represent the heavy and light chain
CC variable domains of various clones of a human monoclonal antibody
CC which binds to an epitope of glycoprotein F of respiratory syncytial
CC virus (RSV). These antibodies may be used as a reagent for the
CC diagnosis of RSV disease and other viral mucosal diseases, eg.
CC influenza virus, rhinovirus and coronavirus. They are particularly
CC useful in ameliorating RSV when delivered directly to the lungs, and
CC may also be used for treating pneumonia and bronchiolitis.
SQ Sequence 109 AA:

Query Match 87.6%; Score 656; DB 9; Length 109;
Best Local Similarity 86.0%; Pred. No. 8,35e-40;
Matches 92; Conservative 10; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltsgpgtltspgeratlsrscasqslsnnnylawyqkqgqaprllygsstrgtgipdr 61
QY 1 aeltsgpgtltspgeratlsrscasqslsnnnylawyqkqgqaprllygsstrgtgipdr 60
Db 62 rfsqsgstgdtltlsrlepedfavyycqygnsvytfgggtkleik 108
QY 61 rfsqsgstgdtltlsrlepedfavyycqygnsvytfgggtkleik 106

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RESULT 14
ID R54317 standard: protein: 104 AA
AC R54317
DE Anti-HIV gp120 immunoglobulin light chain variable region s6
DE Human immunodeficiency virus: HIV1; glycoprotein gp120; epitope;
KW neutralisation: monoclonal antibody; kappa light chain;
KW variable region; framework: complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..18
FT /label= FR1
FT Region 19..30
FT /label= CDR1
FT Region 31..45
FT /label= FR2
FT Region 46..52
FT /label= CDR2
FT Region 53..84
FT /label= FR3
FT Region 85..93
FT /label= CDR3
FT Region 94..104
FT /label= FR4
FT /label= FR4
PN W09602273-A1
PD 01-FEB-1996
PF 11-JUL-1995; U08743
PR 18-JUL-1994; US-276852
PA (SCR1 ) SCRIPOS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAb's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, s6. A MAb containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in-vivo virus infectivity assay
CC by 50 % at a concentration of less than 100 ng of anti-gp120, and
CC binds mature gp120 preferentially over the precursor gp160. The MAb
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 104 AA:

Query Match 86.8%; Score 650; DB 9; Length 104;
Best Local Similarity 87.4%; Pred. No. 2.38e-39;
Matches 90; Conservative 9; Mismatches 3; Indels 1; Gaps 1;

Db 1 qspqtlslpgeratlsrscasqslsnnylawyqgkpgqaprllygsstratgipdrfsq 60
QY 5 QSPQTLSLSPGERATLSRSPASQSLSSKYLAWYQKQKQAPPLFIYDASSRATGIPDPFSG 64
Db 61 gsgtdftltisrlpepfavvyccqgynsvytfqggtkleik 103
QY 65 SGSGTDFTLISRLPEPFDAVYVYCCQYGTTPR-TFGQGTKEIK 106

Search completed: Tue Feb 24 07:31:32 1998
Job time : 32 secs.

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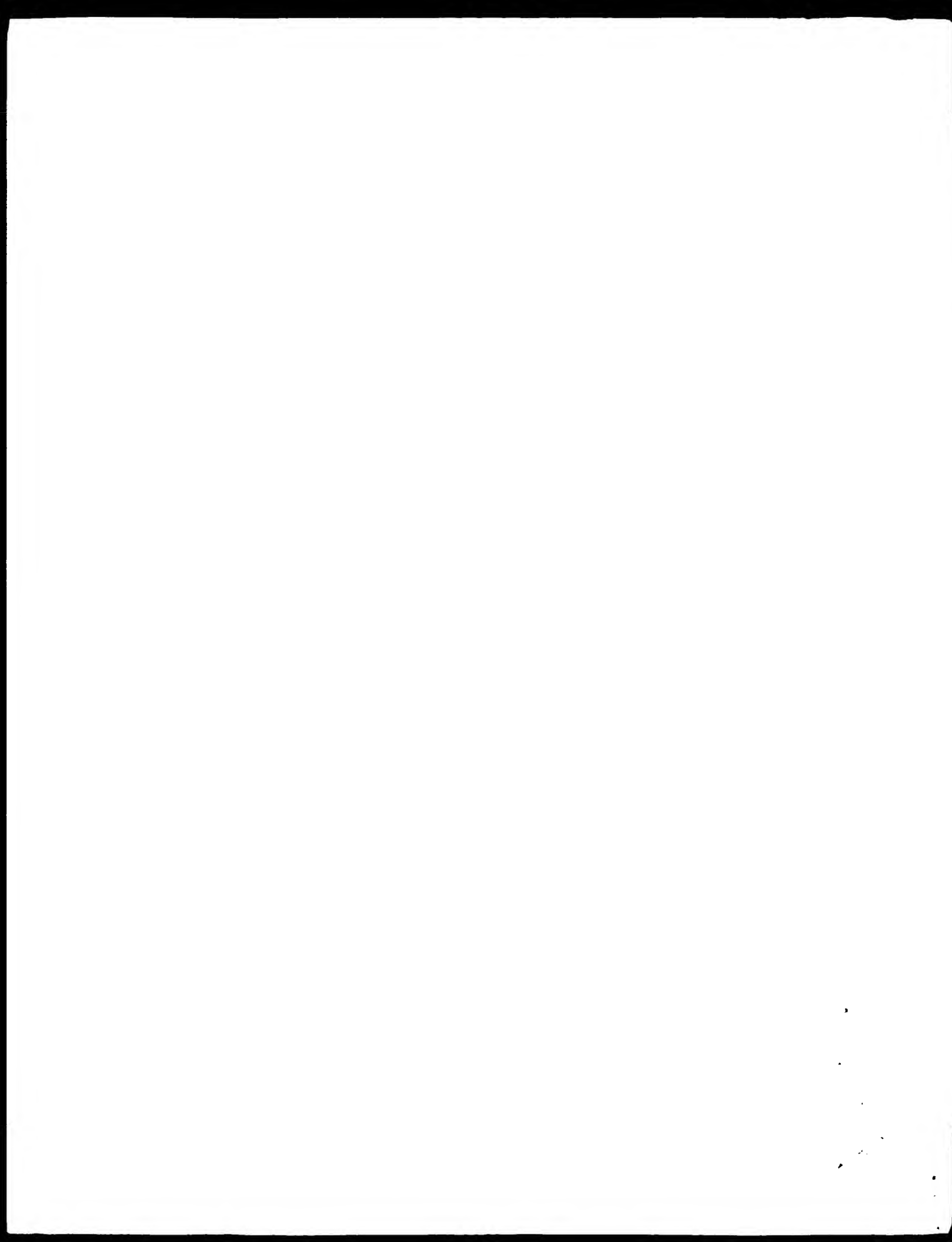
RESULT 15
ID W01274 standard: Protein: 104 AA.
AC W01274;
DE 29-JAN-1997 (first entry)
DE VL region of HIV neutralising MAb, clone s6.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
KW MAB: HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..18
FT /label= FR1
FT Region 19..30
FT /label= CDR1
FT Region 31..45
FT /label= FR2
FT Region 46..52
FT /label= CDR2
FT Region 53..84
FT /label= FR3
FT Region 85..93
FT /label= CDR3
FT Region 94..104
FT /label= FR4
FT /label= FR4
PN W09407922-A.
PD 14-APR-1994
PF 30-SEP-1993; U09428
PR 30-SEP-1992; ES-35448
PA (SCR1 ) SCRIPOS RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immunotherapy
PS Example: Page 186-187; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54317 neutralises HIV1
CC gp120.
SQ Sequence 104 AA:

Query Match 86.8%; Score 650; DB 9; Length 104;
Best Local Similarity 87.4%; Pred. No. 2.38e-39;
Matches 90; Conservative 9; Mismatches 3; Indels 1; Gaps 1;

Db 1 qspqtlslpgeratlsrscasqslsnnylawyqgkpgqaprllygsstratgipdrfsq 60
QY 5 QSPQTLSLSPGERATLSRSPASQSLSSKYLAWYQKQKQAPPLFIYDASSRATGIPDPFSG 64
Db 61 gsgtdftltisrlpepfavvyccqgynsvytfqggtkleik 103
QY 65 SGSGTDFTLISRLPEPFDAVYVYCCQYGTTPR-TFGQGTKEIK 106

Search completed: Tue Feb 24 07:31:32 1998
Job time : 32 secs.

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WIREHILL (IM)

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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:27:53 1998; MasPar time 7.38 Seconds
Tabular output not generated. 437.627 Million cell updates/sec

Title: >US-08-844-215-13
Description: (1-106) from US08844215 pep
Perfect Score: 728
Sequence: 1 AELTQSPSSLSAFVGDPRVI CQGSVTPPTPTFGGKVEVK 106

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pirs3
1:unann1 2:unann2 3:unann3 4:unann4 5:unann5 6:unann6 7:unann7 8:unann8 9:unann9 10:unann10 11:unann11 12:unann12 13:unann13 14:unann14 15:unann15 16:unann16 17:unann17 18:unann18 19:unann19 20:unann20 21:unann21 22:unann22 23:unann23 24:unann24 25:unann25 26:unann26 27:unann27 28:unann28 29:unann29 30:unann30 31:unann31 32:unann32 33:unann33 34:unann34 35:unann35 36:unann36 37:unann37 38:unann38 39:unann39 40:unann40 41:unann41 42:unann42 43:unann43 44:unann44 45:unann45 46:unann46 47:unann47 48:unann48 49:unann49 50:unann50 51:unann51 52:unann52 53:unann53 54:unann54 55:unann55 56:unann56 57:unann57 58:unann58 59:unann59 60:unann60 61:unann61 62:unann62 63:unann63 64:unann64 65:unann65 66:unann66 67:unann67 68:unann68 69:unann69 70:unann70 71:unann71 72:unann72 73:unann73 74:unann74 75:unann75 76:unann76 77:unann77 78:unann78 79:unann79 80:unann80 81:unann81 82:unann82 83:unann83 84:unann84 85:unann85 86:unann86 87:unann87 88:unann88 89:unann89 90:unann90 91:unann91 92:unann92 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864:unann864 865:unann865 866:unann866 867:unann867 868:unann868 869:unann869 870:unann870 871:unann871 872:unann872 873:unann873 874:unann874 875:unann875 876:unann876 877:unann877 878:unann878 879:unann879 880:unann880 881:unann881 882:unann882 883:unann883 884:unann884 885:unann885 886:unann886 887:unann887 888:unann888 889:unann889 890:unann890 891:unann891 892:unann892 893:unann893 894:unann894 895:unann895 896:unann896 897:unann897 898:unann898 899:unann899 900:unann900 901:unann901 902:unann902 903:unann903 904:unann904 905:unann905 906:unann906 907:unann907 908:unann908 909:unann909 910:unann910 911:unann911 912:unann912 913:unann913 914:unann914 915:unann915 916:unann916 917:unann917 918:unann918 919:unann919 920:unann920 921:unann921 922:unann922 923:unann923 924:unann924 925:unann925 926:unann926 927:unann927 928:unann928 929:unann929 930:unann930 931:unann931 932:unann932 933:unann933 934:unann934 935:unann935 936:unann936 937:unann937 938:unann938 939:unann939 940:unann940 941:unann941 942:unann942 943:unann943 944:unann944 945:unann945 946:unann946 947:unann947 948:unann948 949:unann949 950:unann950 951:unann951 952:unann952 953:unann953 954:unann954 955:unann955 956:unann956 957:unann957 958:unann958 959:unann959 960:unann960 961:unann961 962:unann962 963:unann963 964:unann964 965:unann965 966:unann966 967:unann967 968:unann968 969:unann969 970:unann970 971:unann971 972:unann972 973:unann973 974:unann974 975:unann975 976:unann976 977:unann977 978:unann978 979:unann979 980:unann980 981:unann981 982:unann982 983:unann983 984:unann984 985:unann985 986:unann986 987:unann987 988:unann988 989:unann989 990:unann990 991:unann991 992:unann992 993:unann993 994:unann994 995:unann995 996:unann996 997:unann997 998:unann998 999:unann999 1000:unann1000 1001:unann1001 1002:unann1002 1003:unann1003 1004:unann1004 1005:unann1005 1006:unann1006 1007:unann1007 1008:unann1008 1009:unann1009 1010:unann1010 1011:unann1011 1012:unann1012 1013:unann1013 1014:unann1014 1015:unann1015 1016:unann1016 1017:unann1017 1018:unann1018 1019:unann1019 1020:unann1020 1021:unann1021 1022:unann1022 1023:unann1023 1024:unann1024 1025:unann1025 1026:unann1026 1027:unann1027 1028:unann1028 1029:unann1029 1030:unann1030 1031:unann1031 1032:unann1032 1033:unann1033 1034:unann1034 1035:unann1035 1036:unann1036 1037:unann1037 1038:unann1038 1039:unann1039 1040:unann1040 1041:unann1041 1042:unann1042 1043:unann1043 1044:unann1044 1045:unann1045 1046:unann1046 1047:unann1047 1048:unann1048 1049:unann1049 1050:unann1050 1051:unann1051 1052:unann1052 1053:unann1053 1054:unann1054 1055:unann1055 1056:unann1056 1057:unann1057 1058:unann1058 1059:unann1059 1060:unann1060 1061:unann1061 1062:unann1062 1063:unann1063 1064:unann1064 1065:unann1065 1066:unann1066 1067:unann1067 1068:unann1068 1069:unann1069 1070:unann1070 1071:unann1071 1072:unann1072 1073:unann1073 1074:unann1074 1075:unann1075 1076:unann1076 1077:unann1077 1078:unann1078 1079:unann1079 1080:unann1080 1081:unann1081 1082:unann1082 1083:unann1083 1084:unann1084 1085:unann1085 1086:unann1086 1087:unann1087 1088:unann1088 1089:unann1089 1090:unann1090 1091:unann1091 1092:unann1092 1093:unann1093 1094:unann1094 1095:unann1095 1096:unann1096 1097:unann1097 1098:unann1098 1099:unann1099 1100:unann1100 1101:unann1101 1102:unann1102 1103:unann1103 1104:unann1104 1105:unann1105 1106:unann1106 1107:unann1107 1108:unann1108 1109:unann1109 1110:unann1110 1111:unann1111 1112:unann1112 1113:unann1113 1114:unann1114 1115:unann1115 1116:unann1116 1117:unann1117 1118:unann1118 1119:unann1119 1120:unann1120 1121:unann1121 1122:unann1122 1123:unann1123 1124:unann1124 1125:unann1125 1126:unann1126 1127:unann1127 1128:unann1128 1129:unann1129 1130:unann1130 1131:unann1131 1132:unann1132 1133:unann1133 1134:unann1134 1135:unann1135 1136:unann1136 1137:unann1137 1138:unann1138 1139:unann1139 1140:unann1140 1141:unann1141 1142:unann1142 1143:unann1143 1144:unann1144 1145:unann1145 1146:unann1146 1147:unann1147 1148:unann1148 1149:unann1149 1150:unann1150 1151:unann1151 1152:unann1152 1153:unann1153 1154:unann1154 1155:unann1155 1156:unann1156 1157:unann1157 115

#title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40367

#status preliminary; translation not shown

#molecule_type mRNA

#residues 1-127 #label KLE

#cross-references EMBL:X72477

CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology

KEYWORDS heterotetramer: immunoglobulin

SUMMARY #length 127 #molecular-weight 13919 #checksum 8394

Query Match 89.4%; Score 651; DB 7; Length 127;

Best Local Similarity 88.6%; Pred. No. 1.52e-71;

Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 20 gmtqspsslsasvdrvtitcrasqsisnylnwvqrkpkapkllyaaasslsgvpsrf 79

Qy 2 ELTQSPSSLSAFVGDVPTITCPASQGISPNLNWYQKPGTAPKVLIIYAASSLSQSGVPSRF 61

Db 80 sgsqsgtdftltisslqpedfatyyccqsyntptfsggtkveik 124

Qy 62 SGSGSGTDFTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 3

ENTRY B49047 #type fragment

TITLE IgM monoclonal strational autoantibody kappa chain variable

ORGANISM region, IgM STRAB SA-1A kappa chain V region - human

DATE #formal_name Homo sapiens #common_name man

19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change

28-Apr-1995

ACCESSIONS B49047

REFERENCE A49047

#authors Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.;

Capra, J.D.

#journal Eur J Immunol (1992) 22:2231-2236

#title Human monoclonal strational autoantibodies isolated from

thymic B lymphocytes of patients with myasthenia gravis use

VH and VL gene segments associated with the autoimmune

repertoire.

#cross-references M01D:92387224

#accession B49047

#status preliminary

#molecule_type nucleic acid

#residues 1-108 #label VIC

#cross-references NCBI:113209

#experimental_source thymic B lymphocytes

#note sequence extracted from NCBI backbone

CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology

SUMMARY #length 108 #checksum 1741

Query Match 88.2%; Score 642; DB 7; Length 108;

Best Local Similarity 88.6%; Pred. No. 2.70e-70;

Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 3 gmtqspsslsasvdrvtitcrasqsisnylnwvqrkpkapkllyaaasslsgvpsrf 62

Qy 2 ELTQSPSSLSAFVGDVPTITCPASQGISPNLNWYQKPGTAPKVLIIYAASSLSQSGVPSRF 61

Db 63 sgsqsgtdftltisslqpedfatyyccqsyntptfsggtkveik 107

Qy 62 SGSGSGTDFTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 4

ENTRY S40370 #type complete

TITLE Ig kappa chain - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change

16-Aug-1996

ACCESSIONS S40370

REFERENCE S40312

#authors Klein, R.; Jaenichen, R.; Zachau, H.G.

#journal Eur J Immunol (1993) 23:3248-3271

#title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40370

#status preliminary; translation not shown

#molecule_type mRNA

#residues 1-122 #label KLE

#cross-references EMBL:X72480

CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology

KEYWORDS heterotetramer: immunoglobulin

SUMMARY #length 122 #molecular-weight 13257 #checksum 567

Query Match 88.2%; Score 642; DB 7; Length 122;

Best Local Similarity 87.6%; Pred. No. 2.70e-70;

Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Db 17 qltqspsslsasvdrvtitcrasqsisflhwvgnlqkpkkllyaaasslsgvpsrf 76

Qy 2 ELTQSPSSLSAFVGDVPTITCRASQGISRNLAWYQKPGTAPKVLIIYAASSLSQSGVPSRF 61

Db 77 sgsqsgtdftltisslqpedfatyyccqsyntptfsggtkveik 121

Qy 62 SGSGSGTDFTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 5

ENTRY S47182 #type complete

TITLE Ig kappa chain - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change

16-Aug-1996

ACCESSIONS S47182

REFERENCE S47181

#authors McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

#submission submitted to the EMBL Data Library, June 1994

#description Cloning and analysis of IgM anti-thyroglobulin autoantibodies

from patients with Hashimoto's thyroiditis.

#accession S47182

#status preliminary

#molecule_type mRNA

#residues 1-108 #label MCI

#cross-references EMBL:X79786

CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology

KEYWORDS heterotetramer: immunoglobulin

SUMMARY #length 108 #molecular-weight 11655 #checksum 2422

Query Match 87.8%; Score 639; DB 7; Length 108;

Best Local Similarity 87.7%; Pred. No. 7.05e-70;

Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 2 teltqspsslsasvdrvtitcrasqsisnylnwvqrkpkapkllyaaasslsgvpsrf 61

Qy 1 AFUTQSPSSLSAFVGDVPTITCPASQGISPNLNWYQKPGTAPKVLIIYAASSLSQSGVPSRF 60

Db 62 fsgsgsgtdftltisslqpedfatyyccqsyntptfsggtkveik 107

Qy 61 FSGSGSGTDFTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 6

ENTRY S31998 #type fragment

TITLE Ig kappa chain - human (fragment)

ORGANISM #formal_name Homo sapiens #common_name man

DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change

16-Aug-1996

ACCESSIONS S31998

REFERENCE S31977

#authors Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan,

S.M.; Rapoport, B.

#submission submitted to the EMBL Data Library, June 1992

#description Lack of promiscuity in autoantigen-specific H and L chain

combinations as revealed by human H and L chain "roulette".


```

#accession S31598
#status Preliminary
#molecule_type mRNA
#residues 1-109 ##label POR
#cross-references EMBL:Z15081
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 6177

Query Match 87.8%; Score 639; DB 7; Length 109;
Best Local Similarity 87.5%; Pred. No. 7.05e-70;
Matches 91; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 4 mtgspsslsasvdrvtitcrasgissaylnwygqkpkpkllyasaslgspvrsf 63
QY 3 LTQSPSSLSAFVSDPVITTFASGSIISPLNWNVQKRPSTAPKVLIIYAASLSGVPSPFS 52
Db 64 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 63 SSGSGTDFILIIISLQPEFAIYYQQSYIIIPRIFGQTKVEVK 106

RESULT 7
ENTRY K1HCHU #type complete
TITLE Ig kappa chain V-1 region (Hau) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
ACCESSIONS S02574; A01868
REFERENCE S02572;
#authors Steiner, V.; Chang, J.Y.
#journal FEBS Lett (1987) 222:6-10
#title Chemical modification of the carboxyl groups of protein
#cross-references MUID:88005152
#accession S02574
#status preliminary
#molecule_type protein
#residues 1-109 ##label STE
REFERENCE A01868
#authors Watanabe, S.; Hilschmann, N.
#journal Hoppe-Seyler's Z. Physiol. Chem. (1970) 351:1291-1295
#title The primary structure of a monoclonal kappa-type
#cross-references MUID:71032830
#accession A01868
#molecule_type protein
#residues 1-108 ##label WAT
#note This is a Bence Jones protein.
COMMENT GENETICS
#gene GDB:IGKV1
COMP-EX #cross-references GDB:136264
#cross-references GDB:136264
an immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds; in some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
FEATURE
SUMMARY #disulfide_bonds #status predicted
#length 109 #molecular_weight 11772 #checksum 7448

Query Match 85.9%; Score 632; DB 2; Length 109;
Best Local Similarity 84.8%; Pred. No. 6.61e-69;
Matches 89; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Db 3 qmtgspsslsasvdrvtitcrasgissaylnwygqkpkpkllyasaslgspvrsf 62
QY 2 ELTQSPSSLSAFVSDPVITTFASGSIISPLNWNVQKRPSTAPKVLIIYAASLSGVPSPFS 61

#accession S31598
#status Preliminary
#molecule_type mRNA
#residues 1-109 ##label POR
#cross-references EMBL:Z15074
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 6130

Query Match 85.9%; Score 625; DB 7; Length 109;
Best Local Similarity 82.7%; Pred. No. 6.19e-68;
Matches 86; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 4 mtgspsslsasvdrvtitcrasgissaylnwygqkpkpkllyasaslgspvrsf 63
QY 3 LTQSPSSLSAFVSDPVITTFASGSIISPLNWNVQKRPSTAPKVLIIYAASLSGVPSPFS 52
Pt 64 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 63 SSGSGTDFILIIISLQPEFAIYYQQSYIIIPRIFGQTKVEVK 106

RESULT 8
ENTRY S44122 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-1995
ACCESSIONS S44122
REFERENCE S44105
#authors Hawkins, P.E.; Zhu, P.; Czeck, M.; Winter, G.; Hamlin,
#submission T.J.; Stevenson, F.K.
#description submitted to the EMBL Data Library, March 1994
#description Idiotype vaccination against human B-cell lymphoma: rescue
of variable region gene sequences from biopsy material for
assembly as single chain fv "personal" vaccine.
#accession S44122
#status preliminary
#molecule_type DNA
#residues 1-108 ##label HAW
#cross-references EMBL:Z31390
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 108 #molecular_weight 11750 #checksum 3040

Query Match 86.4%; Score 629; DB 7; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.72e-68;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Db 3 qmtgspsslsasvdrvtitcrasgissaylnwygqkpkpkllyasaslgspvrsf 62
QY 2 ELTQSPSSLSAFVSDPVITTFASGSIISPLNWNVQKRPSTAPKVLIIYAASLSGVPSPFS 61
Db 63 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 62 SSGSGTDFILIIISLQPEFAIYYQQSYIIIPRIFGQTKVEVK 106

RESULT 9
ENTRY S31978 #type fragment
TITLE Ig kappa chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
ACCESSIONS S31978
REFERENCE S31977
#authors Portolano, S.; Chazrenbalk, G.D.; Hutchison, S.J.; McLachlan,
#submission S.M.; Rapoport, B.
#description submitted to the EMBL Data Library, June 1992
#description Lack of promiscuity in autoantigen-specific H and L chain
combinations as revealed by human H and L chain "doublets".
#accession S31978
#status preliminary
#molecule_type mRNA
#residues 1-109 ##label POR
#cross-references EMBL:Z15074
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 6130

Query Match 85.9%; Score 625; DB 7; Length 109;
Best Local Similarity 82.7%; Pred. No. 6.19e-68;
Matches 86; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 4 mtgspsslsasvdrvtitcrasgissaylnwygqkpkpkllyasaslgspvrsf 63
QY 3 LTQSPSSLSAFVSDPVITTFASGSIISPLNWNVQKRPSTAPKVLIIYAASLSGVPSPFS 52
Pt 64 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 63 SSGSGTDFILIIISLQPEFAIYYQQSYIIIPRIFGQTKVEVK 106

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QY 63 GSGSGTDTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 10
ENTRY S40317 #type complete
TITLE Ig kappa chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
16-Aug-1996
ACCESSIONS S40317
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. (1993) 23:3248-3271
#journal
#title Expressed human immunoglobulin chi genes and their
#accession hypermutation.
#status S40317
#molecule_type preliminary; translation not shown
#residues 1-129 ##label KLE
#cross-references EMBL:X72427
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 129 #molecular-weight 13997 #checksum 8930

Query Match 85.9%; Score 625; DB 7; Length 129;
Best Local Similarity 83.8%; Pred. No. 6.19e-68; Indels 0; Gaps 0;
Matches 88; Conservative 10; Mismatches 7;

Db 24 qmtgspsslsldrvttitcrasqstgtylnwvqqkpkapkllygasslqsgvpsrf 83
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 ELTQSPSSLSAFVGDRTVITCRASQSI SRNLNMYQKPGTAPKVLIVAASSLQSGVPSRF 61

Db 84 sgsgsgtftltisslqpedfatyyccqstypptfgggtkveik 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SSGSGTDTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 11
ENTRY K1HUOU #type complete
TITLE Ig kappa chain V-I region (Ou) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE #text_change 06-Sep-1996
ACCESSIONS A01872
REFERENCE A94242
#authors Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
#journal Science (1970) 169:56-59
#title Macroglobulin structure: variable sequence of light and heavy
chains.
#cross-references MUID:70201507
#accession A01872
#molecule_type protein
#residues 1-108 ##label KOH
#note the sequence of the C region, which has the Inv (3)
marker, is also given
COMMENT This chain was isolated from a Waldenstrom's macroglobulin
GENETICS #gene
#cross-references GDB:136264
COMPLEX An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer
FEATURE 23-88
SUMMARY #disulfide_bonds #status predicted
#length 108 #molecular-weight 11777 #checksum 3565

Query Match 85.4%; Score 622; DB 2; Length 108;
Best Local Similarity 68.6%; Pred. No. 1.61e-67; Indels 0; Gaps 0;
Matches 72; Conservative 28; Mismatches 5;

QY 3 qmtzspsslsasvqbrvttitcrasstissylbwyzzkpkapblliyaaabihsgvpsrf 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 ELTQSPSSLSAFVGDRTVITCRASQSI SRNLNMYQKPGTAPKVLIVAASSLQSGVPSRF 61

Db 63 sgsgsgtftltisslqpedfatyycczsyssptfggtkzlik 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SSGSGTDTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 12
ENTRY S31981 #type fragment
TITLE Ig kappa chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
16-Aug-1996
ACCESSIONS S31981
REFERENCE Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan,
S.M.; Rapoport, B.
#submission submitted to the EMBL Data Library, June 1992
#description Lack of promiscuity in autoantigen-specific H and L chain
combinations as revealed by human H and L chain "roulette".
#accession S31981
#status preliminary
#molecule_type mRNA
#residues 1-109 ##label POR
#cross-references EMBL:Z15077
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 4724

Query Match 85.2%; Score 620; DB 7; Length 109;
Best Local Similarity 83.7%; Pred. No. 3.05e-67; Indels 0; Gaps 0;
Matches 87; Conservative 11; Mismatches 6;

Db 4 mtgspsslsasvqbrvttitcrasqdisrylnwvqqkpkapkllygasslqsgvpsrf 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 3 LTQSPSSLSAFVGDRTVITCRASQSI SRNLNMYQKPGTAPKVLIVAASSLQSGVPSRF 62

Db 64 sgsgsgtftltisslqpedfatyyccqstypptfgggtkveik 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 GSGSGTDTLTITSLQPEDFATYYCQSYTTPRTFGQGTKEVK 106

RESULT 13
ENTRY K1HUDE #type complete
TITLE Ig kappa chain V-I region (Dee) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE #text_change 06-Sep-1996
ACCESSIONS A01865
REFERENCE A01865
#authors Milstein, C.P.; Deverson, E.V.
#journal Biochem. J. (1971) 123:945-958
#title The amino acid sequence of a human kappa light chain.
#cross-references MUID:72053133
#accession A01865
#molecule_type protein
#residues 1-108 ##label MIL
#note the C region of this chain as the Inv (3) marker
GENETICS #gene
#cross-references GDB:136264
COMPLEX An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer
FEATURE 23-88
SUMMARY #disulfide_bonds #status predicted

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MORFAL (TM)

Release 2.1D John F Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:27:18 1998; MasPar time 4.94 Seconds
Tabular output not generated.
454,834 Million cell updates/sec

Title: >US-08-844-215-13
Description: (1-106) from US08844215.pep
Perfect Score: 728
Sequence: 1 AELTQSPSSLSAFVGPVTL..... CQGSYTPFTFGQIKVEVK 106

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 40.195; Variance 69.494; scale 0.578

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES			
Result No	Score	Query Match Length DA ID	Description Pred. No
1	632	86.8 108 5	KV1H_HUMAN IG KAPPA CHAIN V-I RE 4 76e-119
2	622	85.4 108 5	KV1N_HUMAN IG KAPPA CHAIN V-I RE 1 09e-116
3	617	84.8 108 5	KV1E_HUMAN IG KAPPA CHAIN V-I RE 1 64e-115
4	610	83.8 108 5	KV1W_HUMAN IG KAPPA CHAIN V-I RE 7 29e-114
5	606	83.2 108 5	KV1P_HUMAN IG KAPPA CHAIN V-I RE 6 37e-113
6	601	82.6 108 5	KV1G_HUMAN IG KAPPA CHAIN V-I RE 5 49e-108
7	585	80.4 107 5	KV1D_HUMAN IG KAPPA CHAIN V-I RE 4 77e-107
8	581	79.8 108 5	KV1F_HUMAN IG KAPPA CHAIN V-I RE 1 22e-105
9	575	79.0 108 5	KV1S_HUMAN IG KAPPA CHAIN V-I RE 1 81e-104
10	570	78.3 108 5	KV1K_HUMAN IG KAPPA CHAIN V-I RE 3 10e-104
11	569	78.2 108 5	KV1T_HUMAN IG KAPPA CHAIN V-I RE 5 32e-104
12	568	78.0 108 5	KV1B_HUMAN IG KAPPA CHAIN V-I RE 9 12e-104
13	568	78.0 108 5	KV1X_HUMAN IG KAPPA CHAIN V-I RE 1 35e-102
14	567	77.9 108 5	KV1V_HUMAN IG KAPPA CHAIN V-I RE 1 35e-102
15	562	77.2 108 5	KV1Y_HUMAN IG KAPPA CHAIN V-I RE 1 35e-102
16	562	77.2 108 5	KV1Q_HUMAN IG KAPPA CHAIN V-I RE 3 97e-102
17	560	76.4 108 5	KV1A_HUMAN IG KAPPA CHAIN V-I RE 6 80e-102
18	559	76.8 108 5	KV1M_HUMAN IG KAPPA CHAIN V-I RE 1 72e-100
19	553	76.0 108 5	KV1C_HUMAN IG KAPPA CHAIN V-I RE 2 95e-100
20	552	75.8 108 5	KV1L_HUMAN IG KAPPA CHAIN V-I RE 8 65e-100
21	550	75.5 108 5	KV1O_HUMAN IG KAPPA CHAIN V-I RE 7 44e-99
22	545	75.0 108 5	KV1P_HUMAN IG KAPPA CHAIN V-I RE 7 44e-99

RESULT ID	KV1H_HUMAN	STANDARD:	PRT:	108 AA.
AC	P01600			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V-I REGION (HAU).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA, METAZOA, CHOPEATA, VERTEBRATA, TETRAPODA, MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE: 71032830.			
RX	MEDLINE: 71032830.			
RA	WATANABE S, HILSCHMANN N; CHEM 351:1201-1205(1970).			
RL	HOPPE-SELYER S; PHYSIOL 1-1: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.			
CC	-1- THIS IS A BENCE-JONES PROTEIN.			
CC	-1- THIS IS A BENCE-JONES PROTEIN.			
DP	PIP: A01868; K1HUHU.			
DR	BSP: P01607; 1FVC.			
KW	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	DOMAIN 35 49			
FT	DOMAIN 50 56			
FT	DOMAIN 57 88			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DISULFID 23 88			
FT	NON_TER 108 108			
SC	SEQUENCE 108 AA: 11671 MW: 682586 CPO32:			
Query Match 86.9%; Score 632; DB 5; Length 108;				
Best Local Similarity 84.8%; Pred. No. 4.76e-119;				
Matches 89; Conservative 8; Mismatches 8; Indels 0; Gaps 0;				
Db	3 qntqspsslsasvgrdvtrcrasissyswvqgkfkfkapqlylaasalspsrpt: 12			
CY	3 ELTQSPSSLSAFVGPVTLCHASLSKSNMWLYVLSIALKVLVAASLSLSGVSPF 61			
Cb	63 svsgsttdtllissiqpedfatyyccqytlpssfqdtrveik 107			
QY	62 SCGSGIDFILTITSLQPEDFATYYCQGSYTPFTFGQIKVEVK 106			
RESULT ID	KV1N_HUMAN	STANDARD:	PRT:	108 AA.

AC P01505;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (OU).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE; 70201507.
 RA KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
 RL SCIENCE 163:56-59(1970).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
 CC -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
 DP PIP; A01872; KIHUW.
 DR HSP; P01607; 2FGW.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 45 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 4809785 CRC32;
 Query Match 85.4%; Score 622; DB 5; Length 108.
 Best Local Similarity 68.6%; Pred No. 1 09e-116; Indels 0; Gaps 0;
 Matches 72; Conservative 28; Mismatches 5;
 Db 3 qmtqspsslsasvdrvtitorasqsisnylnwyqkpgkpkaplliyaasslqsgvpsrf 62
 QY 2 ELTQSPSSLSAFVGVGRVTITCPASQISPNLNWYQKPGTAPKVLIIYAASSLQSGVPSRF 61
 Db 63 sgsqsgtbfittisslcpbfatyycczasyssptfgzgrizik 107
 QY 62 SSGSGSDFTLITISLOPEDFATYYCCQSYTTPFTFGGQTKVEVK 106
 RESULT 3
 ID KVIH_HUMAN STANDARD; PRT: 108 AA.
 AC P01597;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (DEE).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE; 72054133
 RA MILSTEIN C.P., DEVERSON E.V.;
 RL BIOCHEM. J. 123:945-958(1971).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DP PIP; A01865; KIHUW.
 DR HSP; P01607; 1FVC.
 KW IMMUNOGLOBULIN V REGION
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11661 MW; 1D844F3 CRC32;
 Query Match 84.8%; Score 617; DB 5; Length 108;

Best Local Similarity 83.7%; Pred No. 1 64e-115;
 Matches 87; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
 Db 3 zmtqspsslsasvdrvtitorasqsisnylnwyqkpgkpkaplliyaasslqsgvpsrf 62
 QY 2 ELTQSPSSLSAFVGVGRVTITCPASQISPNLNWYQKPGTAPKVLIIYAASSLQSGVPSRF 61
 Db 63 sgsqsgtbfittisslcpbfatyycczasyssptfgzgrizik 106
 QY 62 SSGSGSDFTLITISLOPEDFATYYCCQSYTTPFTFGGQTKVEVK 105
 RESULT 4
 ID KVIH_HUMAN STANDARD; PRT: 129 AA.
 AC P04431;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE; 85014148.
 RA KLOBECK H.G., COMBES-ATO G., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
 DR EMBL; X00965; G296644; ALT_TERM
 DR PIR; A01883; KIHUW.
 DP HSP; P01507; 2FGW.
 KW IMMUNOGLOBULIN V REGION; SIGNAL
 FT SIGNAL 1 22
 FT CHAIN 23 129
 FT DOMAIN 23 45
 FT DOMAIN 46 56
 FT DOMAIN 57 71
 FT DOMAIN 72 78
 FT DOMAIN 79 110
 FT DOMAIN 111 119
 FT DOMAIN 120 129
 FT DISULFID 45 110
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14069 MW; 9a935172 CRC32;
 Query Match 83.8%; Score 610; DB 5; Length 129;
 Best Local Similarity 84.8%; Pred. No. 7 29e-114; Indels 0; Gaps 0;
 Matches 89; Conservative 8; Mismatches 8;
 Db 25 qmtqspsslsasvdrvtitorasqsisnylnwyqkpgkpkaplliyaasslqsgvpsrf 84
 QY 2 ELTQSPSSLSAFVGVGRVTITCPASQISPNLNWYQKPGTAPKVLIIYAASSLQSGVPSRF 61
 Db 85 sgsqsgtbfittisslcpbfatyycczasyssptfgzgrizik 129
 QY 62 SSGSGSDFTLITISLOPEDFATYYCCQSYTTPFTFGGQTKVEVK 106
 RESULT 5
 ID KVIH_HUMAN STANDARD; PRT: 108 AA.
 AC P01610;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (WEA).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE; 83273707.
 RA GONI F., FRANGIONE B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 80:4837-4841(1983).
 CC -1- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST

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CC 3.4-PURIFIED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR: A01876; K1HUE.
DR HSP: P01607; 2FCW.
KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 35 49 FRAMEWORK 2
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 98 107 FRAMEWORK 4
FT DISULFID 23 88 BY SIMILARITY
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11840 MW: 826251 CPG32:

Query Match 83.2% Score 601; DB 5; Length 108;
Best Local Similarity 82.1%; Pred. No. 6.37e-113;
Matches 83; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 3 qmtqpslsasvgrvritcrasqinditwyqgkpkapkvliyaasalsqgvsrff 62
QY 2 ELIQSPSSLSAIVGDRVITCPASQISPNLNWYQCKPKTAPKVLIIYAASLSQGVSPRF 61

Db 53 ssgsgstftltisslqpfatyyclq-yssfpwfgggtkveik 107
QY 52 SGSGSGTFTLTISLPEDFAIYYCQGSYIT-PTTFGGGKVEIK 106

RESULT 5
ID KVIF_HUMAN STANDARD: PRT: 108 AA:
AC P01599:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (GAL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75059322.
RA LAURE C J, WATANABE S, HILSCHMANN N.
HOPE-SEYLER S Z. PHYSIOL CHEM 354:1503-1504(1973)
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR PIR: A01847; K1HUGL.
DR HSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 35 49 FRAMEWORK 2
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 98 107 FRAMEWORK 4
FT DISULFID 23 88 BY SIMILARITY
FT NON_TER 108 108
SQ SEQUENCE 108 AA: CCAEAAD2 CPG32:

Query Match 82.5%; Score 601; DB 5; Length 108;
Best Local Similarity 79.0%; Pred. No. 9.56e-112;
Matches 83; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 3 qmtqpslsasvgrvritcrasqinditwyqgkpkapkvliyaasalsqgvsrff 62
QY 2 ELIQSPSSLSAIVGDRVITCPASQISPNLNWYQCKPKTAPKVLIIYAASLSQGVSPRF 61

Db 53 ssgsgstftltisslqpfatyyclq-yssfpwfgggtkveik 107
QY 52 SGSGSGTFTLTISLPEDFAIYYCQGSYIT-PTTFGGGKVEIK 106

RESULT 6
ID KVIF_HUMAN STANDARD: PRT: 108 AA:
AC P01599:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (GAL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75059322.
RA LAURE C J, WATANABE S, HILSCHMANN N.
HOPE-SEYLER S Z. PHYSIOL CHEM 354:1503-1504(1973)
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR PIR: A01847; K1HUGL.
DR HSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 35 49 FRAMEWORK 2
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 98 107 FRAMEWORK 4
FT DISULFID 23 88 BY SIMILARITY
FT NON_TER 108 108
SQ SEQUENCE 108 AA: CCAEAAD2 CPG32:

Query Match 82.5%; Score 601; DB 5; Length 108;
Best Local Similarity 79.0%; Pred. No. 9.56e-112;
Matches 83; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 3 qmtqpslsasvgrvritcrasqinditwyqgkpkapkvliyaasalsqgvsrff 62
QY 2 ELIQSPSSLSAIVGDRVITCPASQISPNLNWYQCKPKTAPKVLIIYAASLSQGVSPRF 61

Db 53 ssgsgstftltisslqpfatyyclq-yssfpwfgggtkveik 107
QY 52 SGSGSGTFTLTISLPEDFAIYYCQGSYIT-PTTFGGGKVEIK 106

RESULT 7
ID KVIF_HUMAN STANDARD: PRT: 107 AA:
AC P01596:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (CAP).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75075135.
RA MILSTEIN C P, DEVERSON E V.
EPR. J BIOCHEM. 49:377-391(1974).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01864; K1HUGP.
DR HSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION: GLYCOPROTEIN.
FT CARBOHYD 28 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA: 11703 MW: 84895FD CPG32:

Query Match 80.4%; Score 595; DB 5; Length 107;
Best Local Similarity 77.1%; Pred. No. 5.49e-108;
Matches 81; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

Db 3 qmtqpslsasvgrvritcrasqinditwyqgkpkapkvliyxssslsqgvsrff 62
QY 2 ELIQSPSSLSAIVGDRVITCPASQISPNLNWYQCKPKTAPKVLIIYAASLSQGVSPRF 61

Db 53 ssgsgstftltisslqpfatyyclq-yssfpwfgggtkveik 105
QY 52 SGSGSGTFTLTISLPEDFAIYYCQGSYIT-PTTFGGGKVEIK 106

RESULT 8
ID KVIF_HUMAN STANDARD: PRT: 108 AA:
AC P01598:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (EU).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 71064023.
RA GOTTLIEB P D, CUNNINGHAM P A, PUTISHAUSER H, EDELMAN G M.
BIOCHEMISTRY 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE: 71064027.
RA GALL W E, EDELMAN G M.
BIOCHEMISTRY 9:3188-3196(1970).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01866; K1HUEU.
DR HSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 35 49 FRAMEWORK 2
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 98 107 FRAMEWORK 4
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 9AF455E5 CPG32:

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CC      -1- THIS IS A RENCE-JONES PROTEIN.
DOR      FIR: A01869; KIHUKA.
DOR      HSSP: P01607; 1IGM.
KKW      IMMUNOGLOBULIN V REGION: RENCE-JONES PROTEIN.
DOR      DOMAIN 1 23 FRAMEWORK 1.
DOR      DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
DOR      DOMAIN 35 49 FRAMEWORK 2.
DOR      DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
DOR      DOMAIN 57 88 FRAMEWORK 3.
DOR      DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
DOR      DOMAIN 98 107 FRAMEWORK 4.
DOR      DOMAIN 108 108 BY SIMILARITY.
DOR      NON_TER 108 108
DOR      SEQ SEQUENCE 108 AA; 11900 MW; 41EC730E CRC32;

Query Match 78.3%; Score 570; DB 5; Length 108;
Best Local Similarity 71.4%; Pred. No. 1,81e-104;
Matches 75; Conservative 18; Mismatches 12; Indels 0; Gaps

Ddb 3 qmtqspstlsvsggrttitceasqdvlyfhwvgqkqkqpklliraaasietarpsrf 62
CQY 2 ELTGSPSSLSAFLVGUFVITTCFASQSSISNLMWYCKKPTAPKVLIIYAASSIQSGVPSRF 61

Ddb 63 sgqgsdtbfttissvzpzbfatyqczyldiprfggatkvdk 107
CQY 62 SGSGSGTDFTLITSLQDFELFAIYQVQSYTPP-IFGQKIKVEVK 106

RESULT 11
ID KVT_HUMAN STANDARD; PFT: 109 AA.
AC P01612;
DOR 21-JUL-1986 (PEL 01, CREATED)
DOR 21-JUL-1986 (PEL 01, LAST SEQUENCE UPDATE)
DOR 01-JAN-1988 (PEL 06, LAST ANNOTATION UPDATE)
DOR IG KAPPA CHAIN V-1 REGION (MEV).
DOR HMO SAPIENS (HUMAN).
DOR EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DOR EUTHERIA; PRIMATES
DOR [1]
DOR SEQUENCE.
DOR MEDLINE: 83081018.
DOR EULIZ M., LINKE R.P.;
DOR HOPPE-SYLER S 2. PHYSIOL. CHEM 363:1347-1359(1982).
DOR -1- ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.
DOR -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DOR FIR: A01879; KIHUKA
DOR HSSP: P01607; 2FGW
DOR IMMUNOGLOBULIN V REGION
DOR DOMAIN 1 23 FRAMEWORK 1.
DOR DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
DOR DOMAIN 35 49 FRAMEWORK 2.
DOR DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
DOR DOMAIN 57 88 FRAMEWORK 3.
DOR DOMAIN 89 98 COMPLEMENTARITY-DETERMINING 3.
DOR DOMAIN 99 108 FRAMEWORK 4.
DOR DISULFID 23 88
DOR NON_TER 109 109
DOR SEQ SEQUENCE 109 AA; 11870 MW; D74FEECL CRC32;

Query Match 78.2%; Score 569; DB 5; Length 109;
Best Local Similarity 76.4%; Pred. No. 3,10e-104;
Matches 81; Conservative 11; Mismatches 13; Indels 1; Gaps

Ddb 3 qmtqspstlsasvgrdviltorasqsdvlylhwvgkqkqpkllifdtstlsgvpsrf 62
CQY 2 ELTGSPSSLSAFLVGUFVITTCFASQSSISNLMWYCKKPTAPKVLIIYAASSIQSGVPSRF 61

Ddb 63 sgqrstdflltisslpddfatvycqgsytpertfgagttvdik 108
CQY 62 SGSGSGTDFTLITSLQDFELFAIYQVQSYTPP-IFGQKIKVEVK 106

RESULT 12

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ID  KV1X_HUMAN          STANDARD:          PRI: 108 AA.
AC  P04594:
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE  01-JAN-1988 (PEP. 06, LAST ANNOTATION UPDATE)
DE  IG KAPPA CHAIN V-I REGION (AU)
OS  HOMO SAPIENS (HUMAN)
OC  EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC  EUTHERIA: PRIMATES:
RN  [1]
RP  SEQUENCE.
RX  MEDLINE: 72189444.
RA  SCHIEHL H., HILSCHMANN N.:
RL  HOPPE-SEYLER'S Z. PHYSIOL. CHEM 353:345-370(1972)
RN  [2]
RP  X-RAY CRYSTALLOGRAPHY.
RX  MEDLINE: 77022433.
RA  FEHLMAYER H., SCHIFFER M., EPP O., COLMAN P.M., LATTMAN E.E.:
RA  SCHWAGER P., STEIGEMANN W., SCHRAMM H.J.:
RL  BIOPHYS. STRUCT. MECH. 1:139-146(1975)
CC  -!- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR
CC  REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF
CC  THE KAPPA CHAIN PEI
CC  -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC  -!- THIS IS A BENCE-JONES PROTEIN.
DR  PIR: A01862; K1HUAU.
DR  HSSP: P01607; 1FGV.
KW  IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT  DOMAIN 1 23 FRAMEWORK 1
FT  DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1
FT  DOMAIN 35 49 FRAMEWORK 2
FT  DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT  DOMAIN 57 88 FRAMEWORK 3
FT  DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3
FT  DOMAIN 98 107 FRAMEWORK 4
FT  DISULFID 23 88 BY SIMILARITY.
FT  NON_TER 108 108
SQ  SEQUENCE 108 AA; 11939 MW; R455AF00 CRC32:

Query Match 78.0%; Score 568; DB 5; Length 108;
Best Local Similarity 77.4%; Pred. No. 5,32e-104;
Matches 82; Conservative 13; Mismatches 9; Indels 2; Gaps 2.

Db  3 gmtqspsslsasvdrvtitcradnfnlswyqgkpkapklitydasnlesgvsrf 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  2 ELTQSPSSLSAFVGPVITTPASQISPNLNWYQKPGTAPKVLIVAASSLSGVSPPF 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  63 sgsgsgahtftisslqpedfatyyccqdydl-pwtfggqtkveik 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  62 SGSGSGIDFTLTITSLQPEDFAIYQQQ-SYIPIPIFGQTKVEK 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
ID  KV1X_HUMAN          STANDARD:          PRI: 129 AA.
AC  P04432:
DT  13-AUG-1987 (REL. 05, CREATED)
DT  13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE  01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE  IG KAPPA CHAIN PREPREGOP V-I REGION (DAUDI)
OS  HOMO SAPIENS (HUMAN)
OC  EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC  EUTHERIA: PRIMATES:
RN  [1]
RP  SEQUENCE.
RX  MEDLINE: 85014148.
RA  KLOECK H.G., COMBRIATO G., ZACHAU H.G.:
RL  NUCLEIC ACIDS RES. 12:5995-7006(1984).
DR  EMBL: X02134; G185822;
DR  EMBL: X00966; G296685; A17_TERM.
DR  PIR: A01884; K1HUDI.
DR  HSSP: P01607; 1FGV.
KW  IMMUNOGLOBULIN V REGION: SIGNAL.
FT  SIGNAL 1 22

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FT  CHAIN 23 129 IG KAPPA CHAIN V-I REGION (DAUDI).
FT  DOMAIN 23 45 FRAMEWORK 1.
FT  DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT  DOMAIN 57 71 FRAMEWORK 2.
FT  DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT  DOMAIN 79 110 FRAMEWORK 3.
FT  DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT  DOMAIN 120 129 FRAMEWORK 4.
FT  DISULFID 45 110 BY SIMILARITY.
FT  NON_TER 129 129
SQ  SEQUENCE 129 AA; 14235 MW; 05B40B5E CRC32:

Query Match 78.0%; Score 568; DB 5; Length 129;
Best Local Similarity 74.3%; Pred. No. 5,32e-104;
Matches 78; Conservative 15; Mismatches 12; Indels 0; Gaps 0.

Db  25 gmtqspsslsasvdrvtitcradnfnlswyqgkpkapklitydasnlesgvsrf 84
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  2 ELTQSPSSLSAFVGPVITTPASQISPNLNWYQKPGTAPKVLIVAASSLSGVSPPF 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  85 sgsgsgahtftisslqpedfatyyccqdydl-pwtfggqtkveik 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  62 SGSGSGIDFTLTITSLQPEDFAIYQQQ-SYIPIPIFGQTKVEK 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
ID  KV1V_HUMAN          STANDARD:          PRI: 108 AA.
AC  P04430:
DT  13-AUG-1987 (REL. 05, CREATED)
DT  13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE  01-JAN-1988 (PEP. 06, LAST ANNOTATION UPDATE)
DE  IG KAPPA CHAIN V-I REGION (PAN)
OS  HOMO SAPIENS (HUMAN)
OC  EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC  EUTHERIA: PRIMATES:
RN  [1]
RP  SEQUENCE.
RX  MEDLINE: 86174817.
RA  DWULET F.E., O'CONNOR T.P., BENSON M.D.:
RL  MOL. IMMUNOL. 23:73-78(1986).
DR  PIR: A01878; K1HUBN.
DR  HSSP: P01607; 1FGV.
KW  IMMUNOGLOBULIN V REGION: AMYLOID.
FT  DOMAIN 1 23 FRAMEWORK 1.
FT  DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT  DOMAIN 35 49 FRAMEWORK 2.
FT  DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT  DOMAIN 57 88 FRAMEWORK 3.
FT  DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT  DOMAIN 98 107 FRAMEWORK 4.
FT  DISULFID 23 88 BY SIMILARITY.
FT  NON_TER 108 108
SQ  SEQUENCE 108 AA; 11840 MW; 0D44DA0A CRC32:

Query Match 77.9%; Score 567; DB 5; Length 108;
Best Local Similarity 77.1%; Pred. No. 9,12e-104;
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0.

Db  3 gmtqspsslsasvdrvtitcradnfnlswyqgkpkapklitydasnlesgvsrf 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  2 ELTQSPSSLSAFVGPVITTPASQISPNLNWYQKPGTAPKVLIVAASSLSGVSPPF 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  63 sgsgsgahtftisslqpedfatyyccqdydl-pwtfggqtkveik 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  62 SGSGSGIDFTLTITSLQPEDFAIYQQQ-SYIPIPIFGQTKVEK 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ID  KV1Y_HUMAN          STANDARD:          PRI: 108 AA.
AC  P80362:
DT  01-NOV-1995 (REL. 32, CREATED)
DT  01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT  01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-I REGION (WAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTERATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE: 95086080.
 RA HUANG D.-B., CHANG C.-H., AINSWORTH C., BRUENGER A.T., EULITZ M.,
 RA SOLOMON A., STEVENS F.J., SCHIFFER M.;
 RL BIOCHEMISTRY 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE: 81267384.
 RA STEVENS F.J., WESTHOIM F.A., PANAGIOTOPoulos N., SCHIFFER M.,
 RA POPP P.A., SOLOMON A.;
 RL J. MOL. BIOL. 147:185-193(1981).
 CC -!- THIS IS A RENCE-JONES PROTEIN.
 DR PDB: 1WT1; 01-NOV-94.
 KW IMMUNOGLOBULIN V REGION: RENCE-JONES PROTEIN; 3D-STRUCTURE.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN PEF 2).
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA: 11737 MW; 41A2388C CRC32;

Query Match 77.2%; Score 562; DB 5; Length 108;
 Best Local Similarity 76.4%; Pred. No. 1.35e-102;
 Matches 81; Conservative 14; Mismatches 9; Indels 2; Gaps 2;
 Db 3 qmtqspsslsasvgrvritcrasgdtitvynvfwgqpggqpkvliygasiletgypsr 62
 QY 2 ELTQSPSSLSAFVGRVITCRASGISISRNLNWYQQRSTAPKVLIIYAASSLSQSGVPSRF 61
 Db 63 sgsqsgtdfttisslqpeditatyyccq-ydtlpltfgggktvdik 107
 QY 62 SSGSGGTDFTLTITSLOPEDFATYYCOOSYTT-PRTFQGGTKVEVK 106

Search completed: Tue Feb 24 07:27:34 1998
 Job time : 16 secs.

W O E R E L I
***** (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by Intelligenetics, Inc.
MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:55:23 1998; MasPar time 4.27 Seconds
Tabular output not generated.

Title: >US-08-844-215-13
Description: (1-106) from US08844215.ppep
Perfect score: 728
Sequence: 1 AELTQSPSSLSAFVGPVTI... CQSYTTPFTFGGKVEVK 106
Scoring table: PAM 150
Gap 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:pcr90 9:pcr91
10:pcr92 11:pcr93 12:pcr94 13:pcr95 14:pcr96
Statistics: Mean 27.078; Variance 147.594; scale 0.183
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	659	90.5	107	13	PCT-US95-0 Sequence 105, Applicat	1 45e-41	
2	659	90.5	107	7	US-08-276- Sequence 105, Applicat	1 45e-41	
3	651	89.4	107	7	US-08-276- Sequence 104, Applicat	5 98e-41	
4	651	89.4	107	13	PCT-US95-0 Sequence 104, Applicat	5 98e-41	
5	635	87.2	108	13	PCT-US95-0 Sequence 109, Applicat	1 02e-39	
6	635	87.2	108	7	US-08-276- Sequence 109, Applicat	1 02e-39	
7	629	86.4	108	7	US-08-276- Sequence 102, Applicat	2 96e-39	
8	629	86.4	108	13	PCT-US95-0 Sequence 102, Applicat	2 96e-39	
9	627	86.1	104	13	PCT-US95-0 Sequence 106, Applicat	4 21e-39	
10	627	86.1	104	7	US-08-276- Sequence 106, Applicat	4 21e-39	
11	625	85.9	107	7	US-08-300- Sequence 66, Applicat	6 01e-39	
12	625	85.9	107	13	PCT-US95-1 Sequence 66, Applicat	1 46e-38	
13	625	85.9	111	7	US-08-276- Sequence 150, Applicat	6 01e-39	
14	625	85.9	111	13	PCT-US95-0 Sequence 150, Applicat	6 01e-39	
15	620	85.2	107	11	PCT-US93-0 Sequence 18, Applicat	1 46e-38	
16	620	85.2	104	7	US-08-300- Sequence 69, Applicat	1 46e-38	
17	620	85.2	104	13	PCT-US95-1 Sequence 69, Applicat	1 46e-38	
18	613	84.2	107	13	PCT-US95-0 Sequence 84, Applicat	5 03e-38	
19	613	84.2	107	7	US-08-276- Sequence 84, Applicat	5 03e-38	
20	611	83.9	107	13	PCT-US95-0 Sequence 103, Applicat	7 17e-38	
21	611	83.9	107	7	US-08-276- Sequence 103, Applicat	7 17e-38	
22	607	83.4	107	7	US-08-276- Sequence 82, Applicat	1 45e-37	

23	607	83.4	107	13	PCT-US95-0	Sequence 82, Applicati	1 45e-37
24	607	83.4	109	11	PCT-US93-0	Sequence 1, Applicatio	1 45e-37
25	607	83.4	214	11	PCT-US93-0	Sequence 40, Applicati	1 45e-37
26	607	83.4	233	11	PCT-US93-0	Sequence 25, Applicati	1 45e-37
27	606	83.2	214	11	PCT-US93-0	Sequence 39, Applicati	1 74e-37
28	605	83.1	109	11	PCT-US93-0	Sequence 3, Applicatio	2 07e-37
29	604	83.0	107	11	PCT-US93-0	Sequence 17, Applicati	2 47e-37
30	601	82.6	107	13	PCT-US95-1	Sequence 67, Applicati	4 21e-37
31	601	82.6	107	7	US-08-300-	Sequence 67, Applicati	4 21e-37
32	601	82.6	110	7	US-08-300-	Sequence 70, Applicati	4 21e-37
33	601	82.6	110	13	PCT-US95-1	Sequence 70, Applicati	4 21e-37
34	598	82.1	237	9	PCT-US91-0	Sequence 26, Applicati	7 15e-37
35	589	80.9	108	7	US-08-478-	Sequence 84, Applicati	3 51e-36
36	588	80.8	106	7	US-08-276-	Sequence 83, Applicati	4 19e-36
37	588	80.8	106	13	PCT-US95-0	Sequence 83, Applicati	4 19e-36
38	581	79.8	107	7	US-08-477-	Sequence 2, Applicatio	1 44e-35
39	581	79.8	107	7	US-07-942-	Sequence 12, Applicati	1 44e-35
40	581	79.8	107	6	US-08-477-	Sequence 17, Applicati	1 44e-35
41	581	79.8	107	6	US-07-634-	Sequence 102, Applicat	1 44e-35
42	581	79.8	107	6	US-07-634-	Sequence 17, Applicati	1 44e-35
43	581	79.8	107	6	US-07-634-	Sequence 2, Applicatio	1 44e-35
44	581	79.8	107	6	US-07-634-	Sequence 70, Applicati	1 44e-35
45	581	79.8	107	6	US-08-477-	Sequence 70, Applicati	1 44e-35

ALIGNMENTS

RESULT 1 PCT-US95-08743-105 STANDARD: PRT: 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 105, Application PC/TUS9508743.
XX
CC Sequence 105, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0 Version #1 25 (FPO)
CC CURRENT APPLICATION DATA
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 09/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 105:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11573 MW: 66905 CN:
Query Match 90.5%; Score 659; DB 13; Length 107;
Best Local Similarity 90.5%; Pred. No. 1 45e-41;
Matches 95, Conservative 6, Mismatches 4, Indels 0, Gaps 0;

Db	1	ELTQSPSSLSAFVGPVTIIPASUSISSYLNWYQWKPAPKPLLIYAASLSQGVPSRF	60
QY	2	ELTQSPSSLSAFVGPVTIIPASUSISSYLNWYQWKPAPKPLLIYAASLSQGVPSRF	61
Db	61	SSGSGTDTLTITSSLOPDPATYYCCQSYSTPQTFGGGKLEIK	105
QY	62	SSGSGTDTLTITSSLOPDPATYYCCQSYSTPQTFGGGKLEIK	106

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RESULT      2
ID    US-08-276-852-105   STANDARD: PPT: 107 AA.
XX
AC
XXXXXX
XX
DT    01-JAN-1900
XX
DE    Sequence 105, Application US/08276852.
XX
DE    Sequence 105, Application US/08276852.
CC
CC    Patent No. 5652138
CC    GENERAL INFORMATION:
CC    APPLICANT: Burton, Dennis R
CC    APPLICANT: Barbas, Carlos F
CC    APPLICANT: Lerner, Richard A
CC    TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC    TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC    NUMBER OF SEQUENCES: 170
CC    CORRESPONDENCE ADDRESS
CC    ADDRESSEE: The Scripps Research Institute, Office of
CC    ADDRESSEE: Patent Counsel
CC    STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC    STREET: Mail Drop Tpc8
CC    CITY: La Jolla
CC    STATE: CA
CC    COUNTRY: USA
CC    ZIP: 92037
CC    COMPUTER READABLE FORM:
CC    MEDIUM TYPE: Floppy disk
CC    COMPUTER: IBM PC compatible
CC    OPERATING SYSTEM: PC-DOS/MS-DOS
CC    SOFTWARE: Patent In Release #1.0, Version #1.25
CC    CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER: 05/08/276,852
CC    FILING DATE: 18-JUL-1994
CC    CLASSIFICATION: 514
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: US 08/178,302
CC    FILING DATE: 30-SEP-1993
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: US 07/954,148
CC    FILING DATE: 30-SEP-1992
CC    ATTORNEY/AGENT INFORMATION:
CC    NAME: Fitting, Thomas
CC    REGISTRATION NUMBER: 34,163
CC    REFERENCE/DOCKET NUMBER: SCR1452P
CC    TELECOMMUNICATION INFORMATION:
CC    TELEPHONE: 619-554-2037
CC    TELEFAX: 619-554-6312
CC    INFORMATION FOR SEQ ID NO: 105:
CC    SEQUENCE CHARACTERISTICS:
CC    LENGTH: 107 amino acids
CC    TYPE: amino acid
CC    TOPOLOGY: linear
CC    MOLECULE TYPE: protein
CC    SEQUENCE 107 AA: 11573 MW: 66005 CN:
SQ
Query Match 90.5%; Score 659; DB 7; Length 107;
Best Local Similarity 90.5% Pref No. 1 45e-41;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db      1 ELTQSFSLSSVGPVTITTPASQSISSYLNWYQQKPKAPKLLIYAASSLQSQVSPF 60
        |||||
Qy      2 ELTQSFSLSSAFVQGFVITTPASQSISSRLRWYQQKPGTAPEKVLIIYAASSLQSQVSRF 61
        |||||

Db      61 SGGSGGTDFLTISLSLOPEFAFYCOQSYSTPTQTGQQTLEIK 105
        |||||
Qy      62 SGGSGGTDFLTISLSLOPEFAFYCOQSYTPRTFGQGTKEVK 106
        |||||

RESULT      3
ID    US-08-276-852-104   STANDARD: PPT: 107 AA.
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DT 01-JAN-1900
XX Sequence 104, Application PC/TUS9508743.
XX Sequence 104, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 104:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11608 MW: 58127 CN:

Query Match 89.4% Score 651; DB 13; Length 107;
Best Local Similarity 90.5%; Pred. No. 5.98e-41;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPSSLSASVGDRTVITTCRASQJINNYLNWYQKPKAKPLIIYASNTIGSVPSRF 60
QY 2 ELTQSPSSLSAFVGDRTVITTCRASQISRNINWYQKPKGTAPKVLIIYAASSIGSVPSRF 61

Db 61 SSGSGTDFTLTIISLQPEDFATYVQQSYTPRTFGGKLEIK 105
QY 62 SSGSGTDFTLTIISLQPEDFATYVQQSYTPRTFGGKLEIK 106

RESULT 5
ID PCT-US95-08743-109 STANDARD: PRT: 108 AA
XX xxxxxx
XX 01-JAN-1900
XX Sequence 109, Application PC/TUS9508743.
XX GENERAL INFORMATION:
XX APPLICANT:
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX NUMBER OF SEQUENCES: 170
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: PCT/US95/08743
XX FILING DATE: 11-JUL-1995
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 08/276,852
XX FILING DATE: 18-JUL-1994
XX INFORMATION FOR SEQ ID NO: 109:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 108 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
XX MOLECULE TYPE: protein
XX SEQUENCE 108 AA: 11820 MW: 67709 CN:

CC MOLECULE TYPE: protein
SQ SEQUENCE 108 AA: 11820 MW: 67709 CN:

Query Match 87.2% Score 635; DB 13; Length 108;
Best Local Similarity 84.9%; Pred. No. 1.02e-19;
Matches 90; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 1 ELTQSPSSLSASVGDRTVITTCRASQJINNYLNWYQKPKAKPLIIYASNTIGSVPSRF 60
QY 2 ELTQSPSSLSAFVGDRTVITTCRASQISRNINWYQKPKGTAPKVLIIYAASSIGSVPSRF 61

Db 61 SSGSGTDFTLTIISLQPEDFATYVQQSYTPRTFGGKLEIK 106
QY 62 SSGSGTDFTLTIISLQPEDFATYVQQSYTPRTFGGKLEIK 106

RESULT 6
ID US-08-276-852-109 STANDARD: PRT: 108 AA
XX xxxxxx
XX 01-JAN-1900
XX Sequence 109, Application US/98276852.
XX GENERAL INFORMATION:
XX APPLICANT: Burton, Dennis R
XX APPLICANT: Barbas, Carlos F
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX NUMBER OF SEQUENCES: 170
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: The Scripps Research Institute, Office of:
XX ADDRESSEE: Patent Counsel
XX STREET: 10666 No 56321stth Torrey Pines Road, Suite 220,
XX CITY: La Jolla
XX STATE: CA
XX COUNTRY: USA
XX ZIP: 92037
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: PatentIn Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/276,852
XX FILING DATE: 18-JUL-1994
XX CLASSIFICATION: 514
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 08/178,302
XX FILING DATE: 30-SEP-1993
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 07/954,148
XX FILING DATE: 30-SEP-1992
XX ATTORNEY/AGENT INFORMATION:
XX NAME: Fitting, Thomas
XX REGISTRATION NUMBER: 34,163
XX REFERENCE/DOCKET NUMBER: SC91452P
XX TELECOMMUNICATION INFORMATION:
XX TELEPHONE: 519-554-2937
XX TELEFAX: 519-554-6312
XX INFORMATION FOR SEQ ID NO: 109:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 108 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
XX MOLECULE TYPE: protein
SQ SEQUENCE 108 AA: 11820 MW: 67709 CN:

Query Match 87.2%; Score 635; DB 7; Length 108;
 Best Local Similarity 84.9%; Pred. No. 1.02e-39;
 Matches 90; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 1 ELTQSPSSLSASVGDRTITTCRASQTSINYNWYQCKPKAPKLLIYGASNLQSGVPSPF 60
 QY 2 ELTQSPSSLSAFVGDRTITTCRASQTSINYNWYQCKPKAPKLLIYGASNLQSGVPSPF 61

Db 61 SSGSGTDFLTLSLQPEDFATYCCQSYNTPTWTFGGTKVEIK 106
 QY 62 SSGSGTDFLTLSLQPEDFATYCCQSYTTP-RTFGQTKVEIK 106

RESULT 7
 ID US-08-276-852-102 STANDARD: PRT: 108 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 102, Application US/08276852.
 XX CC Sequence 102, Application US/08276852.
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: the Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220.
 CC CITY: Mail Drop TPC8
 CC STATE: La Jolla
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCPI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 102:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 108 AA; 11664 MW; 68213 CN;

Query Match 86.4%; Score 629; DB 7; Length 108;
 Best Local Similarity 86.8%; Pred. No. 2.96e-39;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 ELTQSPSSLSASVGDRTITTCRASQTSINYNWYQCKPKAPKLLIYGASNLQSGVPSPF 60
 QY 2 ELTQSPSSLSAFVGDRTITTCRASQTSINYNWYQCKPKAPKLLIYGASNLQSGVPSPF 61

Db 61 SSGSGTDFLTLSLQPEDFATYCCQSYNTPTWTFGGTKVEIK 106
 QY 62 SSGSGTDFLTLSLQPEDFATYCCQSYTTP-RTFGQTKVEIK 106

RESULT 8
 ID PCT-US95-08743-102 STANDARD: PRT: 108 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 102, Application PC/TUS9508743.
 XX CC Sequence 102, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
 CC INFORMATION FOR SEQ ID NO: 102:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 108 AA; 11664 MW; 68213 CN;

Query Match 86.4%; Score 629; DB 13; Length 108;
 Best Local Similarity 86.8%; Pred. No. 2.96e-39;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 ELTQSPSSLSASVGDRTITTCRASQTSINYNWYQCKPKAPKLLIYGASNLQSGVPSPF 60
 QY 2 ELTQSPSSLSAFVGDRTITTCRASQTSINYNWYQCKPKAPKLLIYGASNLQSGVPSPF 61

Db 61 SSGSGTDFLTLSLQPEDFATYCCQSYNTPTWTFGGTKVEIK 106
 QY 62 SSGSGTDFLTLSLQPEDFATYCCQSYTTP-RTFGQTKVEIK 106

RESULT 9
 ID PCT-US95-08743-106 STANDARD: PRT: 104 AA
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 106, Application PC/TUS9508743.
 XX CC Sequence 106, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 106:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 104 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 104 AA: 11248 MW: 63942 CN:
Query Match 86.1%; Score 627; DB 13; Length 104;
Best Local Similarity 88.2%; Pred. No. 4.21e-39;
Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Db 1 QSPSSLSASVGRVTITCRASQTSISYLNWYQKPKAPKLLIYAASSLSQGVSPFSGG 60
QY 5 QSPSSLSAFVGRVTITCRASQTSISRNLNWYQKPGTAPKVLIIYAASSLSQGVSPFSGS 64
Db 61 GSGDTFTLIISLQPEDFATYYCOQSYSTPTFGQTKLEIK 102
QY 65 GSGDTFTLIISLQPEDFATYYCOQSYTTPRTFGQTKVEVK 106
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ID US-08-276-852-106 STANDARD: PRT: 104 AA.
XX xxxxxx
DT 01-JAN-1900
DE Sequence 106, Application US/08276852.
CC Sequence 106, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SC1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 106:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 104 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 104 AA: 11248 MW: 63942 CN:
Query Match 86.1%; Score 627; DB 7; Length 104;
Best Local Similarity 89.2%; Pred. No. 4.21e-39;
Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Db 1 QSPSSLSASVGRVTITCRASQTSISYLNWYQKPKAPKLLIYAASSLSQGVSPFSGG 60
QY 5 QSPSSLSAFVGRVTITCRASQTSISRNLNWYQKPGTAPKVLIIYAASSLSQGVSPFSGS 64
Db 61 GSGDTFTLIISLQPEDFATYYCOQSYSTPTFGQTKLEIK 102
QY 65 GSGDTFTLIISLQPEDFATYYCOQSYTTPRTFGQTKVEVK 106
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ID US-08-300-386A-66 STANDARD: PRT: 107 AA.
XX xxxxxx
DT 01-JAN-1900
DE Sequence 66, Application US/08300386A.
CC Sequence 66, Application US/08300386A
CC Patent No. 5667988
CC GENERAL INFORMATION:
CC APPLICANT: Barbas, Carlos F, III
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGH
T CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10666 No. 5667988th Torrey Pines Road, IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/300,386A
CC FILING DATE: 02-SEP-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/836,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:

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CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 66:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11611 MW: 68881 CN:

Query Match      85.9%; Score 625; DB 7; Length 107;
Best Local Similarity 85.7%; Pred. No. 6,01e-39;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Db 1 EMTQSPSSLSASVGRVITTCRASQISISYINWYQKPKAPKLLIYAASTLQSGVPSRF 60
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XX xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 66, Application PC/TUS9511235.
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CC Sequence 66, Application PC/TUS9511235
CC GENERAL INFORMATION:
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLORULIN LIGH
T CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10666 North Torrey Pines Road, TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11235
CC FILING DATE: 01-SEP-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/300,386
CC FILING DATE: 02-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/825,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148

CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 66:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11611 MW: 68881 CN:

Query Match      85.9%; Score 625; DB 13; Length 107;
Best Local Similarity 85.7%; Pred. No. 6,01e-39;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Db 1 EMTQSPSSLSASVGRVITTCRASQISISYINWYQKPKAPKLLIYAASTLQSGVPSRF 60
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Qy 2 ELTQSPSSLSAFVGDVPTITCRASQISIRNLNMYQKPKGTAPKVLIIYAASSLQSGVPSRF 61
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   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 SGGSGTDFLTITSLQPEDFATYYCQOSYSTPTFTFGGKTVEVK 106
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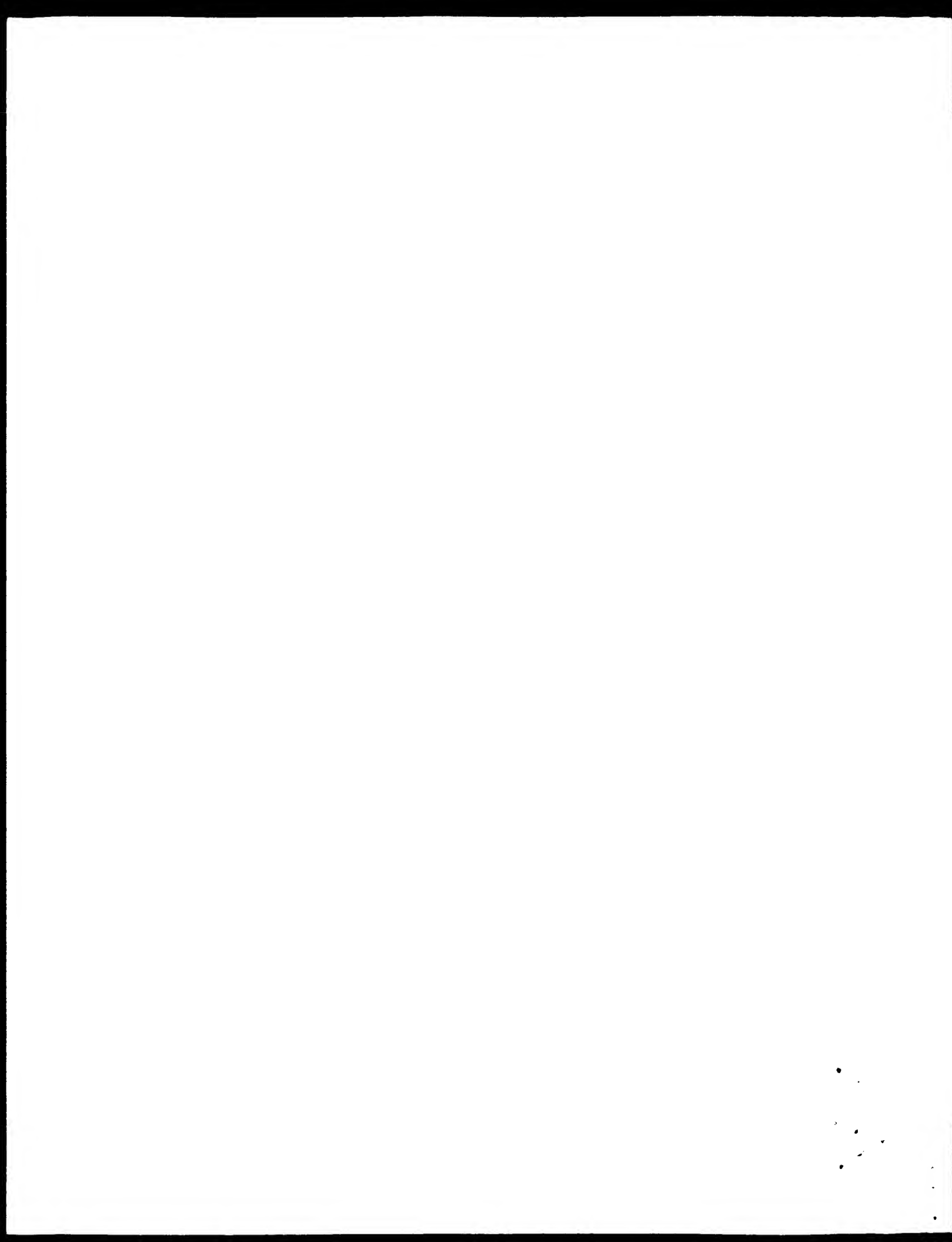
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XX xxxxxx
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DT 01-JAN-1900
XX
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XX
CC Sequence 150, Application: US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
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  STANDARD:
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  XXXXXX
  01-JAN-1900
  Sequence 18, Application PC/TUS9307832.
  Sequence 18, Application PC/TUS9307832
  GENERAL INFORMATION:
  APPLICANT: Genetech, Inc
  TITLE OF INVENTION: Immunoglobulin Variants
  NUMBER OF SEQUENCES: 40
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Genetech, Inc
  STREET: 460 Point San Bruno Blvd
  CITY: South San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94080
  COMPUTER READABLE FORM:
  MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: patin (Genetech)
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/US93/07832
  FILING DATE: 19930820
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/715272
  FILING DATE: 14-JUN-1991
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US92/05126
  FILING DATE: 15-JUN-1992
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/934373
  FILING DATE: 21-AUG-1992
  ATTORNEY/AGENT INFORMATION:
  NAME:
  REGISTRATION NUMBER:
  REFERENCE/DOCKET NUMBER: 709P2PCT
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415/952-9881
  TELEFAX 910/371-7168
  INFORMATION POP SEQ ID NO: 18:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 107 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  SEQUENCE 107 AA; 11629 MW; 67250 CN;
  Query Match 85.2%; Score 620. Da 11: Length
  Best Local Similarity 84.8%; Pred. No. 1,45e-38;
  Matches 89; Conservative 8; Mismatches 8; Indel:
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  2 ELATQSPSSLSAFAVGRVITTCFASQSISRNINWYQKPGTAPKVLIIYAAS
  Db 63 SGSGSGTDFLITLSSLOPEDFATYVQGSYLSLWIFSGGTKVEIK 107
  QY :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  62 SGSGSGTDFLITLSSLOPEDFATYVQGSY:IPRTFGGTKVEVK 105
  Search completed: Tue Feb 24 07:55:30 1998
  Job time : 7 secs.

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WQESREH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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Distribution rights by IntelliGenetics, Inc.
MPsrch_Fp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:28:42 1998: Maxstar time 6.60 seconds
223.095 Million cell updates/sec
Tabular output not generated.
Title: >US-08-844-215-13
Description: (1-106) from US08844215.pep
Perfect Score: 728
Sequence: 1 AELTQSPSSLSAFVGVPTI.....CQSYTTPRTFGGKTKEVK 106

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13889129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 29.358: Variance 168.648: scale 0.174

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match %	Description
1	669	91.9	Light chain #1 for an
2	659	90.5	Anti-HIV gp120 immuno
3	659	90.5	VL region of HIV neut
4	658	90.4	Human anti-tumour ant
5	651	89.4	Anti-HIV gp120 immuno
6	651	89.4	VL region of HIV neut
7	640	87.9	Anti-TGF beta-2 scFv
8	635	87.2	VL region of HIV neut
9	635	87.2	Anti-HIV gp120 immuno
10	629	86.4	Anti-HIV gp120 immuno
11	629	86.4	VL region of HIV neut
12	627	86.1	Anti-HIV gp120 immuno
13	627	86.1	VL region of HIV neut
14	626	86.0	Anti-TGF beta-1 scFv
15	626	86.0	CEA-specific antibody
16	625	85.9	VL of Fab, Mt 41 12,
17	625	85.9	Anti-HIV gp41 immunog
18	620	85.2	CEA-specific antibody
19	619	85.0	Light chain #2 for an
20	618	84.3	Human anti-PSV monocl

21	616	84.6	114 20	W13928	Light chain #4 for an
22	613	84.2	107 10	R54305	Anti-HIV gp120 immuno
23	613	84.2	107 19	W01263	VL region of HIV neut
24	611	83.9	107 10	R54259	Anti-HIV gp120 immuno
25	611	83.9	107 6	R30770	Consensus humanised m
26	611	83.9	107 19	W01282	VL region of HIV neut
27	611	83.9	113 20	W13926	Light chain #2 for an
28	608	83.5	128 12	R54234	Humanized antibody 12
29	608	83.5	128 12	R54264	CDP-grafted 1243-212
30	607	83.4	107 19	W01261	VL region of HIV neut
31	607	83.4	107 10	R54303	Anti-HIV gp120 immuno
32	607	83.4	109 9	R47039	Sequence of the light
33	607	83.4	109 9	R30762	Light chain variable
34	607	83.4	233 6	R30777	PH2-a 6 humanised mu
35	605	83.1	107 7	R38592	Human lambda light ch
36	602	82.7	125 14	R54759	Anti-human IL-4 human
37	602	82.7	133 16	R87057	CDR grafted anti-IL-5
38	601	82.6	108 2	R80516	Anti-human IL-4 human
39	601	82.6	111 2	R81246	Anti-pseudomonas aeru
40	601	82.6	111 2	R81970	Anti-pseudomonas aeru
41	600	82.4	109 8	R40955	Human germ-line gene
42	599	82.3	109 9	R47041	Sequence of the conse
43	599	82.3	127 22	W1817	Humanised mouse anti
44	598	82.3	214 7	R43338	Completely humanised
45	598	82.1	234 7	R38162	Sequence of the kappa

ALIGNMENTS

RESULT 1
ID W13922 standard; Protein: 114 AA.
AC W13922;
DE Light chain #1 for anti-HB virus antibody.
DT 15-MAY-1997 (first entry)
KW Antibody; heavy chain; light chain; variable region; human; monoclonal;
KW Complementarity determining region; human; adr type hepatitis B virus;
KW HB virus; CDP; virus antigen; anti-HB antibody; vaccine.
OS Homo sapiens.
PN J09020798-A.
PD 21-JAN-1997.
FF 11-JUL-1995; 174752.
PR 11-JUL-1995; JP-174752.
PA (ASAH) ASAH KASEI KOGYO KK.
DR WPI: 97-140911/13.
DR N-PSDB; T60117.
PT Human anti-Hepatitis B antibody - used in a adr type HB virus
PT vaccine
PS Claim 7; page 10-11; 20pp; Japanese.
CC W13921-W13928 represent the sequences for the heavy and light chains of
CC the human monoclonal antibodies of the invention. The antibody of the
CC invention preferably contains the sequence represented by W13912 in the
CC complementarity determining region-1 (CDR-1) of the heavy chain variable
CC region. The antibody of the invention also contains the sequence
CC represented by W13913 in the CDR-3 of the light chain variable region.
CC the antibody is capable of binding to adr type hepatitis B (HB) virus
CC antigen. A human anti-HB virus monoclonal antibody preparation which is
CC highly safe and is effective to adr type HB virus can be provided, using
CC the monoclonal antibody. It can also be used as a vaccine against HB
CC infection.
SQ Sequence 114 AA;

Query Match 91.9% Score 659; DR 20; Length 114;
Best Local Similarity 91.4%; Pred. No. 3,36e-39;
Matches 96; Conservative 5; Mismatches 4; Indels 0; Gaps 0
Db 2 emtqpsstlsavqgryvritcrasissylawvqgkpkakplliyaaslsqgvnsrf 61
Qy 2 ELUTSPSSLSAFVGVPTIIPASVSPNINWVQKKIPAKVLIIVAASSLQSVSPSR 61
Db 62 ssgsgtdftltkisslqpdafatyyvqgsgysptffgqgktkveik 106
Qy 62 SSGSGSDINFTLTLSQEDTALVYVYVSYIIPFPGVSIKVEVK 106

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RESULT 2
ID R54261 standard; protein: 107 AA.
AC R54261;
DI 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region b27.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
PN W09407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U093328.
PR 30-SEP-1992; US-954148.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Claim 5; Page 190; 248pp; English
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54261 neutralises HIV1
CC gp120.
SQ Sequence 107 AA;

Query Match 90.5%; Score 659; DR 10; Length 107;
Best Local Similarity 90.5%; Pred NO. 1.80e-38;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltgspsslsasvqdrvtitcrasqssissylwvqgkqkpklliyaaasslqsgvpsrf 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2 ELTQTSRSSLSAFVGDVRVTITCRASQSSISRNLNWYQQKPGTAPKVLIIYAASSLQSGVPSRF 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 sgsqsgtdftltisslqpedfatyyccqgsystpqtfgqgkkleik 105
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 SGSGSGTDFTLTITSLQPEDFATYYCQQSYTTPPTFGQGTKEVK 106
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
ID W01284 standard; protein: 107 AA.
AC W01284;
DI 29-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone b27.
KW Heavy chain, light chain, variable region, VH; monoclonal antibody.
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1

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FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
PN W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743
PR 18-JUL-1994; US-278952.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example; Fig 11; 365pp; English.
CC The sequences given in W01261-Q2 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the V2
CC gene clone, b27. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

Query Match 90.5%; Score 659; DB 19; Length 107;
Best Local Similarity 90.5%; Pred NO. 1.80e-38;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltgspsslsasvqdrvtitcrasqssissylwvqgkqkpklliyaaasslqsgvpsrf 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2 ELTQTSRSSLSAFVGDVRVTITCRASQSSISRNLNWYQQKPGTAPKVLIIYAASSLQSGVPSRF 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 sgsqsgtdftltisslqpedfatyyccqgsystpqtfgqgkkleik 105
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 SGSGSGTDFTLTITSLQPEDFATYYCQQSYTTPPTFGQGTKEVK 106
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
ID W22842 standard; protein: 132 AA.
AC W22842;
DI 12-SEP-1997 (first entry)
DE Human anti-tumour antigen antibody light chain variable region.
KW Human, tumour antigen; cancer; monoclonal; antibody, light chain;
KW variable region; medicine; pharmacology; biochemistry; CDR.
KW complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= sig_peptide
FT Peptide 23..132
FT /label= mat_peptide
FT Region 46..56
FT /label= CDR_1
FT Region 72..78
FT /label= CDR_2
FT Region 111..119
FT /label= CDR_3
PN J09100300-A.
PD 15-APR-1997.
PF 03-OCT-1995; 278266.
PR 03-OCT-1995; JP-278266.
PA (HAGI/) HAGIWARA Y.
DR WPI; 97-276746/25.

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DR N-PSDB: T75423.
 PT Anticancer human monoclonal antibody variable region sequences - and
 PS Claim 9: Page 11; 14pp; Japanese.
 CC The present sequence is a human anti-tumour antigen
 CC monoclonal antibody (MAB) light chain variable region, useful in
 CC medicine, pharmacology and biochemistry, the isotype of a MAB
 CC secreted by the human/human hybridoma HT was determined to be mu
 CC and kappa. Human MAB was purified, and the antigen recognised by
 CC human MAB CLN⁺-IOM identified by western blotting.
 SQ Sequence 132 AA;

Query Match 90.4%; Score 658; DB 22; Length 132;

Best Local Similarity 89.5%; Pred. No. 2,13e-38;

Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 25 gntqpslsasvdrvtitorasqsssylnwqgkpgkpklliyaaasslsgvpsrf 84
 QY 2 ELTQSPSSLSAFVGRPVITITCPASQSSISPNLNWYQKPGTAPKVI IYAASSLSQGVPSRF 61

Db 35 ssgsgstftltisslqpedfatyyqgqsystrtfqggtkveik 129

QY 62 SSGSGSIUFIILIIISLQPEFAIYYQWQSYTIIPFQSGIKVEVK 106

RESULT 5

ID R54260 standard; Protein: 107 AA.

DE Anti-HIV gp120 immunoglobulin light chain variable region b22.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 1..21

FT /label= FR1

FT Region 22..33

FT /label= CDR1

FT Region 34..48

FT /label= FR2

FT Region 49..55

FT /label= CDR2

FT Region 56..67

FT /label= FR3

FT Region 68..95

FT /label= CDR3

FT Region 96..107

FT /label= FR4

PN W09407022-A

PD 14-APR-1994.

PR 30-SEP-1993; m09328

PA (SCPI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA.

WPI: 94-14515/16.

PT New human monoclonal antibodies neutralising HIV - react with

PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo

PT or in vitro diagnosis and for passive immuno-therapy

PS Claim 5: Page 183; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR

CC amplification using primers specific for heavy and light chain

CC variable regions. The amplification products were inserted into a

CC diclontonic vector to produce a library of fragments. E.coli XL1

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAB regions on their surface. Panning

CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VK region sequence R54260 neutralises HIV1

CC gp120.

SQ Sequence 107 AA;

Query Match 89.4%; Score 651; DB 10; Length 107;

Best Local Similarity 90.5%; Pred. No. 6.90e-38;

Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltqpslsasvdrvtitorasqsssylnwqgkpgkpklliyaaasslsgvpsrf 60

QY 2 ELTQSPSSLSAFVGRPVITITCPASQSSISPNLNWYQKPGTAPKVI IYAASSLSQGVPSRF 61

Db 61 ssgsgstftltisslqpedfatyyqgqsystrtfqggtkveik 105

QY 62 SSGSGSIUFIILIIISLQPEFAIYYQWQSYTIIPFQSGIKVEVK 106

RESULT 6

ID W01283 standard; Protein: 107 AA.

AC W01283;

DE 29-JAN-1997 (first entry)

DE VL region of HIV neutralising MAB, clone b22 and B35.

KW Heavy chain; light chain; variable region; VH; monoclonal antibody;

KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;

KW virus infectivity assay; precursor gp120; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 1..21

FT /label= FR1

FT Region 22..32

FT /label= CDR1

FT Region 33..47

FT /label= FR2

FT Region 48..54

FT /label= CDR2

FT Region 55..86

FT /label= FR3

FT Region 87..95

FT /label= CDR3

FT Region 96..107

FT /label= FR4

PN W0950273-A1.

PD 01-FEB-1996.

PR 11-JUL-1995; U08743.

PR 18-JUL-1994; US-276852.

PA (SCPI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA.

WPI: 96-179601/18

PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in

PT passive immuno-therapy and detection of HIV infection.

PS Example: Fig 11; 366pp; English.

CC The sequences given in W01261-92 represent the light chain variable

CC regions (VL) of a series of monoclonal antibodies (MAB's) which are

CC immunoreactive with HIV glycoprotein gp120 and are capable of

CC neutralising HIV. This sequence represents the sequence of the VL

CC gene clones, b22 and B35. A MAB containing this VL sequence has the

CC capacity to reduce HIV infectivity titre in an in vivo virus

CC infectivity assay by 50 % at a concentration of less than 700 ng

CC of antibody/ml, and binds mature gp120 preferentially over the

CC precursor gp160. The MAB may be used for determining immunocompetence

CC of a human anti-HIV antibody and in the detection of HIV infection.

SQ Sequence 107 AA;

Query Match 89.4%; Score 651; DB 19; Length 107;

Best Local Similarity 90.5%; Pred. No. 6.90e-38;

Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltqpslsasvdrvtitorasqsssylnwqgkpgkpklliyaaasslsgvpsrf 60

QY 2 ELTQSPSSLSAFVGRPVITITCPASQSSISPNLNWYQKPGTAPKVI IYAASSLSQGVPSRF 61

Db 61 ssgsgstftltisslqpedfatyyqgqsystrtfqggtkveik 105

QY 62 SSGSGSIUFIILIIISLQPEFAIYYQWQSYTIIPFQSGIKVEVK 106

RESULT 7

ID W15524 standard; Protein: 108 AA.

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AC W1524;
DT 27-NOV-1997 (first entry)
DE Anti-TGF beta-2 scFv antibody 6-H1 VL domain.
KW Transforming growth factor beta-2, TGF-beta-2, human,
KW antibody engineering; scFv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis.
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy; chain shuffling.
OS Chimeric Homo sapiens;
FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..56
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 89..97
FT /label= CDR3
FT /note= "complementarity determining region 3"
PN G82305921-A
PD 23-APR-1997
PF 07-OCT-1996; 020920.
PR 19-JAN-1996; GB-001081.
PR 06-OCT-1995; GB-020486.
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
DR WPI: 97-215360/20.
DR N-PSDB; T60371.
DT Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
PS Claim 5; Fig 2b(1); 184pp; English.
CC This polypeptide sequence comprises the VL domain of human scFv
CC antibody 2A-H1 (also known as 6H1), which is specific for
CC transforming growth factor (TGF) beta-2. It is encoded by a gene
CC (T60371) obtd. from a light chain shuffle repertoire of a peripheral
CC blood lymphocyte library. The antigen-binding domains of human
CC antibodies (see W1522-40) to TGF beta-1 and/or beta-2 can be used
CC to counter the adverse effects of TGF beta, such as (i) promotion
CC of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis,
CC arterial injury, proliferative retinopathy, retinal detachment,
CC adult respiratory distress syndrome, liver cirrhosis, post
CC myocardial infarction, post-angioplasty restenosis, scleroderma,
CC vascular disorders, cataract, glaucoma, or esp. neural scarring and
CC glomerulonephritis, also (not claimed) osteoporosis), or (ii)
CC immune and inflammatory diseases (e.g. rheumatoid arthritis,
CC macrophage deficiency diseases or macrophage pathogen infection).
CC Nucleic acids encoding human antibody VH and VL can be used for
CC prodn. of recombinant antigen-binding domains. These are highly
CC specific, have low dissociation constants (pref. less than 5 nM)
CC and low IC50s for neutralisation.
SQ Sequence 108 AA;
Query Match 87.9%; Score 640; DB 23; Length 108;
Best Local Similarity 84.6%; Pred No 4 37e-37;
Matches 88; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Db 4 mtqspsslsasvdrvtitcrasqisnlywqqkpkapkllykastlesgvsrfs 63
QY 3 LTQSPSSLSAFVGDVRTITCPASQSISRNLMWYQKPKTAPKVLIIYAASSLQSGVPSPF 62
Db 64 gsgsgtftltisslqpedfatyccqsystrptfgggtkvdk 107
QY 63 GSGSGTDFLTITSLQPEDFATYYCQSYTTPRTFGGQTKVEVK 106

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RESULT 8
ID W01288 standard; Protein: 108 AA.
AC W01288;
DE 29-JAN-1997 (first entry)
DI VL region of HIV neutralising MAB, clone B8.
KW Heavy chain, light chain, variable region, VH, monoclonal antibody,
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
PN W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PF 18-JUL-1994; US-276852
PA (SCRI ) SCRIpps RES INST
PI Barbas CF, Burton DR, Lerner RA;
PI WPI: 96-179601/18.
DR Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
FT passive immunotherapy and detection of HIV infection.
PS Example; Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK1
CC gene clone, B8. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/mL, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;
Query Match 87.2%; Score 635; DB 19; Length 108;
Best Local Similarity 84.9%; Pred No 1.01e-36;
Matches 90; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 1 eitqspsslsasvdrvtitcrasqisnlywqqkpkapkllykastlesgvsrfs 60
QY 2 ELTQSPSSLSAFVGDVRTITCPASQSISRNLMWYQKPKTAPKVLIIYAASSLQSGVPSPF 61
Db 61 gsgsgtftltisslqpedfatyccqsystrptfgggtkvdk 106
QY 62 GSGSGTDFLTITSLQPEDFATYYCQSYTTPRTFGGQTKVEVK 106
RESULT 9
ID R54320 standard; protein: 108 AA
AC R54320;
DE 10-NOV-1994 (first entry)
DI Anti-HIV gp120 immunoglobulin light chain variable region B8.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1

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FT /Region 22...33
 FT /label- CDR1 34...48
 FT /Region 49...55
 FT /label- FR2 56...87
 FT /Region 88...96
 FT /label- FR3 97...108
 FT /label- CDR3
 FT /label- FR4
 PN W09407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993: U09328.
 PI (SCFI) SCFIPPS PES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 94-135515/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PI gp120 or gp41 and nucleic acid encoding them. Useful for in vivo
 PI or in vitro diagnosis and for passive immuno-therapy
 PS Example: Page 192-193; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54320 neutralises HIV1
 CC gp120.
 SQ Sequence 108 AA;

Query Match 87.2%; Score 635; DB 9; Length 108;
 Best Local Similarity 84.9%; Pred. No. 1.0le-36;
 Matches 90; Conservative 10; Mismatches 5; Indels 1; Gaps 1;
 Db 1 elqtspsslsasvdrvtitcrasqslslnwvqgkpgkapklliyaaasslqgysrff 50
 QY 2 ELTQSPSSLSAFVSDRVITITCRASQSLSPNLSNLYQVQKPGTAPKVIYAAASSLSGVSPPSF 51
 Db 61 sgsusgtfttisslqpedfatycqsyntppwtfggatkveik 106
 QY 62 SGSGSGTDFTLTITSLOPEDFATYCOOSYITP-RFGQGTKEVK 106

RESULT 10
 ID R54258 standard; protein: 108 AA.

AC R54258;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region b8.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.

Key	Location/Qualifiers
FT /Region	1..21
FT /label- FR1	
FT /Region	22...33
FT /label- CDR1	
FT /label- FR2	34...48
FT /Region	49...55
FT /label- CDR2	
FT /label- FR3	56...87
FT /Region	88...96
FT /label- CDR3	
FT /label- FR4	97...108
PN W09407922-A.	
PD 14-APR-1994	

PF 30-SEP-1993: U09328.
 PI (SCFI) SCFIPPS PES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 94-135515/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PI gp120 or gp41 and nucleic acid encoding them. Useful for in vivo
 PI or in vitro diagnosis and for passive immuno-therapy
 PS Claim 5; Page 188; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54258 neutralises HIV1
 CC gp120.
 SQ Sequence 108 AA;

Query Match 86.4%; Score 629; DB 10; Length 108;
 Best Local Similarity 86.9%; Pred. No. 2.76e-36;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 elqtspsslsasvdrvtitcrasqslslnwvqgkpgkapklliyaaasslqgysrff 50
 QY 2 ELTQSPSSLSAFVSDRVITITCRASQSLSPNLSNLYQVQKPGTAPKVIYAAASSLSGVSPPSF 51
 Db 61 sgsusgtfttisslqpedfatycqsyntppwtfggatkveik 106
 QY 62 SGSGSGTDFTLTITSLOPEDFATYCOOSYITP-RFGQGTKEVK 106

RESULT 11
 ID W01281 standard; protein: 108 AA.

AC W01281;
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b8.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.

Key	Location/Qualifiers
FT /Region	1..21
FT /label- FR1	
FT /Region	22...32
FT /label- CDR1	
FT /label- FR2	33...47
FT /Region	48...54
FT /label- CDR2	
FT /label- FR3	55...86
FT /label- FR3	
FT /label- CDR3	87...96
FT /Region	97...108
FT /label- FR4	
PN W09502273-A1.	
PD 01-FEB-1996	
PF 11-JUL-1995: U08743.	
PR 18-JUL-1994: US-278852.	
PA (SCFI) SCFIPPS PES INST.	
PI Barbas CF, Burton DR, Lerner RA;	
DR WPI: 96-179601/18.	
PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in PI passive immunotherapy and detection of HIV infection.	
PS Example; Fig 11; 366pp; English.	
CC The sequences given in W01261-92 represent the light chain variable CC regions (VL) of a series of monoclonal antibodies (MAB's) which are CC immunoreactive with HIV glycoprotein gp120 and are capable of CC neutralising HIV. This sequence represents the sequence of the Jk4 CC gene clone, b8. A MAB containing this VL sequence has the capacity	

CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAb
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA:

Query Match 86.4%, Score 629, DB 19, Length 108.
 Best Local Similarity 86.8%; Pred. No. 2.76e-36;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 eltcpslssasvqdrvtitcrasqtsissylnwvqqkpkapkllyaaasslqsgvpsrf 60
 QY 2 ELTCPSLSASFVGDVPTITCRASQTSISRNWVQQKPGTAPKVLIIYAASSLSQSGVPSRF 61
 Db 61 sgsgsgtdftltisslqpedfatyyccqsyssipptlfgggtkveik 106
 QY 62 SGSGSGTDFTLTITSLQPEDFATYYCQOSYTPP-TFGQGTKEVK 106

RESULT 12
 ID P54318 standard: protein: 104 AA
 AC R54318;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region s4.
 KW Human immunodeficiency virus: HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT Region 1..18
 FT /label= FR1
 FT Region 19..29
 FT /label= CDR1
 FT Region 30..44
 FT /label= FR2
 FT Region 45..51
 FT /label= CDR2
 FT Region 52..83
 FT /label= FR3
 FT Region 84..92
 FT /label= CDR3
 FT Region 93..104
 FT /label= FR4
 PN W09602273-A.
 PD 14-APR-1994.
 PF 30-SEP-1993; U09328.
 PR 30-SEP-1992; US-954148.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Example: Page 190-191; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAb regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54318 neutralises HIV1
 CC gp120
 SQ Sequence 104 AA:

Query Match 86.1%; Score 627; DB 9; Length 104;
 Best Local Similarity 88.2%; Pred No 3.86e-36;
 Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 qspsslsasvqdrvtitcrasqtsissylnwvqqkpkapkllyaaasslqsgvpsrf 60
 QY 5 QSPSSLSAFVGDVPTITCRASQTSISPNLNWVQQKPGTAPKVLIIYAASSLSQSGVPSRF 64

Db 61 sgsgtdftltisslqpedfatyyccqsyssipptlfgggtkveik 102
 QY 65 GS3TDFTLTITSLQPEDFATYYCQOSYTPP-TFGQGTKEVK 106

RESULT 13
 ID W01285 standard: Protein: 104 AA.

AC W01285;
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAb, clone s4.
 KW Heavy chain; light chain; variable region; VH, monoclonal antibody;
 KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..18
 FT /label= FR1
 FT Region 19..29
 FT /label= CDR1
 FT Region 30..44
 FT /label= FR2
 FT Region 45..51
 FT /label= CDR2
 FT Region 52..83
 FT /label= FR3
 FT Region 84..92
 FT /label= CDR3
 FT Region 93..104
 FT /label= FR4
 PN W09602273-A.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-275352.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.

PT Monoclonal antibody; binding to VL/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example: Fig 11; 366pp; English
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAb's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, s4. A MAb containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAb
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 104 AA:

Query Match 86.1%; Score 627; DB 19; Length 104;
 Best Local Similarity 88.2%; Pred. No. 3.86e-36;
 Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

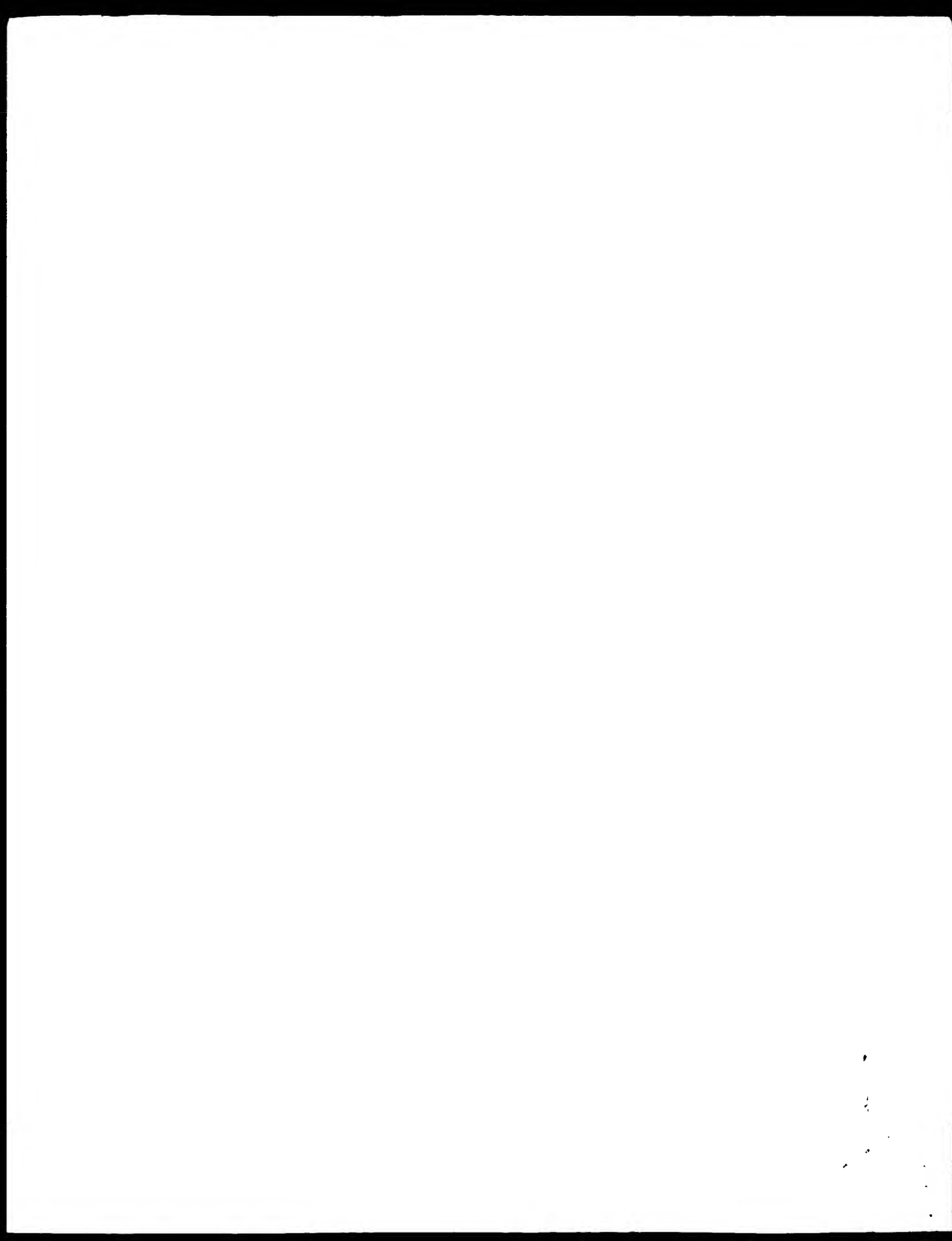
Db 1 qspsslsasvqdrvtitcrasqtsissylnwvqqkpkapkllyaaasslqsgvpsrf 60
 QY 5 QSPSSLSAFVGDVPTITCRASQTSISPNLNWVQQKPGTAPKVLIIYAASSLSQSGVPSRF 64
 Db 61 sgsgtdftltisslqpedfatyyccqsyssipptlfgggtkveik 102
 QY 65 GS3TDFTLTITSLQPEDFATYYCQOSYTPP-TFGQGTKEVK 106

RESULT 14
 ID W15539 standard: Protein: 108 AA.

AC W15539;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-1 scfv antibody 31G9 VL domain.
 KW Transforming growth factor beta-1; TGF-beta-1; human;
 KW antibody engineering; scfv; phage display; lung fibrosis.

KW arterial injury: proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction: post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy
 OS Homo sapiens.
 PN GB2305421-A
 PD 23-APR-1997.
 PF 07-OCT-1996: G20920.
 PR 19-JAN-1996: GB-001081.
 PR 06-OCT-1995: GB-020486.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 PF WPI: 97-215365/20
 DR N-PSDB: T60385.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis.
 PT immune and inflammatory disease
 PS Claim 15: Fig 1a(iii): 184pp: English.
 CC This polypeptide sequence comprises the VL domain of human scFv
 CC antibody 31G9, which is specific for transforming growth factor
 CC (TGF) beta-1. Antigen-binding domains of human antibodies (see
 CC W15222-40) to TGF beta-1 and/or beta-2 can be used to counter the
 CC adverse effects of TGF beta, such as (i) promotion of fibrosis (in
 CC dermal, ocular or keloid scarring, lung fibrosis, arterial injury,
 CC proliferative retinopathy, retinal detachment, adult respiratory
 CC distress syndrome, liver cirrhosis, post myocardial infarction,
 CC post-angioplasty restenosis, scleroderma, vascular disorders,
 CC cataract, glaucoma, or esp. neural scarring and glomerulonephritis,
 CC also (not claimed) osteoporosis), or (ii) immune and inflammatory
 CC diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases
 CC or macrophage pathogen infection). Nucleic acids encoding human
 CC antibody VH and VL can be used for prodn. of recombinant antigen-
 CC binding domains. These are highly specific, have low dissociation
 CC constants (pref. less than 5 nM) and low IC50s for neutralisation
 SQ Sequence 108 AA:
 Query Match 86.0%; Score 626; DB 23; Length 108;
 Best Local Similarity 84.6%; Pred NO 4 56e-36;
 Matches 88; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 Db 4 mtqspstiasvqdrvtitcrasqgisslawyqqkqgrapkvllykastlesyrprfs 63
 QY 3 LTQSPSSLSAFVGDRTITCRASQSIISRNUNWYQKPKTAPKVLIIYAASSIQSGVSPFS 62
 Db 64 qsgstqdtltlisslqpedfatyyqqgsystptwtfqgqtkleik 107
 QY 63 GSGSGTDFLTIIISLQPELFATYYCQSYTTPRTFGGQTKVEVK 106
 RESULT 15
 ID W19894 standard; Protein: 108 AA.
 AC W19894;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VL variant T06D8 sequence.
 KW Carcinoembryonic antigen: CEA; human; antibody: scFv;
 KW tumour marker: lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 CH Chimeric synthetic.
 FH Key Location/Qualifiers
 FT Region 24...34
 FT /label- CDR1
 FT /note- "complementarity determining region 1"
 FT Region 50..59
 FT /label- CDR2
 FT /note- "complementarity determining region 2"
 FT Region 89..97

FT /label- CDR3
 FT /note- "complementarity determining region 3"
 PN W09720932-A1.
 PD 12-JUN-1997.
 PF 09-DEC-1996: G03043.
 PR 11-OCT-1996: GB-021295.
 PR 07-DEC-1996: GB-025004.
 PR 23-MAY-1996: GB-010824.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 PI WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer
 PS Claim 4; Fig 4: 128pp: English.
 CC This polypeptide sequence comprises the light chain variable region
 CC (VL), T06D8, obtained by light chain shuffling of the VL CDR3 of
 CC human carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19885). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1 x 10⁻⁸ M. is non-cross-reactive
 CC with human liver cells, and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19875-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. An example of a claimed pairing
 CC is T06D8 VL with CEA6 VH. (A) is used to detect cells expressing
 CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing
 CC cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 108 AA:
 Query Match 86.0%; Score 626; DB 23; Length 108;
 Best Local Similarity 84.6%; Pred. No. 4 56e-36;
 Matches 88; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 Db 4 mtqspstiasvqdrvtitcrasqgisslawyqqkqgrapkvllykastlesyrprfs 63
 QY 3 LTQSPSSLSAFVGDRTITCRASQSIISRNUNWYQKPKTAPKVLIIYAASSIQSGVSPFS 62
 Db 64 qsgstqdtltlisslqpedfatyyqqgsystptwtfqgqtkleik 107
 QY 63 GSGSGTDFLTIIISLQPELFATYYCQSYTTPRTFGGQTKVEVK 106
 Search completed: Tue Feb 24 07:29:15 1998
 Job time : 33 secs.



WATERLH

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:25:45 1998; Maspar time 7.39 Seconds
441.114 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-12
Description: (1-107) from US08844215.pep
Perfect Score: 769
Sequence: 1 AELTQSPGTLISLVSEPATI CQYQSPPTFGGKVEIK 107

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30459580 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir53
1:unnn1 2:unnn2 3:unnn3 4:unnn4 5:unnn5 6:unnn6 7:unnn7
8:unnn8 9:unnn9 10:unnn10 11:unnn11 12:unnn12
13:unnn13 14:unnn14 15:unnn15 16:unnn16 17:unnn17
18:unnn18

Statistics: Mean 40.232; Variance 142.182; scale 0.292

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	688	89.5	109	7 H30601	Ig kappa chain V-III	1 87e-63
2	687	89.3	109	7 F44151	Ig kappa chain V-III	2 45e-63
3	685	89.2	114	7 S45375	Ig kappa chain V-J r	3 20e-63
4	685	89.1	107	7 P03655	Ig kappa chain V-III	4 18e-63
5	681	88.6	109	7 A30608	Ig kappa chain V-III	1 22e-62
6	679	88.3	109	7 B30601	Ig kappa chain V-III	2 09e-62
7	676	87.9	108	7 C30608	Ig kappa chain V-III	4 66e-62
8	676	87.9	109	7 C30601	Ig kappa chain V-III	4 66e-62
9	675	87.9	129	2 K3HUT1	Ig kappa chain V-III	4 66e-62
10	675	87.8	109	7 D30601	Ig kappa chain V-III	6 08e-62
11	675	87.8	129	7 S45369	Ig kappa chain V-III	6 08e-62
12	675	87.8	134	7 S45375	Ig kappa chain V-III	6 08e-62
13	673	87.5	129	2 K3HUT1	Ig kappa chain V-III	1 04e-61
14	672	87.4	109	7 C30608	Ig kappa chain V-III	1 36e-61
15	672	87.4	109	2 K3HUT1	Ig kappa chain V-III	1 36e-61
16	671	87.3	109	7 P03655	Ig kappa chain V-III	1 77e-61
17	671	87.3	129	7 S45369	Ig kappa chain V-III	1 77e-61
18	669	87.0	109	7 C30607	Ig kappa chain V-III	3 03e-61
19	669	87.0	109	2 K3HUT1	Ig kappa chain V-III	3 03e-61
20	666	86.6	108	7 H44151	Ig kappa chain V-III	6 76e-61

21	666	86.6	109	7 G30601	Ig kappa chain V-III	6 76e-61
22	666	86.6	110	7 E30607	Ig kappa chain V-III	6 76e-61
23	666	86.6	129	7 S45375	anti-Sm antibody VL	6 76e-61
24	663	86.2	109	7 F30601	Ig kappa chain V-III	1 51e-60
25	662	86.1	110	7 S20635	Ig kappa chain V-III	1 97e-60
26	658	85.6	108	2 K3HUT1	Ig kappa chain V-III	5 74e-60
27	658	85.6	108	7 B30608	Ig kappa chain V-III	5 74e-60
28	655	85.2	109	2 K3HUT1	Ig kappa chain V-III	1 28e-59
29	650	84.5	124	7 S20633	Ig kappa chain - hum	4 97e-59
30	649	84.4	130	7 S40360	Ig kappa chain - hum	6 35e-59
31	647	84.1	109	7 S47181	Ig kappa chain - hum	1 08e-58
32	645	83.9	130	7 S20637	Ig kappa chain - hum	1 08e-58
33	645	83.9	129	7 S40325	Ig kappa chain - hum	1 85e-58
34	644	83.7	121	7 S40327	Ig kappa chain - hum	2 42e-58
35	642	83.5	109	2 K3HUT1	Ig kappa chain V-III	4 12e-58
36	641	83.4	108	7 E30609	Ig kappa chain V-III	5 38e-58
37	636	82.7	110	7 S44120	Ig kappa chain V-J r	2 04e-57
38	632	82.2	129	7 A32274	Ig kappa chain V-III	5 92e-57
39	624	81.1	104	7 P03664	Ig kappa chain V-III	5 00e-56
40	624	81.1	131	7 S40346	Ig kappa light chain	5 00e-56
41	622	80.9	127	7 S40380	Ig kappa light chain	8 52e-56
42	618	80.4	145	7 S20631	Ig kappa chain - hum	2 47e-56
43	612	79.6	111	7 S23628	Ig kappa chain V-III	1 22e-54
44	610	79.3	92	7 S37613	Ig kappa chain V-III	2 08e-54
45	608	79.1	108	7 S33988	Ig kappa chain V-III	3 54e-54

ALIGNMENTS

RESULT 1
ENTRY H30601 #type fragment
TITLE Ig kappa chain V-III region (Gar and Flo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS H30601; E30601
REFERENCE Gonl, F. F., Chak, F. P., McGinnis, D., Arjonilla, M.,
#authors Fernandez, J., Carson, D., Solomon, A., Mendez, E.,
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession H30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON1
#accession E30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON2
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin domain
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 5951
Query Match 89.5%; Score 688; DB 7; Length 109;
Best Local Similarity 89.5%; Pred. No. 1.87e-63;
Matches 94; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
Db 4 ltqpgtislsvgepatlscpasqnytsvsgvkwkpsfppfellygsnfnatgtdmf 63
QY 3 lTQSPGTLISLVGEPATLSVSEPATI CQYQSPPTFGGKVEIK 107
Pb 64 sqsgsgrdflltrslrpfafarvyyqgysssttttgggttyleik 108
QY 63 SSSSGTDFLLTRSLRPFARVYYVLYDSPPTFGGKVEIK 107
RESULT 2
ENTRY F44151 #type fragment
TITLE Ig kappa chain V region (JM-01) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man

#authors	Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal	J. Exp. Med. (1992) 175:983-991
#title	Evidence for somatic selection of natural autoantibodies.
#cross-references	MUID:92202880
#accession	PH0965
##status	nucleic acid sequence not shown
##molecule_type	DNA
##residues	1-107 ##label MAR
CLASSIFICATION	##superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
KEYWORDS	
FEATURE	
1-21	#region framework 1\
22-32	#region complementarity-determining 1\
33-48	#region framework 2\
49-54	#region complementarity-determining 2\
55-87	#region framework 3\
88-95	#region complementarity-determining 3
SUMMARY	#length 107 #checksum 7830
Query Match	89.1%; Score 685; DB 7; Length 107;
Best Local Similarity	89.5%; Pred.No. 4,18e-63;
Matches	94; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Db	2 ltspgdtlslsgperatlscrasqsvssylawyqkpgqprrlliygassratgipdrf 61
Qy	3 LTQSPGTLISVGERATLSCRASQNIYSYLGWYQKPGQPRLLIYGASNPATGIPIRFF 62
Db	62 sgsgsgtdftltisrlepedfavvyccqygsspytfgggtkvek 106
Qy	63 SGSGSGTDFLTISRLESEDFAVYYCQYGSPPYTFGGTKVEIK 107
RESULT	5
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TITLE	Ig kappa chain V-II region (Son) - human (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
ACCESSIONS	A30608
REFERENCE	A30601
#authors	Goni, F.R.; Chen, P.P.; McGinniss, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.
#journal	J. Immunol. (1989) 142:3158-3163
#title	Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
#cross-references	MUID:89215279
#accession	A30608
##status	preliminary
##molecule_type	protein
##residues	1-209 ##label GON
CLASSIFICATION	##superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin
KEYWORDS	
SUMMARY	#length 109 #checksum 6031
Query Match	88.6%; Score 681; DB 7; Length 109;
Best Local Similarity	88.6%; Pred. No. 1,22e-62;
Matches	93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Db	4 ltspgdtlslsgperatlscrasqsvssylawyqkpgqprrlliygassratgipnrf 63
Qy	3 LTQSPGTLISVGERATLSCRASQNIYSYLGWYQKPGQPRLLIYGASNPATGIPIRFF 62
Db	64 sgsgsgtdftltisrlepedfavvyccqygsspytfgggtkvek 108
Qy	63 SGSGSGTDFLTISRLESEDFAVYYCQYGSPPYTFGGTKVEIK 107
RESULT	6
ENTRY	B30601 #type fragment
TITLE	Ig kappa chain V-II region (Glo) - human (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change

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16-Aug-1996
ACCESSIONS B30601
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession C30601
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
#length 109 #checksum 5911
SUMMARY
Query Match 88.3%; Score 679; DB 7; Length 109;
Best Local Similarity 89.5%; Pred. No. 2,00e-62;
Matches 94; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
Db 4 ltqspstlspgeratiscrasqsvssylawyqkpgqprlllygassratgipdrf 63
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
QY 3 LTQSPSTLSVGERATISCRASQNIYSGYLQWYQKPGQPPRLIYGCASNRATGIPDRF 62
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
Db 64 ssgsqstftltislepepfavvyccqygsspltfqgatkveik 108
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
QY 63 SSGSGSTFTLTISLESEDFAVYCCQYGSPPYIFGGTKVEIK 107
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109

RESULT 7
ENTRY #type fragment
TITLE Ig kappa chain V-III region (Pie) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS C30608
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession C30608
##status preliminary
##molecule_type protein
##residues 1-108 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
#length 108 #checksum 1607
SUMMARY
Query Match 87.9%; Score 676; DB 7; Length 108;
Best Local Similarity 88.6%; Pred. No. 4.56e-62;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Db 4 ltqspstlspgeratiscrasqsvssylawyqkpgqprlllygassratgipdrf 63
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
QY 3 LTQSPSTLSVGERATISCRASQNIYSGYLQWYQKPGQPPRLIYGCASNRATGIPDRF 62
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
Db 64 ssgsqstftltislepepfavvyccqygsspltfqgatkveik 108
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
QY 63 SSGSGSTFTLTISLESEDFAVYCCQYGSPPYIFGGTKVEIK 107
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108

RESULT 8
ENTRY #type fragment
TITLE Ig kappa chain V-III region (Pay) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS B30601
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession C30601
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
#length 109 #checksum 5911
SUMMARY
Query Match 88.3%; Score 679; DB 7; Length 109;
Best Local Similarity 89.5%; Pred. No. 2.00e-62;
Matches 94; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
Db 4 ltqspstlspgeratiscrasqsvssylawyqkpgqprlllygassratgipdrf 63
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
QY 3 LTQSPSTLSVGERATISCRASQNIYSGYLQWYQKPGQPPRLIYGCASNRATGIPDRF 62
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
Db 64 ssgsqstftltislepepfavvyccqygsspltfqgatkveik 108
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
QY 63 SSGSGSTFTLTISLESEDFAVYCCQYGSPPYIFGGTKVEIK 107
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109

RESULT 9
ENTRY #type complete
TITLE Ig kappa chain precursor V-III region (Hic) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
30-May-1997
ACCESSIONS PL0021
REFERENCE PL0021
#authors Kipps, T.J.; Tomhave, F.; Chen, P.P.; Carson, D.A.;
J. Exp. Med. (1988) 167:840-852
#journal J. Exp. Med. (1988) 167:840-852
#title Autobody-associated kappa light chain variable region
gene expressed in chronic lymphocytic leukemia with little
or no somatic mutation: implications for etiology and
immunotherapy.
#cross-references MUID:88171307
#accession PL0021
##molecule_type mRNA
##residues 1-129 ##label KIP
COMMENT The protein is one of the surface immunoglobulin M autoantibodies
expressed in patients with chronic lymphocytic leukemia.
GENETICS
#gene GDB:IGKV3
#cross-references GDB:136266
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS autoantibody; chronic lymphocytic leukemia, heterotetramer;
immunoglobulin
#domain signal sequence #status predicted #label KIP
#product Ig kappa chain V-III region (Hic) #status
predicted #label MATN
#region V segment
#region complementarity-determining 1\
#region complementarity-determining 2\
#region complementarity-determining 3\
#region J segment (CKI)\
#disulfide_bonds #status predicted
#length 129 #molecular_weight 14070 #checksum 8174

```



```

CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS antibody, chronic lymphocytic leukemia, heterotetramer, immunoglobulin
FEATURE
1-20 domain signal sequence #status predicted #label S1G\
21-129 #product Ig kappa chain V-III region (Hah) #status predicted #label MAT\
21-117 #region V segment\
44-55 #region complementarity-determining 1\
71-77 #region complementarity-determining 2\
110-117 #region complementarity-determining 3\
118-129 #region J segment (JK1)\
43-109 #disulfide bonds #status predicted
SUMMARY
#length 129 #molecular_weight 14073 #checksum 7361
Query Match 87.5% Score 673; DB 2; Length 129;
Best Local Similarity 88.6% Pred. No. 1,046-61;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Db 24 ltspatlsipgeratlscrasqssvslawyqgkqgqaprllygassratgipdrf 83
Qy 3 LTSPGTLSSVGERATLSCPASQNIYSGYLGWYQCKPKCPPLLIYGGASNRATGIPDPF 62
Db 84 sgsqsgtdflltislrepedfavyycqygyspftfgqgkveik 128
Qy 53 SSGSGGIDFLLISRLSESEFAVYVQYQYGSPPYIFGQGKVEIK 107

RESULT 14
ENTRY G30607 #type fragment
TITLE Ig kappa chain V-III region (Kas) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1995
ACCESSION G30607
REFERENCE A30601
#authors Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.
#journal: 2 Immunity (1994) 142 315a-316a
#title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
#cross-references M01D:89215279
#accession G30607
#status Preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY
#length 109 #checksum 4998
Query Match 87.4% Score 672; DB 7; Length 109;
Best Local Similarity 87.6% Pred. No. 1,366-61;
Matches 92; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Db 4 ltspatlsipgeratlscrasqssvslawyqgkqgqaprllygassratgipdrf 63
Qy 3 LTSPGTLSSVGERATLSCPASQNIYSGYLGWYQCKPKCPPLLIYGGASNRATGIPDPF 62
Db 64 sgsqsgtdflltislrepedfavyycqygyspftfgqgkveik 108
Qy 53 SSGSGGIDFLLISRLSESEFAVYVQYQYGSPPYIFGQGKVEIK 107

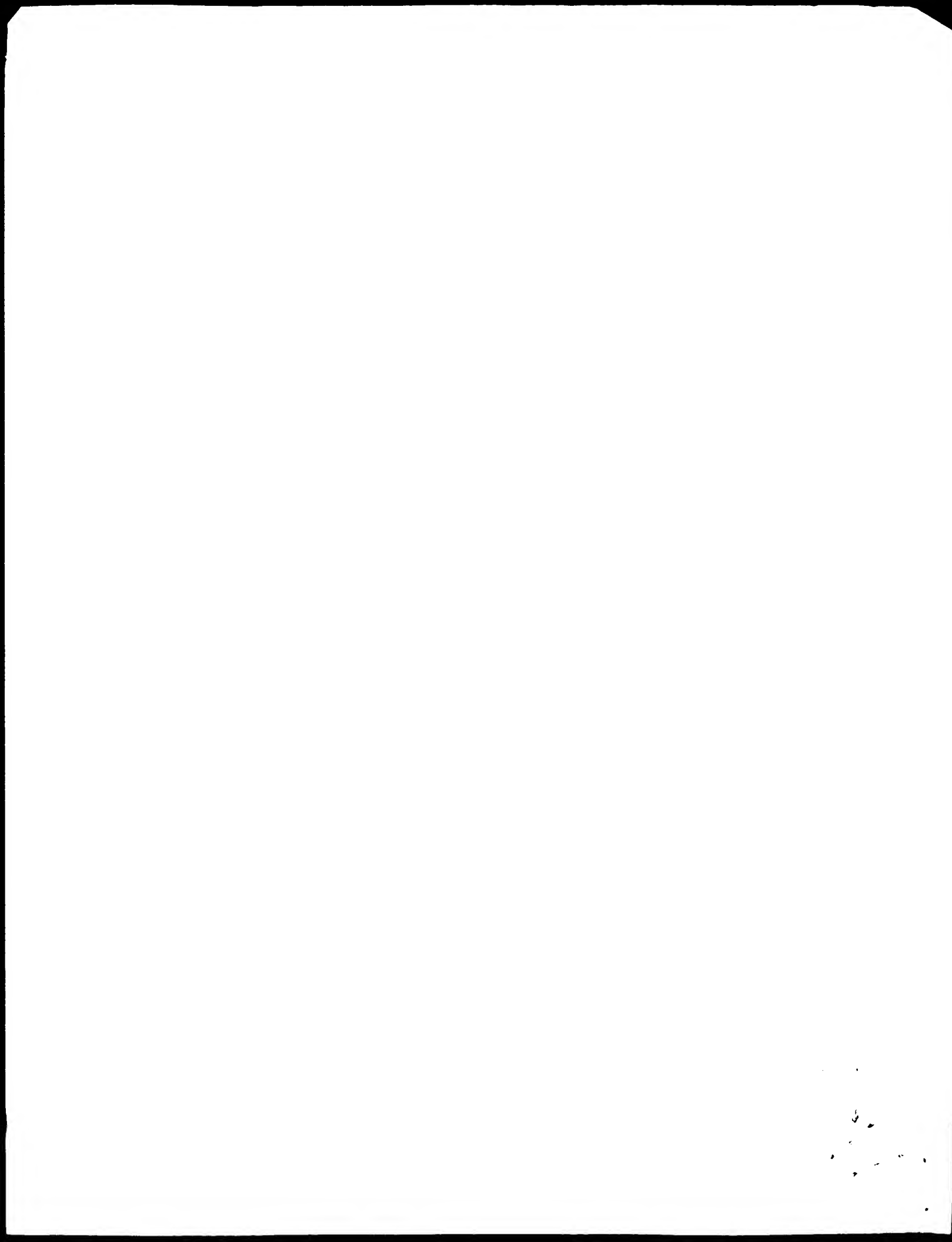
RESULT 15
ENTRY K3H0WL #type complete
TITLE Ig kappa chain V-III region (Wol) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 06-Sep-1995
ACCESSION A01896
REFERENCE A0450

```

```

#authors Andrews, D.W.; Capra, J.D.
#journal Biochemistry (1991) 30:5816-5822
#title Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa group.
#cross-references M01D:82046598
#accession A01896
#molecule_type protein
#residues 1-109 #label AND
COMMENT This chain was isolated from an IgM with anti-gamma globulin activity.
GENETICS
#gene GDB:IGKV3
#cross-references GDB:136266
COMPLEX An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer
FEATURE 23-89
SUMMARY
#disulfide_bonds #status predicted
#length 109 #molecular_weight 11746 #checksum 5360
Query Match 87.4% Score 672; DB 2; Length 109;
Best Local Similarity 90.5% Pred. No. 1,366-61;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Db 4 ltspatlsipgeratlscrasqssvslawyqgkqgqaprllygassratgipdrf 63
Qy 3 LTSPGTLSSVGERATLSCPASQNIYSGYLGWYQCKPKCPPLLIYGGASNRATGIPDPF 62
Db 64 sgsqsgtdflltislrepedfavyycqygyspftfgqgkveik 108
Qy 53 SSGSGGIDFLLISRLSESEFAVYVQYQYGSPPYIFGQGKVEIK 107
Search completed, Tue Feb 24 07:26:07 1998
Tot time: 22 secs

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WATERH

(TM)

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MPsearch_n 3 - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:09:51 1998; Maspar time 53.87 Seconds
Tabular output not generated

Title: >US-08-844-215-15
Description: (1-318) from US08844215.seq
Perfect Score: 318
N.A. Sequence: 1 CAGGTTCAGGTCAGTTCAGG
Comp: CTCGAGTCAGTCAGAGTTC
Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0: Query 0
Searched: 159651 seqs, 57698962 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
Statistics: Mean 8.012; Variance 4.941; scale 1.622
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution

SUMMARIES					
Result	No.	Score	Query Match Length	ID	Description
1	280	88.1	387	C49155	P105 rearranged varia
2	272	85.5	325	C65538	light chain of Amb a1
3	270	84.9	306	C43707	P105VX protein
4	268	84.3	372	T79322	Immunoglobulin r101.2
5	265	83.3	459	C45146	pGEM3 expression vec
6	265	83.3	516	C92547	Expression vector, pp
7	263	82.7	542	T44090	Ulcerative colitis-as
8	263	82.7	446	T15003	603AP33 anti-tetanus
9	263	82.7	446	T79397	Anti-tetanus toxoid 1
10	262	82.4	387	C43706	Xk135-k2
11	262	82.4	900	T79854	Human V-kappa gene vk
12	262	82.4	900	T79854	Human DNA fragment vk
13	262	82.4	900	T79854	DNA fragment vk5.8
14	258	81.1	324	C29756	Gene for Lv region of
15	252	79.2	422	T73654	Anti-lung tumour anti

16	252	79.2	645	T44091	Ulcerative colitis-as
17	241	75.8	1011	N91359	Anti-P. aeruginosa st
18	241	75.8	1011	N91359	Anti-pseudomonas aer
19	233	73.3	924	C18872	Sequence coding huma
20	238	68.6	324	C92549	PM24 2 fragment enco
21	238	68.6	812	C92549	Human V-kappa gene vk
22	238	68.6	812	C92549	Human DNA fragment vk
23	238	68.6	812	C92549	Human DNA fragment vk
24	238	68.6	812	C92549	Human V-kappa gene vk
25	238	68.6	812	C92549	Human DNA fragment vk
26	238	68.6	812	C92549	Human DNA fragment vk
27	238	68.6	812	C92549	Human DNA fragment vk
28	238	68.6	812	C92549	Human DNA fragment vk
29	238	68.6	812	C92549	Human DNA fragment vk
30	238	68.6	812	C92549	Human DNA fragment vk
31	238	68.6	812	C92549	Human DNA fragment vk
32	238	68.6	812	C92549	Human DNA fragment vk
33	238	68.6	812	C92549	Human DNA fragment vk
34	238	68.6	812	C92549	Human DNA fragment vk
35	238	68.6	812	C92549	Human DNA fragment vk
36	238	68.6	812	C92549	Human DNA fragment vk
37	238	68.6	812	C92549	Human DNA fragment vk
38	238	68.6	812	C92549	Human DNA fragment vk
39	238	68.6	812	C92549	Human DNA fragment vk
40	238	68.6	812	C92549	Human DNA fragment vk
41	238	68.6	812	C92549	Human DNA fragment vk
42	238	68.6	812	C92549	Human DNA fragment vk
43	238	68.6	812	C92549	Human DNA fragment vk
44	238	68.6	812	C92549	Human DNA fragment vk
45	238	68.6	812	C92549	Human DNA fragment vk

ALIGNMENTS

RESULT 1
ID Q49155 standard: cDNA: 387 BP.
AC Q49155:
DE 01-NOV-1993 (first entry)
DT F105 rearranged variable region light chain.
KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
KW CCR4 receptor; hydrolase; polymerase chain reaction; PCR; polymerase chain
chain; cytochrome; immune deficiency; ss.
OS Homo sapiens.
FH Key
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58...387
FT /*tag= b
PN W093122322-A.
PD 24-NOV-1993
PF 10-DEC-1992: U10928.
PF 10-DEC-1991: US-894652.
PA (DAND) DANA FARBER CANCER INST INC.
PA (NEWSE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MP, Sodroski JG.
DR WPI: 93-214174/26.
DE P-PSDB: R41286.
PI DNA segments encoding monoclonal antibody - which binds to gp120
PI and neutralises HIV, for treating AIDS, and for diagnosing and
PI monitoring HIV infection
PS Claim 1: Page 72, 1993: English
CC mRNA from the known hybridoma f105 was converted to cDNA and this
CC subjected to PCR amplification using primers corresp. to appropriate
CC parts of the heavy or light chains and having restriction sites to
CC permit cloning. The extension products were isolated and sequenced.
CC The recombinant human monoclonal antibody (MAb) binds to a
CC discontinuous epitope on the HIV gp120 envelope glycoprotein. It
CC blocks the binding of gp120 to the CD4 receptor, and neutralises a broad
CC range of HIV isolates. The MAb may be used to treat immune
CC deficiency, esp. at doses of 0.1-10 mg/kg.
SQ Sequence 387 BP. 86 A. 111 C. 161 G. 87 T.
Query Match 88.1%. Score 280. DB 7. Length 387.

13	acgcagctctccagcagccctgctctgtctccagaggaagaacccaccctctctctcagcag	72
Ddb		
7	acgcagctctccagcagccctgctctgtctccagaggaagaacccaccctctctctcagcag	56
QY		
73	gccagctccagactcttcagcagcaactcacttagcttggtaccagcacacaacctgccaggt	132
Ddb		
67	gccagctccagactcttcagcagcaactcacttagcttggtaccagcacacaacctgccaggt	126
QY		
133	cccaggtctctctatctcactcaccatcaaggtcactctaggcatcccaacagagttcact	192
Ddb		
127	cccaggtctctctatctcactcaccatcaaggtcactctaggcatcccaacagagttcact	186
QY		
193	ggcagtggggtctgggcagcaacttctctccaccatccagcagactggagcttgagattt	252
Ddb		
187	ggcagtggggtctgggcagcaacttctctccaccatccagcagactggagcttgagattt	246
QY		
253	gcagtgattactgtccagcaggtttcgttaactcaacagtgagcttcggccaaggaccacag	312
Ddb		
247	gcagtgattactgtccagcaggtttcgttaactcaacagtgagcttcggccaaggaccacag	306
QY		
313	gttgaatatcaaa	324
Ddb		
307	cttgagatcaaa	318
QY		

RESULT	3	
ID	Q42707 standard; DNA; 390 BP.	
AC	Q42707;	
DT	01-NOV-1993 (first entry)	
DE	F105Vk-F105Jk.	
DE	Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;	
CC	CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;	
CC	chain; epitope; immune deficiency; ss.	
KW	Human sapiens.	
OS	Human sapiens.	
FF	Key	Location/Qualifiers
FT	sig_peptide	1..60
FT	/*tag= a	
FT	mat_protein	61..390
FT	/*tag= b	
FT	misc_RNA	1..351
FT	/*tag= c	
FT	/label= F105Vk	
FT	misc_RNA	352..390
FT	/*tag= d	
FT	/label= F105Jk	
FT	misc_RNA	130 165
FT	/*tag= e	
FT	/label= CDR1	
FT	misc_RNA	211..231
FT	/*tag= f	
FT	/label= CDR2	
FT	misc_RNA	328..354
FT	/*tag= g	
FT	/label= CDR3	
PN	W09312232-A.	
PD	24-JUN-1993.	
PP	10-DEC-1992; F10928	
PP	10-DEC-1991; US-804652.	
PR	(DAND) DANA FAPPEY CANCER INST INC.	
PR	(NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.	
PI	Haseltine WA, Marasco WA, Posner MR, Sodroski JG;	
PI	WPI: 93-214174/26.	
DR	P-PSDB: R38672	
PT	DNA segments encoding monoclonal antibody - which binds to gp120	
PT	and neutralises HIV, for treating AIDS, and for diagnosing and	
PT	monitoring HIV infection	
CC	Disclosure: Page 73-74; 109pp: English.	
CC	the nucleotide sequence of F105 Vk (Q42707 - sequence differs from	
CC	other F105 Vk sequences given elsewhere in the specification) was	
CC	compared with germ-line gene Humk4.5 (U4-795), showing 97.7%	
CC	similarity. By nucleotide sequence analysis, F105 appears to	
CC	be derived from a member of the V _H III subgroup gene family.	
CC	Sequence 390 BP; 86 A; 115 C; 102 G; 87 T;	


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FT misc_RNA 265..291
FT /tag= k
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT misc_RNA 292..324
FT /tag= 1
FT /label= FR4
FT /note= "framework region 4"
PN WO9607754-A1
PD 14-MAR-1996
PF 01-SEP-1995; U11235
PR 02-SEP-1994; US-300386
PA (Scripps) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA
DR WPI: 96-171625/17
PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
PT gene CDR - useful for prodn. of Ig heavy and light chain
PT combinatorial antibody libraries
PS Example 1; Page 84; 125pp; English.
CC T15202 and T15203 are the heavy and light chain variable domains of
CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a pComb3
CC based expression vector. The heavy and light chain variable domains
CC are used in an example to demonstrate the prodn. of antibodies for
CC an antibody library using mutagenic primers. Mutagenic primers of the
CC binding different framework regions linked by a sequence 5' to 5'
CC nucleotides long. Different immunoglobulins produced using the
CC primers may be used to produce antibody libraries having diverse and
CC novel immunospecificities and affinities. By using mutagenic ONS an
CC extremely large population of different randomised binding sites can
CC be created and use of the universal light chain increases the number
CC of combinations which yield functional heterodimeric antibodies.
CC Sequence 646 BP; 162 A; 187 G; 170 G; 127 T;
SQ
Query Match 82.7%; Score 263; DB 25; Length 642;
Best Local Similarity 91.5%; Pred. No. 149e-157; Indels 3; Gaps 1;
Matches 290; Conservative 0; Mismatches 17;
Db 1 gagctccagcagctctccagcagcagctctcttcttctccaggggaaagagcagcctctctc 63
QY 1 GAGCTCAGCAGCTCTCCAGCAGCAGCTCTCTTCTTCTCCAGGGGAAAGAGCAGCCTCTCTC 60
Db 61 tcacagggcagtcacagcagtgtagcaggggagcagcagcagcagcagcagcagcagcag 120
QY 61 TCACAGGGCAGTCACAGCAGTGTTAGCAGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
Db 121 cagggtccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 180
QY 121 CAGGGTCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180
Db 181 tcacagggcagtcacagcagtgtagcaggggagcagcagcagcagcagcagcagcagcag 240
QY 181 TCACAGGGCAGTCACAGCAGTGTTAGCAGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 241 gattttcagcagtcagcagcagtcagcagcagtcagcagcagtcagcagcagtcagcag 297
QY 241 GATTTTCAGCAGTCAGCAGCAGTCAGCAGCAGTCAGCAGCAGTCAGCAGCAGTCAGCAG 297
Db 298 accaaggtgggaactcaaa 315
QY 301 ACCAAGGTGGGAGATCAAA 318
RESULT 9
ID Q70487 standard; cDNA; 646 BP.
AC Q70487;
DI 04-APR-1995 (first entry)
DE Anti-tetanus toxoid light chain cDNA from vector, pC1AP313
KW Polymerase chain reaction; primer; mutagenesis; PCR; amplification;
KW diversity; antibody; complementarity determining region; CDR;
KW framework; constant; light, heavy, phage, immunoglobulin; library; ss.
OS Synthetic.
PN WO9418219-A
PD 18-AUG-1994
PF 02-FEB-1994; U01234
PR 02-FEB-1993; US-012566
PR 28-DEC-1993; US-174674
PA (Scripps) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA
DR WPI: 94-279673/34
PT Oligo-nucleotides - used as PCR primers for producing increased

```

PT diversity antibody libraries, for screening antigens
 PS Claim 21: Page 84-85; 120pp; English.
 CC This sequence represents the light chain coding sequence derived from
 CC the surface display phagemid expression vector, pC3AP313. pC3AP313
 CC contains the bacteriophage gene III and heavy and light chain variable
 CC domain sequences for encoding human Fab antibodies against tetanus toxin.
 CC This sequence was pref. used in the method of the invention for the
 CC production of antibody libraries containing increased diversity. The
 CC sequences given in Q70480-86 are primers which were used for inducing
 CC immunogenesis in a complementary determining region (CDR) of an
 CC immunoglobulin light chain gene. These primers contain a 3' terminus
 CC capable of hybridising to a first framework region, a 5' terminus
 CC capable of hybridising to a second framework region and a nucleotide
 CC sequence between the 5' and 3' termini having the formula [NNK]_n,
 CC where n is 3-24. These primers may be used to produce antibody
 CC libraries with increased antibody diversity by inducing mutagenesis
 CC within the CDR regions of immunoglobulins heavy or light chains that
 CC are displayed on the surface of filamentous phage particles comprising
 CC the library. These primers pref. mutate the light chain CDR3
 SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T,
 Query Match 82.7%; Score 263; DB 12; Length 646;
 Best Local Similarity 93.7%; Pred. No. 1.49e-157;
 Matches 298; Conservative 0; Mismatches 17; Indels 3; Gaps 1;
 Db 1 gaactcaacagtcctcagggaccctgtcttctcaggggaaagaccacccctcc 60
 QY 1 GAGCTCAGCAGCTCTCAGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
 Db 61 tcagagccagtcacagtgtagcagggcctacttagctgtagcagcagaaacctggc 120
 QY 61 TGCAGGCGCCAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 Db 121 caggtccaggtcctcctctctctctctctctctctctctctctctctctct 180
 QY 121 CAGGCTCCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 Db 181 tcaagtgccagtggtctcggagacagactcactctcaccatcagcagactggagcctgaa 240
 QY 181 TTCACTGGCAGTGGGTCTCTGGGACACTTCACTCTCACTCTCACTCTCACT 240
 Db 241 gattttgagtgactactgtcagcagtgatggtgagctcaccgtgg---ttcgggcagaagg 297
 QY 241 GATTTTGCAGTGATTAAGTCTGAGCTTTATGTTAACTCACTCTGAGCTTGGGCAAGGG 300
 Db 298 accaagtggaactcaaa 315
 QY 301 ACCAAGTGGAGATCAAA 318

RESULT 10
 ID Q42706 standard; DNA; 390 BP.
 AC Q42706;
 DT 01-NOV-1993 (first entry)
 DE vk325-Jk2.
 KW Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT /*tag= a 61..390
 FT mat_protein 61..390
 FT /*tag= b 1..351
 FT misc_RNA 1..351
 FT /*tag= c 352..390
 FT /*label= vk325 352..390
 FT misc_RNA 1..165
 FT /*tag= d 1..165
 FT /*label= Jk2 1..165
 FT misc_PNA 1..165
 FT /*tag= e 1..165
 FT /*label= CDRI 1..165

FT misc_RNA 211..231
 FT /*tag= f
 FT /*label= CDR2 328..354
 FT misc_RNA 328..354
 FT /*tag= g
 FT /*label= CDR3
 PN WO9312232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U10928.
 PR 10-DEC-1991; US-804652.
 PA (DAND) DANA FARMER CANCER INST INC.
 PA (NEW) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Mardisco WA, Posner MR, Sodroski JG;
 DR WPI; 93-214174/26.
 DR P-PSDB; R38672.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Disclosure: Page 73-74; 109pp; English.
 CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
 CC other F105 VK sequences given elsewhere in the specification) was
 CC compared with germ-line gene HwK325 (Q42706), showing 97 %
 CC similarity. By nucleotide sequence analysis, F105 appears to
 CC be derived from a member of the V_H III subgroup gene family.
 SQ Sequence 350 BP; 88 A; 115 C; 99 G; 88 T.
 Query Match 82.4%; Score 262; DB 7; Length 390;
 Best Local Similarity 94.0%; Pred. No. 7.19e-157;
 Matches 296; Conservative 0; Mismatches 16; Indels 3; Gaps 1;
 Db 73 acgagctccagacacccctgtcttctcaggggaaagaccacccctcctccag 132
 QY 7 ACGAGCTCCAGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 132
 Db 133 gccagtcagagtgtagcagcagctacttagcctggtaccagcagaaacctggcaggt 192
 QY 67 GCGAGTCAGAGTGTTAGCAGCAATTAATTAGCTGCTAGCAACAGAGAGAGAG 126
 Db 133 gccagtcagagtgtagcagcagctacttagcctggtaccagcagaaacctggcaggt 192
 QY 127 CCGAGGCT 186
 Db 253 ggcagtggtgctgggacagactcactctcaccatcagcagagtgagcctaaagatttt 312
 QY 187 GSCATGGGCTGGGACAGAAATTCACTCTTACCAATACAGAGAGAGAGAGAG 246
 Db 313 gcagtgattactgtcagcaaatatgataactccgtttgtctacacttttggcagggagcc 372
 QY 247 GAGGTGATTAAGTCTGAGCTTTAAGGAACTCACTGAGG---ACGTTGGGCAAGGAG 403
 Db 373 aagctgggagatcaaa 387
 QY 304 AAGGTGGAGATCAAA 318

RESULT 11
 ID Q78854 standard; DNA; 900 BP.
 AC Q78854;
 DT 07-JUN-1995 (first entry)
 DE Human V-kappa gene vk85.8.
 KW Transgenic mouse; transgenic animal; antibody engineering;
 KW variable region; light chain; minilocus transgene;
 KW chimeric antibody; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..650
 FT /*tag= a 163..350
 FT intron 163..350
 FT /*tag= b 653..659
 FT misc_signal 653..659
 FT /*tag= c
 FT /*label= Splicing_signal
 FT misc_signal 672..680

PD 13-AUG-1996. 574748.
 PF 29-AUG-1996: 574748.
 PP 29-AUG-1996: 574748.
 PP 31-AUG-1996: 574748.
 PP 17-DEC-1991: 574748.
 PP 18-MAR-1992: 574748.
 PP 23-JUN-1992: 574748.
 PP 16-DEC-1992: 574748.
 PA (GENP-) GENPHARM INT INC
 PI Kay RM, Longberg N;
 DR WPI: 96-383736/38.
 DR P-PSDB: W03948.
 PT Prodn. of heterologous human immunoglobulin(s) - by immunising
 PT transgenic mice
 PS Example 21; Fig 43; 94pp; English.
 CC The present sequence is the variable kappa chain gene segment
 CC containing human DNA fragment, vk65.8, which was co-injected along
 CC with the human DNA fragments vk65.3, vk65.5 and vk65.15 into half
 CC day mouse embryo pronuclei, to generate an unrearranged light chain
 CC minilocus transgene. The resulting transgenic mice can be used for
 CC the production of heterologous (i.e. human) antibodies against
 CC specific antigens, this comprises immunising a mouse with a
 CC preselected antigen and collecting antigen binding heterologous
 CC human gamma immunoglobulins.
 SQ Sequence 900 BP. 220 A; 241 C; 201 G; 238 T;
 Query Match 82.4%; Score 262; DB 27; Length 900;
 Best Local Similarity 97.8%; Pred. No. 7.19e-157;
 Matches 268; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Db 375 acgagctccagcagccctgtttgtctccaggggaagagccacctctcctgcagg 434
 QY 7 ACCGAGTCTCCAGGACCCCTGCTTTGTCTCCAGGGGAAGAGCCACCTCTCTGTCAGG 66
 Db 435 gccagtcagagtggttagcagcagctacttagcctggtaccagcagaaacctggccagct 494
 QY 67 GCCAGTCAGAGTGTAGCAGCAATTAATTAGCTGTGTACACAGCAGACCTGGCCAGGCT 126
 Db 495 ccagagctctctatgtagtgcacagcagggccactgggacatccagcagcagctttagt 554
 QY 127 CCACGGCTCTCTATGTATGTGTGATCCAGCAGGGGGGACCTGGCATCCACACAGCTTACT 186
 Db 555 gccagtggtgtctggcagcagcttctcctccatccagcagcagctggagcctgaagatttt 614
 QY 187 GCCAGTGGGTCTGGGACAGATTCATCTCTCACCATCAGCAGACTGGAGCCCTGAAGATT 246
 Db 615 gccagtgattactgtagcagcagctatgtagtgcac 648
 QY 247 GCAGTGTATTACTGTAGCTTTATGTGTAACCTAC 280
 RESULT 14
 ID Q29766 standard, cDNA, 324 BP.
 AC Q29766; (first entry)
 DE Gene for Lv region of human rheumatoid factor antibody.
 KW Light chain; variable region; YES8C; arthritis; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 25 288
 FT /*tag= a
 FT misc.feature 12..24
 FT /*tag= b
 FT /*note= "leader sequence"
 FT misc.feature 72..102
 FT /*tag= c
 FT /*note= "encodes CDR1"
 FT misc.feature 150..168
 FT /*tag= d
 FT /*note= "encodes CDR2"
 FT misc.feature 277..285
 FT /*tag= e
 FT /*note= "encodes CDR3"

PN J04267889-A.
 PD 24-SEP-1992.
 PF 22-FEB-1991: 048704.
 PP 22-FEB-1991: JP-048704
 PA (EZAK/) EZAKI K.
 PA (NISP) NISSHI PHARM CO LTD.
 DR WPI: 92-368404/45.
 DR P-PSDB: R25324
 PT Monoclonal human rheumatoid factor - obt'd by prodn. and
 PT secretion of hybridoma obt'd. from cell fusion of human bone
 PT marrow derived lymphocyte and P3U1 mouse myeloma cell
 PS Disclosure: page 5; 7pp; Japanese.
 CC The sequence shown: encodes the variable region of the light chain of
 CC a human monoclonal antibody rheumatoid factor YES8C. The gene may
 CC be isolated from the bone marrow soln. of a rheumatoid arthritis
 CC patient and used to produce hybridomas, allowing prodn. of the
 CC rheumatoid arthritis factor at constant quality in large quantities.
 CC See also Q29767
 SQ Sequence 324 BP; 72 A; 92 C; 80 G; 80 T;
 Query Match 81.1%; Score 258; DB 5; Length 324;
 Best Local Similarity 97.1%; Pred. No. 1.92e-154;
 Matches 266; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Db 49 acgagctctccagcagccctgtttgtctccaggggaagagccacctctcctgcagg 108
 QY 7 ACCGAGTCTCCAGGACCCCTGCTTTGTCTCCAGGGGAAGAGCCACCTCTCTGTCAGG 66
 Db 109 gccatccagagtgattagcagcagctacttagcctggtaccagcagagacctggccagct 168
 QY 67 GCCAGTCAGAGTGTAGCAGCAATTAATTAGCTGTGTACACAGCAGACTGGCCAGGCT 126
 Db 169 ccagagctctctatgtagtgcacagcagggccactggacatccagcagcagctttagt 228
 QY 127 CCACGGCTCTCTATGTATGTGTGATCCAGCAGGGGGGACCTGGCATCCACACAGCTTACT 186
 Db 229 gccagtggtgtctggcagcagcttctcctccatccagcagcagctggagcctgaagatt 288
 QY 187 GCCAGTGGGTCTGGGACAGATTCATCTCTCACCATCAGCAGACTGGAGCCCTGAAGATT 246
 Db 289 gccagtgattactgtagcagcagctatgtagtgcac 322
 QY 247 GCAGTGTATTACTGTAGCTTTATGTGTAACCTAC 280
 RESULT 15
 ID T33664 standard; cDNA; 402 BP.
 AC T33664;
 DT 10-JUN-1997 (revised)
 DT 14-MAY-1997 (first entry)
 DE Anti-lung tumour antigen monoclonal antibody light chain cDNA.
 KW Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EBV;
 KW Epstein-Barr virus; TB945; human; B cell; screen; antigen;
 KW carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
 KW cell; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..402
 FT /*tag= a
 FT W09628473-A1
 PD 19-SEP-1996.
 PF 18-MAR-1996: U03661.
 PP 16-MAR-1995: US-405034.
 PA (MEDE/) MEDENICA R D.
 PI Mukerjee S;
 DR WPI: 96-433764/43.
 DR P-PSDB: W11155
 PT Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by
 PT Epstein-Barr virus transformation of human lung cancer patient
 PT B-cells, useful in conjunction with other agents for lysis of
 PT tumours
 PS Claim 12; Pages 24-25; 46pp; English.
 CC The present sequence encodes the light chain from the monoclonal



(TM)

MPsrch-nn n.a. - n.a. database search, using Smith-Waterman algorithm.

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Title: >US-08-844-215-15
Description: (1-318) from US9844215 seq

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Perfect Score:	318	1	GAGCTCAGCCGAGTCTCTCCAGG.	CGACCAAGCTGGACATCAAA	318
N.A. Sequence:			CICGAGTGGGCTGAGAGTTC	CTGGTTTCACTTATAGTTT	
Comp:					

Nmatch STD : Dbase C: Query C:

searched: 430261 seqs, 710217276 bases x 2

Post-processing: Minimum Match 08

Listing first 45 summaries

Database: emb1-new7

Database: genbank101

Database:

23:BC11 24:BC12 25:BC13 26:BC14 27:BC15 28:BC16 29:BC17
30:BC18 31:BC19 32:BC20 33:BC21 34:BC212 35:BC213
36:GEN1 37:GEN2 38:GEN3 39:GEN4 40:GEN5 41:GEN6 42:HTG1
43:HTG2 44:HTG3 45:HTG4 46:HTG5 47:INV1 48:INV2 49:INV3
50:INV4 51:INV5 52:INV6 53:INV7 54:INV8 55:INV9 56:INV10
57:INV11 58:INV12 59:MAX1 60:MAX2 61:MAM3 62:VBT1
63:VBT2 64:VPT3 65:VPT4 66:PA1 67:PA2 68:PA3 69:PA4
70:PA5 71:PA6 72:PA7 73:PHG 74:PLN1 75:PLN2 76:PLN3
77:PLN4 78:PLN5 79:PLN6 80:PLN7 81:PLN8 92:PLN9 83:PLN11
84:PR11 85:PR12 86:PR13 87:PR12 88:PR13 89:PR14
90:PR15 91:PR16 92:PR17 93:PR18 94:PR19 95:PR110
96:PR117 97:PR112 98:PR113 99:PR114 100:PR115 101:PR116
102:PR117 103:POD1 104:POD2 105:POD3 106:POD4 107:POD5
108:POD6 109:POD7 110:POD8 111:POD9 112:SEP 113:SYN
114:UNA

Database:

115:VRL1 116:VRL2 117:VRL3 118:VRL4 119:VRL5 120:VRL6
121:VRL7 122:VRL8 123:VRL9 124:VRL10 125:VRL11

Database: genbank-new7

126 BCT 127 GEN 128 HCS 129 HCS 130 INV 131 MAM

132:VPT 133:PHG 134:PLN1 135:PLN2 136:PRI1 137:PRI2

138:ROD 139:SYN 140:INA 141:VPI.

Database: u-emb151_101

142:part1 143:part2

Statistics:	Mean 0.067.	Variance 4.684.	Std. Dev. 2.164
Statistics:	Mean 0.067.	Variance 4.684.	Std. Dev. 2.164

2303050100. Mean 7.95, variance 4.04, S.D. 2.01

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

Result No.	Query			ID	Description	Pred. No.
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1	296	93	1	H5G0K3AQ	Human Ig rearranged k	2,176-23
2	296	93	1	H5G0K3C3	H.sapiens mRNA for Ig	2,176-24
3	295	92.8	402	H5G3GVIC	Human mRNA for Ig kappa	2,176-25
4	294	92.5	447	H5G1GHHH	Human Ig rearranged g	1,836-228
5	292	91.8	402	H5G1GVAN	Human mRNA for Ig kappa	2,176-27
6	291	91.5	324	H5G1KCVG	Homo sapiens Ig kappa	5,420-256
7	290	91.2	324	H5G7K682	Human rearranged IM	5,036-255
8	290	91.2	325	H5MMA855	Human immunoglobulin	5,036-256
9	290	91.2	329	HS1GPHL19	H.sapiens (PF0M16K) m	5,036-259
10	290	91.2	330	HS1JBYVL	H.sapiens immunoglob	5,036-255
11	290	91.2	364	H5M1G3AC	Human Ig rearranged k	5,036-255
12	290	91.2	402	H5M1G3AI	Human Ig active kappa	5,036-255
13	289	90.9	312	HS1GPHL18	H.sapiens (PF0M16K) m	5,036-259
14	289	90.9	318	HS1GPHL20	H.sapiens (PF0M28K) m	3,936-224
15	288	90.6	339	H5M1G3AA	Human Ig active kappa	3,086-223
16	288	89.3	318	H5M1K3VZ	Human displatelet m	1,896-221
17	286	89.9	320	H5M1K3VZ	Human Ig rearranged k	1,896-221
18	286	89.9	324	HS1GVL1TD	H.sapiens mRNA for Ig	1,996-221
19	286	89.9	324	H5G03483	Human clone 3754 Ig k	1,896-221
20	286	89.9	420	HS1G3754	H.sapiens rearranged	1,996-221
21	284	89.3	300	HS1GKCCF	Homo sapiens (clone 1	1,156-219
22	284	89.3	320	H5M1K3AT	Human Ig rearranged k	1,156-219
23	284	89.3	324	H5M1HL1FA	Homo sapiens immunob	1,156-219
24	284	89.3	327	H5274657	H.sapiens mRNA for Im	1,156-219
25	282	88.7	300	H5M1K3BC	Homo sapiens (clone 5	7,056-218
26	282	88.7	300	H5M1K3CP	Homo sapiens (clone 1	7,056-218
27	282	88.7	334	HS003482	Human clone 2681 Ig k	7,056-218
28	282	88.7	333	HS1G28S1	H.sapiens rearranged	7,056-218
29	282	88.7	343	H5M1K3CM	Human Ig rearranged k	7,056-218
30	282	88.7	327	H5M0345L	H.sapiens mRNA for an	7,056-218
31	280	88.1	327	H5M1G1VRD	Human immunoglobulin	4,316-216
32	280	88.1	327	HS0013GA	Human anti-glycoprote	4,316-216
33	279	87.7	321	HS1GK37F	H.sapiens mRNA for Ig	2,360-219
34	278	87.4	327	H5M1K3AF5B	Human Ig rearranged k	2,630-214
35	278	87.4	327	H5M1K3K35C	Human Ig rearranged k	2,630-214
36	278	87.4	351	HS1GK35C	H.sapiens rearranged	2,630-214
37	278	87.4	351	HS1GK35G	H.sapiens rearranged	2,630-214
38	278	87.4	402	HS2P1C18A	H.sapiens rearranged	2,630-214
39	275	86.8	300	HS1GPHL17	H.sapiens (PF-MRKY) m	1,006-212
40	275	86.8	300	HS1GPHK2	Homo sapiens (clone 5	1,006-212
41	275	86.8	327	HS095243	Human clone B54.1 immu	1,006-212
42	275	86.8	327	HS09FBSAG	Human creatinin B. ser	1,006-212
43	275	86.8	327	HS095243	Human clone B53.1 immu	1,006-212
44	275	86.8	327	HS1GK3B1AA	Human Ig rearranged k	1,006-212
45	275	86.8	327	HS1GK3B1AA	Human Ig rearranged k	1,006-212

RESULT	1
LOCUS	HOMIGKAO
DEFINITION	320 bp
ACCESSION	Human Ig rearranged kappa chain V-J-region gene, partial cds.
NID	M28166
KEYWORDS	9185906
SOURCE	J-region; V-region; immunoglobulin light chain; immunoglobulin-kappa.
ORGANISM	Human lymphocyte DNA, from patient PCR with small lymphocytic lymphoma.
REFERENCE	Homo sapiens
AUTHORS	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostei; Primates; Catarrhini, Hominoidea, Homo.
TITLE	1 (bases 1 to 320)
	Pratt, L. F., Massonville, J., Larrick, J., Robbins, B., Banks, P. M. and Kipps, T. J.
	Ig V region gene expression in small lymphocytic lymphoma with little or no somatic hypermutation


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/sex="Female"
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kappa chain; joining region; secreted immunoglobulin"
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KR"
BASE COUNT 74 a 90 c 83 g 65 t
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Best Local Similarity 96.8%; Pred No 3 936-224;
Matches 299; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 61 agtcaaggttagcagagctacttagcctgtaccagcagaacacctggccaggtccc 120
QY 70 AGTCAGAGTGTAGCAGCAATTAATAGCTGTGTACAGCAGAGACCTGGCCAGGCTCC 129
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QY 130 AGGCTCTCATCTATGTCATGTCATGTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 189
Db 181 agtgggtctgggacagctctcaccatcagcagactggagcctgaagatttgc 240
QY 190 AGTGGTCTGGGACAGACTTCACTCTCACTATCAGCAGACTGGAGCTTGAAGATTTTGA 249
Db 241 gtgtattctgtcagcagctatgtgttaactcactcagcagcttcggccagcagcaggtg 300
QY 250 GTGTATTCTGTGAGCTTTATGTAACCTGAGCTTGGACGTTGGCCAGGACCAAGGTG 309
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QY 310 GAGATCAAA 318

RESULT 14
LOCUS HSIGRH20 318 bp RNA PPT 11-APP-1095
DEFINITION H sapiens (RFMP28K) mRNA for immunoglobulin mu chain variable
region, rheumatoid factor (318bp).
ACCESSION 234966
NID g510845
KEYWORDS immunoglobulin mu chain variable region; rheumatoid factor
SOURCE human
ORGANISM Homo sapiens
REFERENCE Eukaryotae: mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata; Eutheria: Primates; Catarrhini; Hominidae: Homo.
AUTHORS Thompson, K.M.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1994) Thompson K. M., I.G.R.I., Immunology, Fr.
Quams Gt.1, Oslo, Norway, 0172
REFERENCE 2 (bases 1 to 318)
AUTHORS Borretzen, M., Randsen, I., Zdarsky, E., Forre, O., Natvig, J.B. and
Thompson, K.M.

TITLE Control of autoantibody affinity by selection against amino acid
replacements in the complementarity-determining regions
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (26): 12917-12921 (1994)
MEDLINE 95108069
FEATURES
Location/Qualifiers
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KPTV"
BASE COUNT 75 a 91 c 86 g 66 t
ORIGIN
Query Match 90.9%, Score 289, DB 91, Length 312;
Best Local Similarity 96.8%; Pred No 3 936-224;
Matches 299; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 1 cagctccagagcaccctgtcttctccaggggaaagagccaccctctctcaggggcc 60
QY 10 CAGTCTCCAGGACCTGTCCTTTGCTCCAGGGAAGAGGAGGAGGAGGAGGAGGAGG 69
Db 61 agtcaaggttagcagcagctacttagcctgtaccagcagaacacctggccaggtccc 120
QY 70 AGTCAGAGTGTAGCAGCAATTAATAGCTGTGTACAGCAGAGACTGGCCAGGCTCC 129
Db 121 aggtcctcatctatgtgtcaccagcagggccactggccatccagcagaggttcagtgcc 180
QY 130 AGGCTCTCATCTATGTCATGTCATGTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 189
Db 181 agtgggtctgggacagctctcaccatcagcagactggagcctgaagatttgc 240
QY 190 AGTGGTCTGGGACAGACTTCACTCTCACTATCAGCAGACTGGAGCTTGAAGATTTTGA 249
Db 241 gtgtattctgtcagcagctatgtgttaactcactcagcagcttcggccagcagcaggtg 300
QY 250 GTGTATTCTGTGAGCTTTATGTAACCTGAGCTTGGACGTTGGCCAGGACCAAGGTG 309
Db 301 gaaatcaaa 309
QY 310 GAGATCAAA 318

RESULT 15
LOCUS HMIGKAA 339 bp mRNA PPT 05-JAN-1995
DEFINITION Human Ig active kappa chain V-region gene NG9, V-kappa-3 mRNA,
partial cds.
ACCESSION K01321
NID g185813
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;
immunoglobulin kappa; immunoglobulin-kappa subgroup VK-5.
SOURCE Human NG9/9.1 hybridoma (mouse plasmacytoma fused with human spleen
cells), cDNA to mRNA, clones NG9/V-kappa-3 and NG9/3.
ORGANISM Homo sapiens
REFERENCE Eukaryotae: mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata; Eutheria: Primates; Catarrhini; Hominidae: Homo.
REFERENCE 1 (bases 100 to 339)

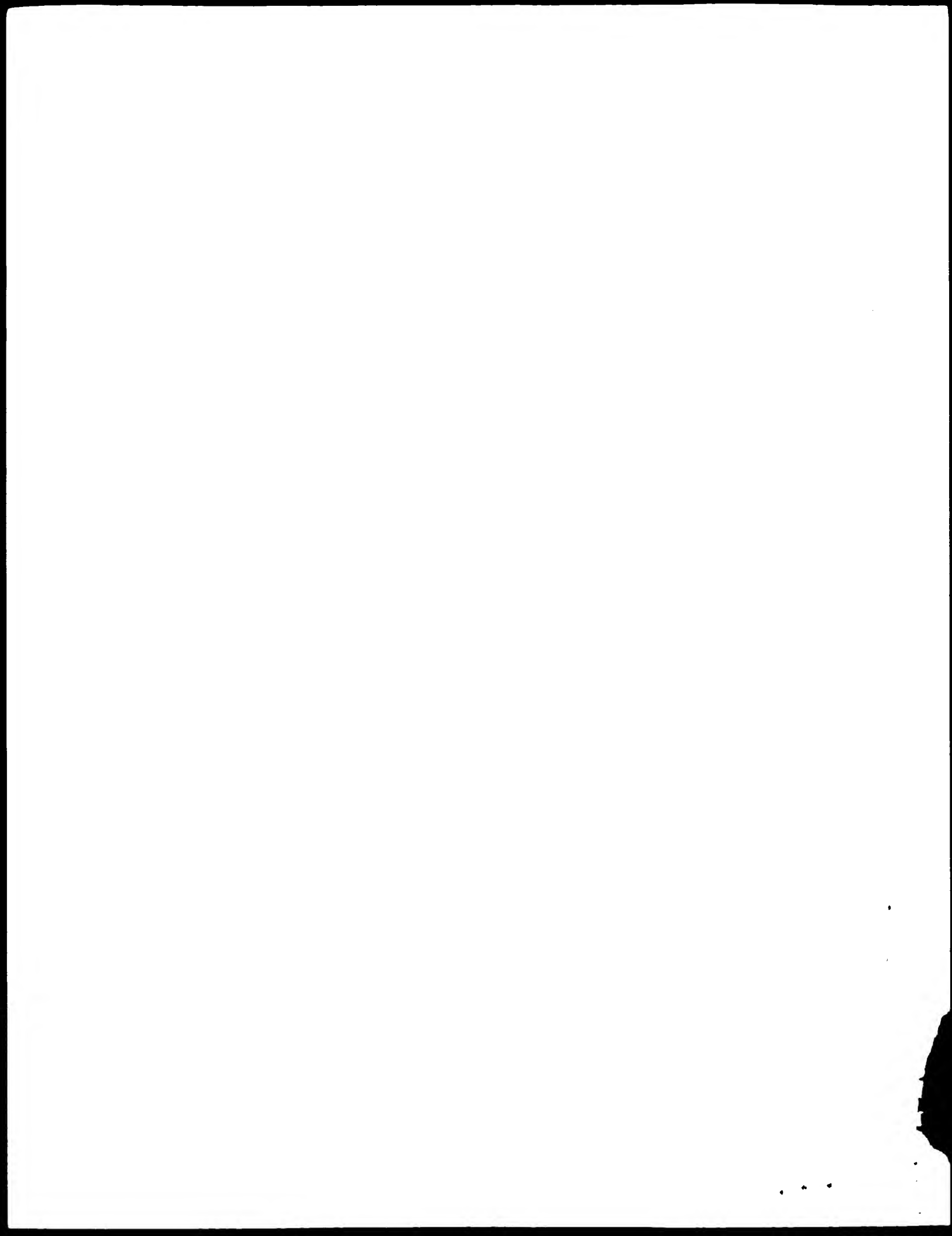
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AUTHORS Bentley,D.L. and Rabbitts,I.H.
 TITLE Human V kappa immunoglobulin gene number: implications for the
 origin of antibody diversity
 JOURNAL Cell 24 (3), 613-623 (1981)
 MEDLINE 81234547
 REFERENCE 2 (bases 1 to 300)
 AUTHORS Bentley,D.L.
 TITLE Most kappa immunoglobulin mRNA in human lymphocytes is homologous
 to a small family of germ-line V genes
 JOURNAL Nature 307 (5945), 77-80 (1984)
 MEDLINE 84093600
 COMMENT [1] and [2] claim that the majority of kappa mRNA (all V-region
 sequences from subgroups 1 and 3) is encoded by approximately 25
 germline V-region genes, and that the total number of human V-kappa
 genes is about 50 or less. Thus, somatic mutation may be the major
 source of human kappa-chain diversity [2]. Compared in [1] and [2]
 with the subgroup V-kappa-1 germline V-region gene HK101.

FEATURES
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 CDS 1..>339 /note="This CDS feature is included to show the
 translation of the corresponding V-region. Presently
 translation qualifiers on V-region features are illegal."
 /codon_start=1
 /db_xref="PID:g185814"
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 FGQTKVEIKR"
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 /note="Ig kappa light chain V-region mature peptide"
 /codon_start=1
 <1..12
 sig_peptide /note="Ig kappa L-chain V-region signal peptide"
 /codon_start=1
 misc_recomb 300..301
 BASE COUNT 79 a 94 c 92 g 74 t
 ORIGIN

Query Match 90.6% Score 288; DB 95; Length 339;
 Best Local Similarity 96.2% Pred. No. 3,08e-223;
 Matches 300; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Db 25 acgagctccagggaccctcttctccagggaagagccaccctctctccag 84
 QY 7 AGCGACTTCAGAGGACCCCTGCTTTGCTCCAGGGAAGAGCCACCCCTCTCTCCAGG 66
 Db 85 gccatcgaadtgttagcagcagctacttaccctgggtaccagagaaacctggccaggct 144
 QY 67 GGCATTCAGAGTGTTAGCAGCAATTAATTAAGCTGTGTACGAGCAGAGACCTGGCCAGGCT 126
 Db 145 cccaggtccctcatctatggtgctaccagcaggccaccctggcatccagacaggttcagt 204
 QY 127 CCCAGGCTCCCTCATCTATGGTGCACTACAGAGAGGAGGACCTGGTCACTCCAGACAGGCTCAGT 186
 Db 205 ggcadtcgctctggagacagcttccactctccatccatccagcagactggagcctgaagatttt 264
 QY 187 GCGAGTGGGTTGGACAGAGATTTCATCTTCACCAICAGATAGACIGGAGCCGIGAGATTIT 246
 Db 265 gcaatgtattacttcagcagctatggtaattccacagtggaagctgggccaagggaacaaag 324
 QY 247 GCAGTGATTAATGTCAGCTTTATGGTAACCTCAGATTGAGAGGTTGGAGAGAGACCAAG 306
 Db 325 atggaatacaaa 336
 QY 307 GTGGAGATCAAA 318

Search completed: Tue Feb 24 07:09:30 1998
 Job time : 544 secs.



1
WIREH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:29:34 1998 Master time 4.94 Seconds
454,909 Million cell updates/sec
Tabular output not generated

Title: >US-08-844-215-14
Description: (1-106) from US08844215.pep
Perfect Score: 749
Sequence: 1 AELTQSPSTLSLSPGEPATL YCCOYGTPTFGQTKVEIK 106

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs 21010398 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 40.434: Variance 69.990: scale 0.578

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB ID	Description	Pred. No.
1	695	92.8	129	5 KV3L_HUMAN IG KAPPA CHAIN PRECUR	1 26e-133
2	679	90.7	129	5 KV3M_HUMAN IG KAPPA CHAIN PRECUR	7 77e-130
3	677	90.4	109	5 KV3E_HUMAN IG KAPPA CHAIN V-III	2 31e-120
4	676	90.3	109	5 KV3D_HUMAN IG KAPPA CHAIN V-III	3 98e-129
5	655	88.8	104	5 KV3A_HUMAN IG KAPPA CHAIN V-III	1 59e-126
6	654	88.0	104	5 KV3G_HUMAN IG KAPPA CHAIN V-III	4 16e-125
7	658	87.9	109	5 KV3C_HUMAN IG KAPPA CHAIN V-III	7 16e-125
8	602	80.4	100	5 KV3K_HUMAN IG KAPPA CHAIN PRECUR	1 11e-111
9	602	80.4	129	5 KV3L_HUMAN IG KAPPA CHAIN PRECUR	1 11e-111
10	600	80.1	104	5 KV3E_HUMAN IG KAPPA CHAIN V-III	3 28e-111
11	599	80.0	129	5 KV3L_HUMAN IG KAPPA CHAIN PRECUR	5 60e-111
12	560	74.8	115	5 KV3L_HUMAN IG KAPPA CHAIN PRECUR	7 62e-102
13	543	72.5	116	5 KV3L_HUMAN IG KAPPA CHAIN PRECUR	7 06e-98
14	540	72.1	108	5 KV1H_HUMAN IG KAPPA CHAIN V-I	3 53e-97
15	531	70.9	108	5 KV1M_HUMAN IG KAPPA CHAIN V-I	4 40e-95
16	530	70.8	108	5 KV1N_HUMAN IG KAPPA CHAIN V-I	7 51e-95
17	524	70.0	108	5 KV1K_HUMAN IG KAPPA CHAIN V-I	1 87e-93
18	523	69.8	107	5 KV1D_HUMAN IG KAPPA CHAIN V-I	3 19e-93
19	521	69.6	108	5 KV1F_HUMAN IG KAPPA CHAIN V-I	9 79e-93
20	519	69.3	114	5 KV4B_HUMAN IG KAPPA CHAIN PRECUR	2 71e-92
21	513	68.5	133	5 KV4C_HUMAN IG KAPPA CHAIN PRECUR	6 69e-91
22	512	68.4	108	5 KV1B_HUMAN IG KAPPA CHAIN V-I	1 14e-90

23	510	68.1	114	5 KV4A_HUMAN IG KAPPA CHAIN V-IV R	3 32e-90
24	510	68.1	129	5 KV1W_HUMAN IG KAPPA CHAIN PRECUR	3 32e-90
25	505	67.4	108	5 KV1P_HUMAN IG KAPPA CHAIN V-I	4 79e-89
26	504	67.3	108	5 KV1V_HUMAN IG KAPPA CHAIN V-I	8 17e-89
27	504	67.3	108	5 KV1R_HUMAN IG KAPPA CHAIN V-I	8 17e-89
28	499	66.6	108	5 KV1Y_HUMAN IG KAPPA CHAIN V-I	1 19e-87
29	498	66.5	108	5 KV1L_HUMAN IG KAPPA CHAIN V-I	2 60e-87
30	497	66.4	108	5 KV1G_HUMAN IG KAPPA CHAIN V-I	3 41e-87
31	496	66.2	108	5 KV1Q_HUMAN IG KAPPA CHAIN V-I	5 82e-87
32	492	65.7	108	5 KV1O_HUMAN IG KAPPA CHAIN V-I	4 60e-86
33	488	65.2	108	5 KV1I_HUMAN IG KAPPA CHAIN V-I	4 12e-85
34	487	65.0	109	5 KV1T_HUMAN IG KAPPA CHAIN V-I	7 01e-85
35	486	64.9	108	5 KV1P_HUMAN IG KAPPA CHAIN V-I	1 19e-84
36	483	64.5	117	5 KV1J_HUMAN IG KAPPA CHAIN PRECUR	5 88e-84
37	482	64.4	108	5 KV1S_HUMAN IG KAPPA CHAIN V-I	1 00e-83
38	481	64.2	112	5 KV1U_HUMAN IG KAPPA CHAIN V-I	1 70e-83
39	479	64.0	129	5 KV1X_HUMAN IG KAPPA CHAIN PRECUR	4 60e-83
40	475	63.6	108	5 KVSP_MOUSE IG KAPPA CHAIN V-V	2 42e-82
41	476	63.6	108	5 KV1C_HUMAN IG KAPPA CHAIN V-I	2 42e-82
42	476	63.6	108	5 KV1J_MOUSE IG KAPPA CHAIN V-V	2 42e-82
43	476	63.6	117	5 KV1E_HUMAN IG KAPPA CHAIN PRECUR	2 42e-82
44	475	63.4	140	5 KV1A_MOUSE IG KAPPA CHAIN PRECUR	4 12e-82
45	474	63.3	112	5 KV2C_HUMAN IG KAPPA CHAIN V-II R	7 01e-82

ALIGNMENTS

RESULT 1
ID KV3L_HUMAN STANDARD: PRI: 129 AA.
AC P18135;
DI 01-NOV-1990 (REL. 16, CREATED)
DI 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DI 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAH).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA:
OC EUTHERIA, PRIMATES.
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.:
J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P10022: K3H0HA.
DR HSP: P01607: IAAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 2044885E CRC32:
Query Match 92.98: Score 695: DB 5: Length 129:
Best Local Similarity 94.14: Pred No. 125e-133:
Matches 99: Conservative 3: Mismatches 2: Indels 1: Gaps 1:
Db 24 1trasptalsgcratiscragssyawlwygkqkqaprllyqasaraaipdrf 83
QY 3 1tspstslspspefatustcpastskylawylxpfpsaprrllyqasaraaipdrf 62
Db 84 sqsgsdftllstslslepedfayvvgqgvgysprfigggtkveik 128
QY 63 SSGSSGIDILSLSLKLEPEDFAVYVCUYGI-PRIFGGSIKVEIK 105

RESULT 2
 ID KV3B_HUMAN STANDARD: PRT: 129 AA.
 AC P18136;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC)
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86171307.
 RA KIPPS T.J., TOMHAVE F., CHEN P.P., CARSON D.A.;
 RL J. EXP. MED. 167:840-852(1988).
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR: P10021; K3HUI.
 DR HSSP; P01607; 1DFB.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).
 FT DOMAIN 21 43 FRAMEWORK 1
 FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; D030C369 CRC32;

Query Match 90.7%; Score 679; DB 5; Length 129;
 Best Local Similarity 91.4%; Pred. No. 7,77e-130;
 Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
 Db 24 ltqspgtlslspgeratlsrlepdafavycqgysvssylyawqkpgqaprllygassratgipdrf 83
 QY 3 LTQSPGTLSPGERATLSRLEPDFAVYCCQYGT-PRTFGGGKVEIK 62
 Db 84 sgsqsgtdftltisrlepdafavycqgysvssylyawqkpgqaprllygassratgipdrf 128
 QY 63 SSGSGGTDFTLSRLEPDFAVYCCQYGT-PRTFGGGKVEIK 106

RESULT 3
 ID KV3B_HUMAN STANDARD: PRT: 109 AA.
 AC P01620;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (SIE).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 82046598.
 RA ANDREWS D.W., CAPRA J.D.;
 RL BIOCHEMISTRY 20:5876-5822(1981).
 CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR: A01892; K3HUI.
 DR HSSP; P01607; 1DFB.
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 00B5DD5D CRC32;
 Query Match 90.4%; Score 677; DB 5; Length 109;

Best Local Similarity 89.5%; Pred. No. 2.31e-129;
 Matches 94; Conservative 8; Mismatches 2; Indels 1; Gaps 1;
 Db 4 ltqspgtlslspgeratlsrlepdafavycqgysvssylyawqkpgqaprllygassratgipdrf 63
 QY 3 LTQSPGTLSPGERATLSRLEPDFAVYCCQYGT-PRTFGGGKVEIK 62
 Db 64 sgsqsgtdftltisrlepdafavycqgysvssylyawqkpgqaprllygassratgipdrf 108
 QY 63 SSGSGGTDFTLSRLEPDFAVYCCQYGT-PRTFGGGKVEIK 106
 RESULT 4
 ID KV3B_HUMAN STANDARD: PRT: 109 AA.
 AC P01623;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (WOL)
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 82046598.
 RA ANDREWS D.W., CAPRA J.D.;
 RL BIOCHEMISTRY 20:5876-5822(1981).
 CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR: A01896; K3HUI.
 DR HSSP; P01607; 1DFB.
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11746 MW; 7D8F5D75 CRC32;

Query Match 90.3%; Score 676; DB 5; Length 109;
 Best Local Similarity 91.4%; Pred. No. 2.04e-129;
 Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
 Db 4 ltqspgtlslspgeratlsrlepdafavycqgysvssylyawqkpgqaprllygassratgipdrf 63
 QY 3 LTQSPGTLSPGERATLSRLEPDFAVYCCQYGT-PRTFGGGKVEIK 62
 Db 64 sgsqsgtdftltisrlepdafavycqgysvssylyawqkpgqaprllygassratgipdrf 108
 QY 63 SSGSGGTDFTLSRLEPDFAVYCCQYGT-PRTFGGGKVEIK 106

RESULT 5
 ID KV3B_HUMAN STANDARD: PRT: 109 AA.
 AC P01622;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (II).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 72188439.
 RA SUPPE L., BARNIKOL H., WATANABE S., HILSCHMANN N.;
 RL HOPPE-SYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972).
 CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01895; K3HUI.
 DR HSSP; P01607; 2IMM.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11788 MW; D03795B1 CRC32;

Query Match 4 38.8% Score 645; DB 5; Length 109;
Best Local Similarity 78.5% Pred No. 156-156;
Matches 94; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

Db 4 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 63
|||||
QY 3 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 62
|||||

Db 64 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 108
|||||
QY 63 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 106
|||||

RESULT 6
ID KV3K_HUMAN STANDARD: PRT: 108 AA.
AC P01619;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-III REGION (NG9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 84093600.
RA BENTLEY D.L.;
RL NATURE 307:77-80(1984).
CC -!- THIS GENE WAS ISOLATED FROM THE NG9/9 1 HYBRIDOMA.
DE PIR: A01894; K3HUG.
DR HSSP: P01607; 1MGP.
KW IMMUNOGLOBULIN V REGION: RENCE-JONES PROTEIN.
FT DISULFID 23 89
FT NON-TER 108 108
SQ SEQUENCE 108 AA: 11635 MW: 4505686E CRC32:

Query Match 88.0% Score 659; DB 5; Length 108;
Best Local Similarity 83.8% Pred. No. 4.156-125;
Matches 88; Conservative 13; Mismatches 3; Indels 1; Gaps 1;

Db 4 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 63
|||||
QY 3 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 62
|||||

Db 64 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 108
|||||
QY 63 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 106
|||||

RESULT 7
ID KV3K_HUMAN STANDARD: PRT: 109 AA.
AC P04205;
DT 20-MAR-1987 (REL. 04, CREATED)
DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-III REGION (NG9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 86230578.
RA NEWKIRK M.; CHEN P.; CARSON D. A.; DOSNETT D.; CAPPA J. D.;
RL MOL. IMMUNOL. 23:239-244(1986).
DR PIR: A01893; K3HUG.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89
FT NON-TER 109 109
SQ SEQUENCE 109 AA: 11830 MW: 8930004A CRC32:

Query Match 87.9% Score 658; DB 5; Length 109;
Best Local Similarity 88.7% Pred No. 7.166-125;
Matches 94; Conservative 7; Mismatches 2; Indels 3; Gaps 1;

Db 4 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 62
|||||
QY 3 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 61
|||||

Db 63 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 108
|||||
QY 62 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 106
|||||

RESULT 8
ID KV3K_HUMAN STANDARD: PRT: 100 AA.
AC P01621;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-III REGION (NG9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 84093600.
RA BENTLEY D.L.;
RL NATURE 307:77-80(1984).
CC -!- THIS GENE WAS ISOLATED FROM THE NG9/9 1 HYBRIDOMA.
DE PIR: A01894; K3HUG.
DR HSSP: P01607; 1MGP.
KW IMMUNOGLOBULIN V REGION: SIGNAL: HYBRIDOMA.
FT NON-TER 1 1
FT CHAIN 5 4
FT SIGNAL 27 93
FT DISULFID 27 93
FT NON-TER 100 100
SQ SEQUENCE 100 AA: 10729 MW: 99A7E223 CRC32:

Query Match 80.4% Score 602; DB 5; Length 100;
Best Local Similarity 89.2% Pred. No. 1.111-111;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 8 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 67
|||||
QY 3 ltsqptslspsgeratlsctasqsvsnflawqgkqgqprlllyvassratgipdrf 62
|||||

Db 68 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 100
|||||
QY 63 ssgsgtdftltisrlepedfavyvccqgsspsstfggqtkveik 95
|||||

RESULT 9
ID KV3K_HUMAN STANDARD: PRT: 128 AA.
AC P06311;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-III REGION (NG9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 86041852.
RA KIMRECH H. G.; MEINFLA.; COMPTON G. S.; ELLMAN A.; KAHN H. J.;
RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
DR EMBL: 200021; G33179; -.
DR PIR: A01899; K3HUG1.
DR HSSP: P01607; 3HEM.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 60

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FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 77 108 FRAMEWORK 3
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 118 128 JK1 SEGMENT
FT DISULFID 43 108 BY SIMILARITY
FT NON_TER 128 128
SQ SEQUENCE 128 AA: 14070 MW: 318E08AF CRC32:

Query Match 80.4%; Score 602; DB 5; Length 128;
Best Local Similarity 86.7%; Pred No 111e-111;
Matches 91; Conservative 6; Mismatches 6; Indels 2; Gaps 2;

Db 24 ltqspgtlslspgeratlsrscasqslsnylawyqkqgsprrlllygastatgiparf 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPGTLSLSPGERATLSRSCASQSLSKYLAWYQKPGQAPRFLFYDASSPATGIPDPF 62

Db 83 sgsgsgtdftllslrlepedfavyycqgyspytfgggtkleik 127
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 SGSGSGTDTLSLSRLEPEDFAVYVCQYQYGT--PRTFGGSGTKVEIK 106

RESULT 10
ID KV3F HUMAN STANDARD; PRT: 109 AA.
AC P01624.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (POM)
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
PA KLAPPER D G., CAPRA J D.
RL ANN INST PASTEUR IMMUNOL 127C:261-271(1976).
CC - THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
DR PIR: A01897; K3HUPM.
DR HSP: P01607; 1DEF.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11922 MW: A0C42C88 CRC32:

Query Match 80.1%; Score 600; DB 5; Length 109;
Best Local Similarity 78.1%; Pred No. 3.26e-111;
Matches 82; Conservative 13; Mismatches 9; Indels 1; Gaps 1.

Db 4 mtqspvtlslspgeratlsrscasqslsnylawyqkqgsprrlllygastatgiparf 63
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPGTLSLSPGERATLSRSCASQSLSKYLAWYQKPGQAPRFLFYDASSPATGIPDPF 62

Db 64 sgsgsgtdftllslrlepedfavyycqgyspytfgggtveik 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 SGSGSGTDTLSLSRLEPEDFAVYVCQYQYGT--PRTFGGSGTKVEIK 106

RESULT 11
ID KV3H HUMAN STANDARD; PRT: 129 AA.
AC P04307.
DT 20-MAR-1987 (REL. 04, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (CLL) (RHENMATOID FACTOR)
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86177570.
RA JIRIK F P., SORGE J., FONG S., HEITZMANN J.G., CHRD J.G., CHEN P.P.,
RA GOLDFEN E., CARSON D.A.
PI PROC NATL ACAD SCI U S A 83:2195-2199(1986).

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DR EMBL: M12740; G553486; -.
DR PIR: A01898; K3HUCI
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (CLL).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 2F344868 CRC32:

Query Match 80.0%; Score 599; DB 5; Length 129;
Best Local Similarity 79.2%; Pred No. 5.60e-111;
Matches 84; Conservative 15; Mismatches 4; Indels 3; Gaps 2;

Db 24 mtqspvtlslspgeratlsrscasqslsnylawyqkqgsprrlllygastatgiparf 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPGTLSLSPGERATLSRSCASQSLSKYLAWYQKPGQAPRFLFYDASSPATGIPDPF 62

Db 83 sgsgsgtdftllslrlepedfavyycqgyspytfgggtveik 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 SGSGSGTDTLSLSRLEPEDFAVYVCQYQYGT--PRTFGGSGTKVEIK 106

RESULT 12
ID KV3I HUMAN STANDARD; PRT: 115 AA.
AC P04433;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932
RA PECH M., ZACHAU H.G.
RL NUCLEIC ACIDS RES 12:9229-9236(1984)
DR EMBL: X01668; -; NOT_ANNOTATED_CDS.
DR PIR: A01400; K3HUVG
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 ~115 IG KAPPA CHAIN V-III REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA: 12575 MW: 37E182FC CRC32:

Query Match 74.8%; Score 560; DB 5; Length 115;
Best Local Similarity 90.9%; Pred. No. 7.52e-102;
Matches 80; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Db 24 ltqspvtlslspgeratlsrscasqslsnylawyqkqgsprrlllygastatgiparf 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPGTLSLSPGERATLSRSCASQSLSKYLAWYQKPGQAPRFLFYDASSPATGIPDPF 62

Db 83 sgsgsgtdftllslrlepedfavyycq 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 SGSGSGTDTLSLSRLEPEDFAVYVCQY 90

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RESULT 13
ID KVAL_HUMAN STANDARD: PRT: 116 AA.
AC P04434
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (PEASMENT)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932
RA PECH M., ZACHAU H.G.:
PE NUCLEIC ACIDS RES 12:9220-9236(1984).
DR EMBL: X02725: -; NOT_ANNOTATED_CDS.
DR PIR: A01901: K3HUVH.
DR HSP: P01607: LMCP.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH)
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 55 FRAMEWORK 2.
FT DOMAIN 56 70 FRAMEWORK 3.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON-TER 116 116
SQ SEQUENCE 116 AA: 12757 MW: 27619C CPC32:
Query Match 72.5% Score 543. DB 5. Length 116.
Best Local Similarity 84.1% Pred No 7 Gap=0.
Matches 74. Conservative 8. Mismatches 6. Indels 0. Gaps 0.

Db 24 mtqspstlsppgervtlscrasqssvssyltwyqqqgqprlllygastratsiparf 83
QY 3 LTQSPGTLSPGEPATLSCPASQSSSKYLAWYQKPGQAPPLFIYUASSPAIGIKVEIK 62

Db 84 sgsqsgtdftlsslpdpfavyycq 111
QY 63 SGSGSGTDFILSLPLEDFAVYVCQ 90

RESULT 14
ID KVAL_HUMAN STANDARD: PRT: 108 AA.
AC P01600.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 05, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (HAU).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES
RN [1]
RP SEQUENCE.
RX MEDLINE: 71032830.
RA WATANABE S., HILSCHMANN N.
RL HORPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1291-1295(1970).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (?) SAKPEP.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01968: KIHUHU.
DR HSP: P01607. IFVC.
KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON-TER 108 108
SQ SEQUENCE 108 AA: 22298C CPC32:
Query Match 70.9% Score 511. DB 5. Length 108.
Best Local Similarity 65.1% Pred No 4 Gap=0.
Matches 69. Conservative 22. Mismatches 12. Indels 2. Gaps 2.

Db 3 qmtspsslsasvdrvtlscrasqssvssyltwyqqqgqprlllygastratsiparf 61
QY 2 ELTSPGTLSPGEPATLSCPASQSSSKYLAWYQKPGQAPPLFIYUASSPAIGIKVEIK 61

Db 62 fsgsgsgtdftlsslpdpfavyycq 107
QY 62 PSGSQSGTDFILSLPLEDFAVYVCQYCT-PPFSGGQIKVEIK 106

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Search completed: Tue Feb 24 07:29:48 1998
Job time : 14 secs.

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FT NON-TER 108 108
SQ SEQUENCE 108 AA: 11671 MW: C9A2EE86 CPC32:
Query Match 72.1% Score 540. DB 5. Length 108.
Best Local Similarity 69.8% Pred No 3.51e-97.
Matches 74. Conservative 19. Mismatches 11. Indels 2. Gaps 2.

Db 3 qmtspsslsasvdrvtlscrasqssvssyltwyqqqgqprlllygastratsiparf 61
QY 2 ELTSPGTLSPGEPATLSCPASQSSSKYLAWYQKPGQAPPLFIYUASSPAIGIKVEIK 61

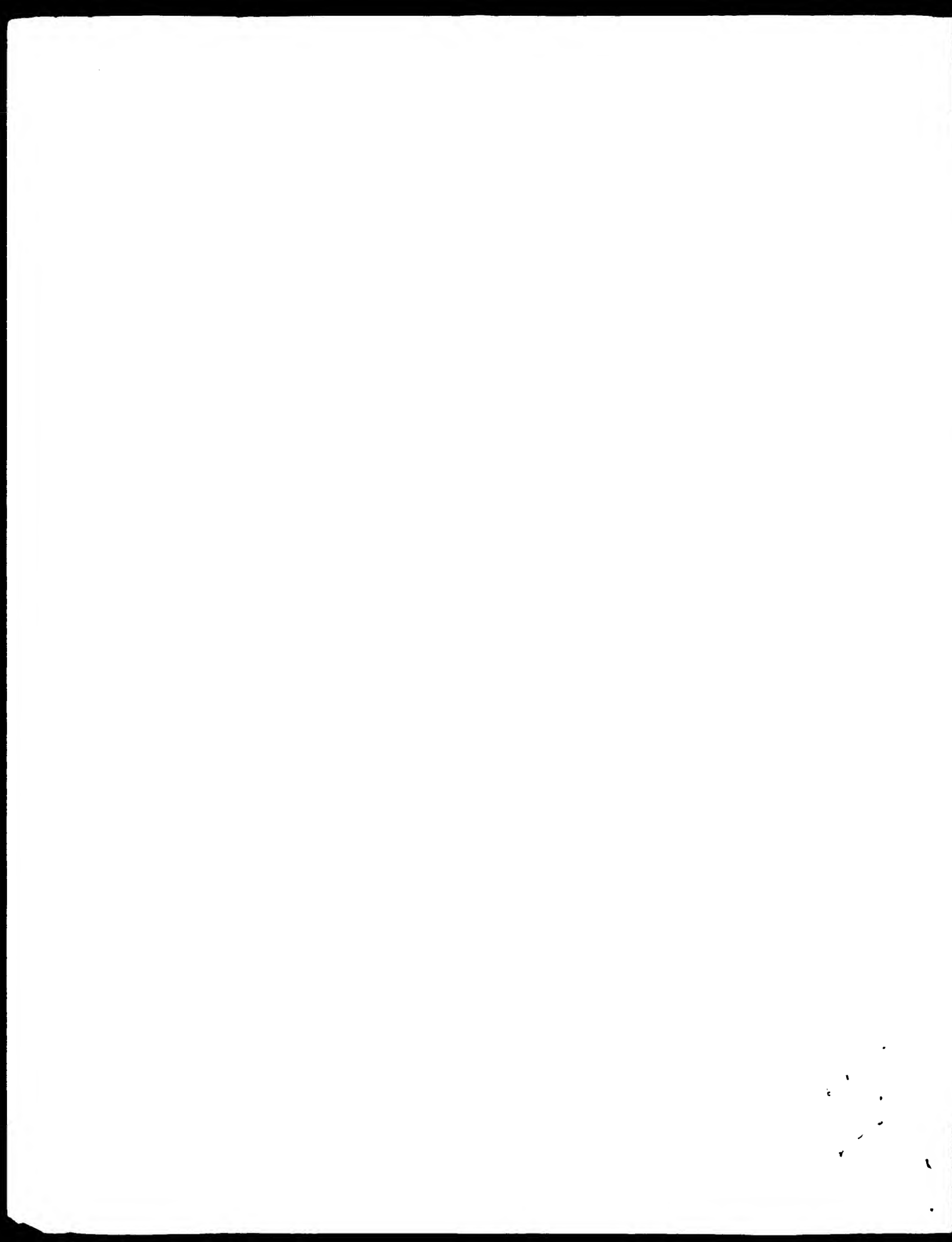
Db 62 fsgsgsgtdftlsslpdpfavyycq 107
QY 62 PSGSQSGTDFILSLPLEDFAVYVCQYCT-PPFSGGQIKVEIK 106

RESULT 15
ID KVAL_HUMAN STANDARD: PRT: 108 AA.
AC P01605.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAY).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES
RN [1]
RP SEQUENCE.
RX MEDLINE: 77038198.
RA CAPPA J.D., KLAPPEP D.G.:
PE SCAND J IMMUNOL 5:677-684(1975).
CC -1- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN FCμ V-III KAPPA CHAIN. WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- THIS CHAIN WAS ISOLATED FROM AN ISM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
DR PIR: A01871: KIHULY.
DR HSP: P01607. 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON-TER 108 108
SQ SEQUENCE 108 AA: 11934 MW: 22298C CPC32:
Query Match 70.9% Score 511. DB 5. Length 108.
Best Local Similarity 65.1% Pred No 4.40e-95.
Matches 69. Conservative 22. Mismatches 12. Indels 2. Gaps 2.

Db 3 qmtspsslsasvdrvtlscrasqssvssyltwyqqqgqprlllygastratsiparf 61
QY 2 ELTSPGTLSPGEPATLSCPASQSSSKYLAWYQKPGQAPPLFIYUASSPAIGIKVEIK 61

Db 62 fsgsgsgtdftlsslpdpfavyycq 107
QY 62 PSGSQSGTDFILSLPLEDFAVYVCQYCT-PPFSGGQIKVEIK 106

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WATER

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPSrch_pp protein - protein database search using Smith-Waterman algorithm

Run on: Tue Feb 24 07:57:16 1998: MasPar time 4.09 Seconds
Tabular output not generated: 131 950 Million cell updates/sec

Title: >US-08-844-215-14
Description: (1-106) from US08844215.pep
Perfect Score: 749
Sequence: 1 AELTQSPGTLSPGERATL.....YCCQYGTPTFGGKTKVEIK 106

Scoring table: PAM 150
Gap 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1.back1 2.51 3.52 4.53 5.54 6.55 7.56 8.PCT90 9.PCT91
10.PCT92 11.PCT93 12.PCT94 13.PCT95 14.PCT96

Statistics: Mean 27.184; Variance 144.390; scale 0.188

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Pred No
1	676	90.3	108	7	US-08-474-	Sequence 86, Applicati	5.02e-44
2	676	90.3	108	7	US-08-487-	Sequence 86, Applicati	5.02e-44
3	676	90.3	108	6	US-08-477-	Sequence 86, Applicati	5.02e-44
4	675	90.3	108	6	US-07-634-	Sequence 86, Applicati	5.02e-44
5	675	90.1	109	13	PCT-US95-0	Sequence 147, Applicat	6.02e-44
6	675	90.1	109	7	US-08-276-	Sequence 99, Applicati	6.02e-44
7	670	89.5	109	7	US-08-276-	Sequence 99, Applicati	1.50e-43
8	670	89.5	109	13	PCT-US95-0	Sequence 86, Applicati	1.50e-43
9	666	88.9	109	7	US-08-276-	Sequence 86, Applicati	3.10e-43
10	666	88.9	109	13	PCT-US95-0	Sequence 86, Applicati	3.10e-43
11	665	88.9	111	13	US-08-276-	Sequence 149, Applicat	3.10e-43
12	665	88.9	111	13	PCT-US95-0	Sequence 90, Applicati	3.10e-43
13	663	88.5	107	13	PCT-US95-0	Sequence 90, Applicati	5.36e-43
14	663	88.5	107	7	US-08-276-	Sequence 90, Applicati	5.36e-43
15	656	87.6	109	11	PCT-US93-0	Sequence 23, Applicati	1.92e-42
16	650	86.8	104	13	PCT-US95-0	Sequence 100, Applicat	5.71e-42
17	650	86.8	104	7	US-08-276-	Sequence 100, Applicat	5.71e-42
18	641	85.6	108	7	US-08-276-	Sequence 110, Applicat	2.94e-41
19	641	85.6	108	13	PCT-US95-0	Sequence 110, Applicat	2.94e-41
20	628	83.8	107	7	US-08-276-	Sequence 87, Applicati	3.12e-40
21	628	83.8	107	13	PCT-US95-0	Sequence 87, Applicati	3.12e-40
22	626	83.4	109	13	PCT-US95-0	Sequence 95, Applicati	4.44e-40

23	626	83.6	108	7	US-08-276-	Sequence 96, Applicati	4.44e-40
24	619	82.6	109	11	PCT-US93-0	Sequence 24, Applicati	1.50e-39
25	618	82.5	112	7	US-08-276-	Sequence 151, Applicat	1.92e-39
26	618	82.5	112	13	PCT-US95-0	Sequence 151, Applicat	1.92e-39
27	616	82.2	104	13	PCT-US95-0	Sequence 94, Applicati	2.76e-39
28	616	82.2	104	7	US-08-276-	Sequence 94, Applicati	2.76e-39
29	612	81.7	105	7	US-08-276-	Sequence 93, Applicati	5.71e-39
30	612	81.7	105	13	PCT-US95-0	Sequence 93, Applicati	5.71e-39
31	611	81.6	116	7	US-08-053-	Sequence 181, Applicat	5.85e-39
32	610	81.4	108	13	PCT-US95-0	Sequence 88, Applicati	8.21e-39
33	610	81.4	108	7	US-08-276-	Sequence 88, Applicati	8.21e-39
34	594	79.3	107	13	PCT-US95-0	Sequence 118, Applicat	1.50e-37
35	594	79.3	107	7	US-08-276-	Sequence 118, Applicat	1.50e-37
36	594	79.3	107	7	US-08-276-	Sequence 116, Applicat	1.50e-37
37	594	79.3	107	13	PCT-US95-0	Sequence 116, Applicat	1.50e-37
38	592	78.9	107	7	US-08-276-	Sequence 117, Applicat	2.58e-37
39	591	78.9	107	13	PCT-US95-0	Sequence 117, Applicat	2.58e-37
40	590	78.8	104	13	PCT-US95-0	Sequence 92, Applicati	3.10e-37
41	590	78.8	104	7	US-08-276-	Sequence 92, Applicati	3.10e-37
42	586	78.2	107	7	US-08-487-	Sequence 63, Applicati	6.39e-37
43	586	78.2	107	6	US-08-477-	Sequence 63, Applicati	6.39e-37
44	586	78.2	107	6	US-08-477-	Sequence 87, Applicati	6.39e-37
45	586	78.2	107	7	US-08-474-	Sequence 63, Applicati	6.39e-37

ALIGNMENTS

RESULT 1							
ID	US-08-474-040-86	STANDARD:	PRI:	108 AA.			
XX	AC	xxxxxx					
XX	XX	01-JAN-1900					
XX	DE	Sequence 86, Application US/08474040.					
XX	CC	Sequence 86, Application US/08474040					
XX	CC	Patent No. 5693761					
CC	CC	GENERAL INFORMATION:					
CC	CC	APPLICANT: QUEEN, Cary L.					
CC	CC	APPLICANT: CO. Man Sung					
CC	CC	APPLICANT: SCHNEIDER, William P					
CC	CC	APPLICANT: LANDOLFI, Nicholas F.					
CC	CC	APPLICANT: COELING, Kathleen E.					
CC	CC	APPLICANT: SELICK, Harold E.					
CC	CC	TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS					
CC	CC	NUMBER OF SEQUENCES: 113					
CC	CC	CORRESPONDENCE ADDRESS:					
CC	CC	ADDRESSEE: Townsend and Townsend Kourie and Crew					
CC	CC	STREET: 379 Lytton Avenue					
CC	CC	CITY: Palo Alto					
CC	CC	STATE: California					
CC	CC	COUNTRY: US					
CC	CC	ZIP: 94301					
CC	CC	COMPUTER READABLE FORM:					
CC	CC	MEDIUM TYPE: Floppy disk					
CC	CC	COMPUTER: IBM PC compatible					
CC	CC	OPERATING SYSTEM: PC-DOS/MS-DOS					
CC	CC	SOFTWARE: Patent in Release #1.0, Version #1.25					
CC	CC	CURRENT APPLICATION DATA:					
CC	CC	APPLICATION NUMBER: US/08474.040					
CC	CC	FILING DATE: 07-JUN-1995					
CC	CC	CLASSIFICATION: 536					
CC	CC	PRIOR APPLICATION DATA:					
CC	CC	APPLICATION NUMBER: US 07/634.278					
CC	CC	FILING DATE: 19-DEC-1990					
CC	CC	APPLICATION NUMBER: US 07/590.274					
CC	CC	FILING DATE: 28-SEP-1990					
CC	CC	PRIOR APPLICATION DATA:					
CC	CC	APPLICATION NUMBER: US 07/410.252					
CC	CC	FILING DATE: 13-FEB-1995					
CC	CC	PRIOR APPLICATION DATA:					
CC	CC	APPLICATION NUMBER: US 07/390.975					

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CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William W.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/PACKET NUMBER: 11R23-062410
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match          90 3%; Score 676; DB 7; Length 108;
Best Local Similarity 91.4%; Pred. No. 5.02e-44;
Matches           96; Conservative      5; Mismatches    43; Indels     1; Gaps

Db   4 LTQSPGTLSPGERATLSCPASQSVSGLYGVQKPGGAPELLVYGASSRATGIPDRF 63
Cc   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Cc   3 LTQSPGTLSPGERATLSCPASQSLSKSLYLAWTQQPQPAPFLFYDASSRATRIPIPRPF 62
Cc   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   64 SSGSGSDTFLLISRLPEDFAVYYCQYGSGLGRITFGQGTKEIK 108
Cc   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Cc   63 SSGSGSDTFLLISRLPEDFAVYYCQYGSF-PPTFGQGTKEIK 106
Cc   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      3
ID          US-09-477-728-86        STANDARD: PRT: 108 AA
XX         xxxxxx
DT          01-JAN-1900
XX
DE          Sequence 86, Application US/08477728
XX
CC          Sequence 86, Application US/08477728
CC          Patent No. 5585089
CC          GENERAL INFORMATION:
CC          APPLICANT: QUEEN, Cary L.
CC          APPLICANT: SCHNEIDER, William P.
CC          APPLICANT: SELICK, Harold E.
CC          TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC          NUMBER OF SEQUENCES: 113
CC          CORRESPONDENCE ADDRESS:
CC          ADDRESSEE: Townsend and Townsend and Crew LLP
CC          STREET: Two Embarcadero Center, 8th Floor
CC          CITY: Palo Alto
CC          STATE: California
CC          COUNTRY: US
CC          ZIP: 94111
CC          COMPUTER READABLE FORM:
CC          MEDIUM TYPE: Floppy disk
CC          COMPUTER: IBM PC compatible
CC          OPERATING SYSTEM: PC-DOS/MS-DOS
CC          SOFTWARE: PatentIn Release #1.0, Version #1.25
CC          CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER: US/08/477,728
CC          FILING DATE: 07-JUN-1995
CC          CLASSIFICATION: 424
CC          PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER: US 07/634,278
CC          FILING DATE: 19-DEC-1990
CC          PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER: US 07,590,874
CC          FILING DATE: 28-SEP-1990

```

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/210,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE: 108 AA; 11590 MW; 54079 CN;

Query Match 90.3% Score 576; DR 6; Length 108;
Best Local Similarity 91.4% Pred No 5 02e-44;
Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Db 4 LTQSPGILSLSPGEPATLSCPASQSVSSYGLWYQKPGGAPRLIYGCASSPATGIPDRF 63
QY 3 LTQSPGILSLSPGEPATLSCPASQSVSSYGLWYQKPGGAPRLIYGCASSPATGIPDRF 62

Db 64 SSGSGTDFTLTIISLEPEDEFAVYCCQYGLGTFQGGIKVEIK 108
QY 63 SSGSGTDFTLTIISLEPEDEFAVYCCQYGT-PRIFGGIKVEIK 105

RESULT 4
ID US-07-634-278-86 STANDARD: PPT: 108 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 86, Application US/07634278.
CC Sequence 86, Application US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: Co Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: CORLING, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 770 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274

CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/210,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE: 108 AA; 11590 MW; 64079 CN;

Query Match 90.3% Score 676; DR 6; Length 108;
Best Local Similarity 91.4% Pred No 5 02e-44;
Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Db 4 LTQSPGILSLSPGEPATLSCPASQSVSSYGLWYQKPGGAPRLIYGCASSPATGIPDRF 63
QY 3 LTQSPGILSLSPGEPATLSCPASQSVSSYGLWYQKPGGAPRLIYGCASSPATGIPDRF 62

Db 64 SSGSGTDFTLTIISLEPEDEFAVYCCQYGLGTFQGGIKVEIK 108
QY 63 SSGSGTDFTLTIISLEPEDEFAVYCCQYGT-PRIFGGIKVEIK 105

RESULT 5
ID PCT-US95-08743-147 STANDARD: PPT: 109 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 147, Application PC/TUS9508743.
CC Sequence 147, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (Epo)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: Pct/us95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 147:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE: 109 AA; 11779 MW; 65550 CN;

Query Match 90.1% Score 675; DR 13; Length 109;
Best Local Similarity 88.7% Pred. No 5 02e-44;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Db 2 AELTSPGTLSPGERVIVSCRASQSSVSNLYAWYQCKPGQAPRLIYGASNRATGIPD 61
 OY 1 AELTSPGTLSPGERATLSRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 60
 Db 62 RFSGSGGTDFTLTISRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 107
 OY 61 RFSGSGGTDFTLTISRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 106

RESULT 6
 ID US-08-276-852-147 STANDARD: PRT: 109 AA.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 147, Application US/08276852.
 CC Sequence 147, Application US/08276852.
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis P
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10466 No 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1992
 CC FILING DATE: 07/954,148
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCRI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 147:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 109 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 109 AA: 11779 MW: 65550 CN;

Query Match 90.1%; Score 675; DB 7; Length 109;
 Best Local Similarity 88.7%; Pred. No. 6.02e-44;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0.

Db 2 AELTSPGTLSPGERVIVSCRASQSSVSNLYAWYQCKPGQAPRLIYGASNRATGIPD 61
 OY 1 AELTSPGTLSPGERATLSRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 60

OY 1 AELTSPGTLSPGERATLSRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 60
 Db 62 RFSGSGGTDFTLTISRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 107
 OY 61 RFSGSGGTDFTLTISRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 106

RESULT 7
 ID US-08-276-852-99 STANDARD: PRT: 108 AA.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 99, Application US/08276852.
 CC Sequence 99, Application US/08276852.
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis P
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC FILING DATE: 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCRI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 99:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 108 AA: 11738 MW: 63142 CN;

Query Match 89.5%; Score 670; DB 7; Length 108;
 Best Local Similarity 89.6%; Pred. No. 1.50e-43;
 Matches 95; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

Db 1 ELTOSPGTLSPGERATLSRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 60
 OY 2 ELTOSPGTLSPGERATLSRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 61
 Db 61 RFSGSGGTDFTLTISRLEPEDEFAVYCCQYSSGSGTGGTKVEIK 106

CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65967 CN;
Query Match 88.9%; Score 666; DB 13; Length 108;
Best Local Similarity 86.8%; Pred No 3 10e-43;
Matches 95; Conservative 6; Mismatches 4; Indels 1; Gaps 1;
Db 1 ELTQSPGTLSPGPRATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 60
QY 2 ELTQSPGTLSPGPRATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 61
Db 61 FSGSGSGDTFTLSISPLEPDEFVAVYCCQYGTSPWTFGGTKVEIK 106
QY 62 FSGSGSGDTFTLSISPLEPDEFVAVYCCQYGTSPWTFGGTKVEIK 106
RESULT 11
ID US-08-276-852-149 STANDARD: PRT: 111 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 149, Application US/08276852.
XX
CC Sequence 149, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10566 No. 56521st Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-534-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA; 11956 MW; 63169 CN;
Query Match 88.9%; Score 666; DB 7; Length 111;
Best Local Similarity 86.8%; Pred No 3 10e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Db 2 AELTQSPGTLSPGPRATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 61
QY 1 AELTQSPGTLSPGPRATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 60
Db 62 FSGSGSGADFTLSISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 107
QY 61 FSGSGSGADFTLSISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 106
RESULT 12
ID PCT-US95-08743-149 STANDARD: PRT: 111 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 149, Application PC/TUS9508743.
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CC Sequence 149, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA; 11956 MW; 63169 CN;
Query Match 88.9%; Score 666; DB 13; Length 111;
Best Local Similarity 86.8%; Pred No 3 10e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Db 2 AELTQSPGTLSPGPRATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 61
QY 1 AELTQSPGTLSPGPRATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 60
Db 62 FSGSGSGADFTLSISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 107
QY 61 FSGSGSGADFTLSISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 106
RESULT 13
ID PCT-US95-08743-90 STANDARD: PRT: 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX

DE • Sequence 90, Application PC/TUS9508743
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 CC Sequence 90, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PC/TUS95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
 CC INFORMATION FOR SEQ ID NO: 90:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 107 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 107 AA: 11705 MW: 62938 CN:
 SQ
 Query Match 88.5% Score 663; DB 13; Length 107;
 Best Local Similarity 85.8% Pred. No. 5,36e-43;
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;
 Db 1 ELTQSPGTLSPGEPATLSCPASOSLSNNYAWYQKPGQAPRLIYSSSTRIGIPDP 60
 QY 2 ELTQSPGTLSPGEPATLSCPASOSLSNNYAWYQKPGQAPRLIYSSSTRIGIPDP 61
 Db 61 FSGGSGSTDTLTISRLPEDEFAVYCYGHYNSVYFGGKLEIK 106
 QY 62 FSGGSGSTDTLTISRLPEDEFAVYCYGHYNSVYFGGKLEIK 106
 RESULT 14
 ID US-08-276-852-90 STANDARD: PRT: 107 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 90, Application US/08276852
 XX
 CC Sequence 90, Application US/08276852
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R.
 CC APPLICANT: Barbas, Carlos F.
 CC APPLICANT: Leiner, Richard A.
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESS: Patent Counsel
 CC STREET: 10665 No. 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCP1452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 90:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 107 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 107 AA: 11705 MW: 62938 CN:
 SQ
 Query Match 88.5% Score 563; DB 7; Length 107;
 Best Local Similarity 85.8% Pred. No. 5,36e-43;
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;
 Db 1 ELTQSPGTLSPGEPATLSCPASOSLSNNYAWYQKPGQAPRLIYSSSTRIGIPDP 60
 QY 2 ELTQSPGTLSPGEPATLSCPASOSLSNNYAWYQKPGQAPRLIYSSSTRIGIPDP 61
 Db 61 FSGGSGSTDTLTISRLPEDEFAVYCYGHYNSVYFGGKLEIK 106
 QY 62 FSGGSGSTDTLTISRLPEDEFAVYCYGHYNSVYFGGKLEIK 106
 RESULT 15
 ID PCT-US93-08786-23 STANDARD: PRT: 109 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 23, Application PC/TUS9308786.
 XX
 CC Sequence 23, Application PC/TUS9308786
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R.
 CC APPLICANT: Barbas, III, Carlos F.
 CC APPLICANT: Chanock, Robert M.
 CC APPLICANT: Murphy, Brian P.
 CC APPLICANT: Crowe, Jr., James E.
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1860 Century Park East, Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08786
 CC FILING DATE: 16-SEP-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:

CC NAME: Wetherell, Jr., Ph.D., John R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD-2791
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 23:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 109 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: rsv 6L; 11L; 21L; anad 22L
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..109
 CC SEQUENCE 109 AA: 12099 MW: 62556 CN;
 Query Match 87.6%; Score 656; DB 11; Length 109;
 Best Local Similarity 86.0%; Pred. No. 1.92e-42;
 Matches 92; Conservative 10; Mismatches 4; Indels 1; Gaps 1;
 Db 2 AELTQSPGTLSPGERATLSRATOSISSNYLAWYQORPGQAPRLIIYGASNRATDIPD 61
 QY 1 AELTQSPGTLSPGERATLSRATOSISSNYLAWYQORPGQAPRLIIYGASNRATDIPD 61
 Db 62 RFSGSGSGTDFTLTISRLEPEDFAMYYCQYDISPYTFGQGTKEIK 108
 QY 61 RFSGSGSGTDFTLTISRLEPEDFAMYYCQYGTPTTFGQGTKEIK 106

Search completed: Tue Feb 24 07:57:22 1998
 Job time : 6 secs.

MUSE RELEASE

Release 2 ID John F Collins, Biocomputing Research Unit
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Distribution rights by IntelliGenetics, Inc.
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:25:09 1998 MasPar time 4.88 Seconds
Tabular output not generated. 464,957 Million cell updates/sec

Title: >US-08-844-215-12
Description: (1-107) from US08844215.pep
Perfect Score: 769
Sequence: 1 AEUOSPGILSLVGERAIL CQVYQSPPVTFGGTKVEIK 107
Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 40.305; Variance 68.586; scale 0.588

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	676	87.9	129	5	KV3M_HUMAN	IG KAPPA CHAIN PRECUR	1.78e-131
2	673	87.5	129	5	KV3L_HUMAN	IG KAPPA CHAIN PRECUR	9.36e-131
3	672	87.4	109	5	KV3E_HUMAN	IG KAPPA CHAIN V-III	1.63e-130
4	669	87.0	109	5	KV3R_HUMAN	IG KAPPA CHAIN V-III	8.58e-130
5	658	85.6	108	5	KV3A_HUMAN	IG KAPPA CHAIN V-III	3.98e-127
6	655	85.2	109	5	KV3D_HUMAN	IG KAPPA CHAIN V-III	1.99e-126
7	642	83.5	109	5	KV3G_HUMAN	IG KAPPA CHAIN V-III	2.63e-123
8	625	81.3	129	5	KV3H_HUMAN	IG KAPPA CHAIN PRECUR	3.12e-119
9	604	78.5	128	5	KV3K_HUMAN	IG KAPPA CHAIN PRECUR	3.30e-114
10	598	77.8	109	5	KV3F_HUMAN	IG KAPPA CHAIN V-III	8.95e-113
11	587	76.3	100	5	KV3C_HUMAN	IG KAPPA CHAIN PRECUR	3.77e-110
12	552	71.8	108	5	KVIM_HUMAN	IG KAPPA CHAIN V-I RE	9.65e-102
13	544	70.7	108	5	KVIA_HUMAN	IG KAPPA CHAIN V-I RE	6.37e-100
14	544	70.7	114	5	KVIA_HUMAN	IG KAPPA CHAIN V-IV R	6.37e-100
15	542	70.5	115	5	KVIL_HUMAN	IG KAPPA CHAIN PRECUR	1.90e-99
16	538	70.0	109	5	KVIN_HUMAN	IG KAPPA CHAIN V-I RE	1.68e-98
17	536	69.7	134	5	KVAC_HUMAN	IG KAPPA CHAIN PRECUR	5.02e-98
18	534	69.4	104	5	KVIH_HUMAN	IG KAPPA CHAIN V-I RE	1.49e-97
19	532	69.2	109	5	KVIB_HUMAN	IG KAPPA CHAIN V-I RE	4.46e-97
20	529	68.9	108	5	KVID_HUMAN	IG KAPPA CHAIN V-I RE	2.28e-96
21	529	68.9	108	5	KVAY_HUMAN	IG KAPPA CHAIN V-I RE	2.24e-96
22	523	69.8	115	5	KV3J_HUMAN	IG KAPPA CHAIN PRECUR	2.28e-96

23	524	68.1	108	5	KV1K_HUMAN	IG KAPPA CHAIN V-I RE	3.47e-95
24	524	68.1	108	5	KV1O_HUMAN	IG KAPPA CHAIN V-I RE	3.47e-95
25	523	68.0	108	5	KV1L_HUMAN	IG KAPPA CHAIN PRECUR	5.98e-95
26	522	67.9	132	5	KV1B_HUMAN	IG KAPPA CHAIN PRECUR	1.03e-94
27	520	67.6	108	5	KV1F_HUMAN	IG KAPPA CHAIN V-I RE	3.06e-94
28	518	67.4	108	5	KV1P_HUMAN	IG KAPPA CHAIN V-I RE	9.10e-94
29	517	67.2	108	5	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE	1.57e-93
30	515	67.0	111	5	KV3M_MOUSE	IG KAPPA CHAIN V-III	4.65e-93
31	509	66.2	108	5	KV1E_HUMAN	IG KAPPA CHAIN V-I RE	1.21e-91
32	508	66.1	108	5	KV1P_HUMAN	IG KAPPA CHAIN V-I RE	2.09e-91
33	508	66.1	111	5	KV3L_MOUSE	IG KAPPA CHAIN V-III	2.09e-91
34	506	65.8	111	5	KV3O_MOUSE	IG KAPPA CHAIN V-III	6.18e-91
35	506	65.8	129	5	KV1W_HUMAN	IG KAPPA CHAIN PRECUR	6.18e-91
36	504	65.5	129	5	KV1X_HUMAN	IG KAPPA CHAIN PRECUR	1.84e-90
37	503	65.4	112	5	KV3E_MOUSE	IG KAPPA CHAIN V-III	3.15e-90
38	503	65.4	135	5	KV3B_MOUSE	IG KAPPA CHAIN PRECUR	3.15e-90
39	501	65.1	108	5	KV1C_HUMAN	IG KAPPA CHAIN V-I RE	9.33e-90
40	501	65.1	111	5	KV3N_MOUSE	IG KAPPA CHAIN V-III	9.33e-90
41	499	64.9	111	5	KV3D_MOUSE	IG KAPPA CHAIN V-III	2.76e-89
42	499	64.9	111	5	KV3H_MOUSE	IG KAPPA CHAIN V-III	2.76e-89
43	496	64.5	110	5	KV3P_MOUSE	IG KAPPA CHAIN V-III	1.40e-88
44	496	64.5	111	5	KV3Q_MOUSE	IG KAPPA CHAIN V-III	1.40e-88
45	495	64.4	109	5	KV1T_HUMAN	IG KAPPA CHAIN V-I RE	2.42e-88

ALIGNMENTS

RESULT 1 STANDARD: PRT: 129 AA.
AC P18136:
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98171307.
RA KIPPS T J, TOMHAVE E, CHEN P P, CAPSON D A.;
PL J EXP MED 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC ANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHO-
CC LEUKEMIA
DR PIR: P10021: K3HUH1.
DR HSSP: P01607: 1DPB.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JKI SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: DD09C169 CRC32:

Query Match 87.9%; Score 576; DB 5; Length 129;
Best Local Similarity 88.6%; Pred. No. 1.78e-131;
Matches 93; Conservative 8; Mismatches 4; Indels 0; Gaps 0

Db 24 ltsqgtlslspgeratiscrasgsvssylawqgkpgqgprlllygssratgipdrf 83
|||||
QY 3 LQSQGTSLSLVGERATISCRASGNIYSGYLOWQQKQGPRLIYGCASNRATGIPDRF 62
|||||
EY 94 ssssgstgftllststslxkxfayvvyggygssgslfsgstkvsk 128
|||||
QY 43 SSSGSGTFTLLSLSESEFAVYVYVGYGSGPTTFGGTAVELY 107
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Best Local Similarity 90.5%; Pred. No. 1.53e-130;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 4 ltqspgtlslspgeratlsctasqsvssylawygkqkqgqprlllygassratgipdrf 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3 LTQSPGTLSSLVGERATLSLCPASQNIYSGYLGMWYQKQKQPPRLIYGASNPATGIPDPF 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 sqsgsgtdftltisrlepedfavyycqygslgrtfgggtkveik 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 SGSGSGTDFTLTISRLESEDFAVYVCOQYGSPPYTFGGGTKEIK 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
ID KV3E_HUMAN STANDARD: PRT: 109 AA
AC P01620;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
RP SEQUENCE
RX MEDLINE: 82046598
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
    ACTIVITY.
CC PIR: A01892; K3HUS1
DP HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 00B5DD5D CRC32;

Query Match 87.0%; Score 669; DB 5; Length 109;
Best Local Similarity 86.7%; Pred. No. 8.58e-130;
Matches 91; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltqspgtlslspgeratlsctasqsvssylawygkqkqgqprlllygassratgipdrf 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3 LTQSPGTLSSLVGERATLSLCPASQNIYSGYLGMWYQKQKQPPRLIYGASNPATGIPDPF 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 sqsgsgtdftltisrlepedfavyycqygslgrtfgggtkveik 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 SGSGSGTDFTLTISRLESEDFAVYVCOQYGSPPYTFGGGTKEIK 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
ID KV3E_HUMAN STANDARD: PRT: 108 AA.
AC P01619;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (B6).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
RP SEQUENCE.
RX MEDLINE: 2:301-304(1969).
RA FEES LETT.
CC -1- THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01891; K3HUR6
DP HSSP: P01607; 1MCP
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 46DAP68E CRC32;

Query Match 85.6%; Score 658; DB 5; Length 108;
Best Local Similarity 80.0%; Pred. No. 3.75e-127;

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Matches 84: Conservative 17: Mismatches 4: Indels 0: Gaps 0:

Db 4 ltsqpatlslsgeratlsrcaalssrgylawygqkqgqprlliyvassratgipdrf 63
 QY 3 LTQSPATLSLSEGEATLSRCAASNIYSYLWYQKPKQPPPLIYCAENPATGIDPDRF 62
 Db 64 sgsasgdtfltlslrlepedfavyycqygssprfsgqtkveik 108
 QY 63 SSGSGDTFTLISRLSEDFAVYCCQYGGSPPIYFGQTKVEIK 107

RESULT 6
 ID KV3D HUMAN STANDARD: PRT: 109 AA.
 AC P04206:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (T1)
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 72188439
 RA SUTER L., BARNIKOL H., WATANABE S., HILSCHMANN N.,
 PL HORPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972)
 CC 1- THE C REGION OF THIS CHAIN HAS THE INV (3) MAPKER.
 CC 1- THIS IS A HENCE-JONES PROTEIN
 PIR: A01895; K3HUT1.
 DR HSSP: P01607; 21MM.
 KW IMMUNOGLOBULIN V REGION: RENGE-JONES PROTEIN.
 FT DISULFID 23 99 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11788 MW: D03795B1 CPG32:

Query Match 85.2%: Score 655: DB 5: Length 109:

Best Local Similarity 85.7%: Pred. No. 1 94e-124:

Matches 90: Conservative 11: Mismatches 4: Indels 0: Gaps 0:

Db 4 ltsqpatlslsgeratlsrcaalssrgylawygqkqgqprlliyvassratgipdrf 63
 QY 3 LTQSPATLSLSEGEATLSRCAASNIYSYLWYQKPKQPPPLIYCAENPATGIDPDRF 62
 Db 64 sgsasgdtfltlslrlepedfavyycqygssprfsgqtkveik 108
 QY 63 SSGSGDTFTLISRLSEDFAVYCCQYGGSPPIYFGQTKVEIK 107

RESULT 7
 ID KV3G HUMAN STANDARD: PRT: 109 AA
 AC P04206:
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (GOL) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 86230578.
 RA NEWKIRK M., CHEN P.P., CARSON D.A., POSNETT D., CAPRA J.D.:
 PL MOL. IMMUNOL. 23:239-244(1986)
 DR PIR: A01894; K3HUGO
 DR HSSP: P01607; 1DPR.
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11840 MW: 893DCC4A CPG32:

Query Match 83.5%: Score 642: DB 5: Length 109:

Best Local Similarity 85.7%: Pred. No. 2 6e-123:

Matches 90: Conservative 9: Mismatches 7: Indels 0: Gaps 0:

Db 4 ltsqpatlslsgeratlsrcaalssrgylawygqkqgqprlliyvassratgipdrf 63
 QY 3 LTQSPATLSLSEGEATLSRCAASNIYSYLWYQKPKQPPPLIYCAENPATGIDPDRF 62
 Db 64 sgsasgdtfltlslrlepedfavyycqygssprfsgqtkveik 108
 QY 63 SSGSGDTFTLISRLSEDFAVYCCQYGGSPPIYFGQTKVEIK 107

RESULT 8
 ID KV3H HUMAN STANDARD: PRT: 129 AA.
 AC P04207:
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (CLL) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86177570.
 RA JIRIK F.P., SORGE J., HEITZMANN J.G., CURD J.G., CHEN P.P.,
 PA GOLDFIEN P., CARSON D.A.:
 PL PROC. NATL. ACAD. SCI. U.S.A. 92:2195-2199(1986).
 DR EMBL: M12740; G553486;
 DR PIR: A01898; K3HUGL
 DR HSSP: P01607; 1AAG.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (CLL).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA: 14475 MW: 2F244868 CPG32:

Query Match 81.3%: Score 625: DB 5: Length 129:

Best Local Similarity 82.1%: Pred. No. 3 12e-119:

Matches 87: Conservative 10: Mismatches 7: Indels 2: Gaps 2:

Db 24 mtqspatlsvsgoratlscrasqsvsnllawygqkqgqprlliyvassratgipdrf 82
 QY 3 LTQSPATLSLSEGEATLSRCAASNIYSYLWYQKPKQPPPLIYCAENPATGIDPDRF 62
 Db 93 sgsasgdtfltlslrlepedfavyycqygssprfsgqtkveik 128
 QY 63 SSGSGDTFTLISRLSEDFAVYCCQYGGSPPIYFGQTKVEIK 107

RESULT 9
 ID KV3K HUMAN STANDARD: PRT: 128 AA.
 AC P06311:
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (IAPC/BL41).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA KLOBECK H.G., MEINDI A., COMBETATON G., SCHIMM A., ZACHAU H.G.:
 PL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: J00021; G33179;
 DR PIR: A01899; K3H041.

OC EUTHERIA; PRIMATES.
[1]
RN
PP SEQUENCE FROM N.A.
FX MEDLINE: 84093600
PA BENTLEY D L.;
CC NATPE 307-77-(1984).
CL -! THIS GENE WAS ISOLATED FROM THE NG9/9 1 HYBRIDOMA.
DR PIR: A01894; K3HUNG.
OR HSP: P01607; IAAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL; HYBRIDOMA.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NG9).
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 99A75223 CPQ32;

Query Match 76.3%; Score 587; DB 5; Length 100;
Best Local Similarity 85.9%; Pred. No. 3,77e-110;
Matches 79; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Db 8 lkspgptlsgpgaralkscraasqssvslwyqkkgqagprlllygastratqpdf 67
QY 3 LFQSPGPTLSUGVKRATLSCRAASQSVSLWYQKKGQAGPRLLLYGASTRATQPDF 62
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 sgasgtfttlrlepdefavyyqgygn 99
 |||||:|||||:|||||:|||||:|||||:|||||:
QY 63 SSGSGTDFTLISRLESEDAFYVYCQYGSP 94
 |||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
ID KVIM_HUMAN STANDARD; PRT: 108 AA.
AC P01605;
DT 21-JUL-1986 (PEL 01, CREATED)
DT 21-JUL-1986 (PEL 01, LAST SEQUENCE UPDATE)
DI 01-JAN-1988 (PEL 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAY).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
PP [1]
PN
RX MEDLINE: 77038198
PL CAPPA J.D., KLAPPER D.G.;
PL SCAND. J. IMMUNOL 5:677-684(1976).
CC -! THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WHICH WHICH IT SHAPES CERTAIN IDIOTYPIC DETERMINANTS.
CC -! THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
CC
DR PIR: A01871; K1HULY.
DR HSP: P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 22228RQC CPQ32;

Query Match 71.8%; Score 552; DB 5; Length 108;
Best Local Similarity 68.2%; Pred. No. a 05e-102;
Matches 73; Conservative 22; Mismatches 9; Indels 3; Gaps 3;

Db 3 qmtpgselvsydvrtlcqasqvay-naylnwvgdggplapkllygastraqvpsf 61
 |||:||||:||||:||||:||||:||||:||||:||||:|||||:
QY 2 ELFCGPATLSSVGERATLSCRAASQSVSLWYQKKGQAGPRLLLYGASTRATQPDF 61
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 fsasgst-dfftllslapadialtycgvnawer-tfgsttkzyevk 107

QY 62 FSGSGGDTLTISRLESEDFAVYCOQYGS-PPTFGQTKVEIK 107

RESULT 13

ID KV1V_HUMAN STANDARD: PRI: 108 AA.
AC P04430:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (BAN)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 86174817.
RA DWULET F E, O'CONNOR T P, BENSON M D.;
PL MOL. IMMUNOL. 23:73-79(1986).
DR PIR: A01878; K1HUBN.
DR HSP: P01607; 1FVC.
KW IMMUNOGLOBULIN V REGION; AMYLOID.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 0D44DA0A CRC32.

Query Match 70.7%; Score 544; DB 5; Length 108.
Best Local Similarity 66.0%; Pred. No. 6.37e-100;
Matches 70; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Db 3 qltqpsissavgrvltitcrasqsv-yvawfqgkpkapksliydastlqsgvpsn 61
QY 2 ELTQSPGTLISVSGEPATLSCPASQNTYSGYLGMWYCKPGCPPPELLIYGASNRATGIPDR 61

Db 62 ftqsgsgtdftltisslpedafayyccqynsyptfgqtkvqik 107
QY 62 FSGSGGDTLTISRLESEDFAVYCOQYGS-PPTFGQTKVEIK 107

RESULT 14

ID KV4A_HUMAN STANDARD: PRI: 114 AA.
AC P01625:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-IV REGION (LEN)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 76004342.
RA SCHNEIDER M., HILSCHMANN N.;
PL HOPPE-SEYLER'S Z PHYSIOL. CHEM. 356:507-557(1975).
DR [2]
RP REVISION TO 9.
RA SALOMON A.;
RL SUBMITTED (AUG-1996) TO THE SWISS-PROT DATA BANK.
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MAPREP.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01933; K4HBLN.
DR HSP: P01507; 1MCP.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 41 55 FRAMEWORK 2.

FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 63 94 FRAMEWORK 3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 113 FRAMEWORK 4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; EEICE0BE CRC32.

Query Match 70.7%; Score 544; DB 5; Length 114.
Best Local Similarity 70.0%; Pred. No. 6.37e-100;
Matches 77; Conservative 20; Mismatches 8; Indels 5; Gaps 2;

Db 4 mtsqpsdlavslgeratlnckssqv-yssnsknvjawyyqkpaqpklliyas-resq 61
QY 3 LTQSPGTLISVSGEPATLSCPASQNT-YSG-----YLGWYCKPSPPELLIYGASNRATG 67

Db 64 vpdfrfsgsgtdftltisslqaedvavyyccqyyspysfqqtkleik 113
QY 58 LPDFFSGSGSGIDFTLTISLSELEFAVYCCQYGSPPYTFGQTKVEIK 107

RESULT 15

ID KV3I_HUMAN STANDARD: PRI: 115 AA.
AC P04433:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PPECUPSCP V-III REGION (V5) (FRAGMENT).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932.
RA PECH M., ZACHAU H.G.;
PL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL: X01668; -; NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HUVG.
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.

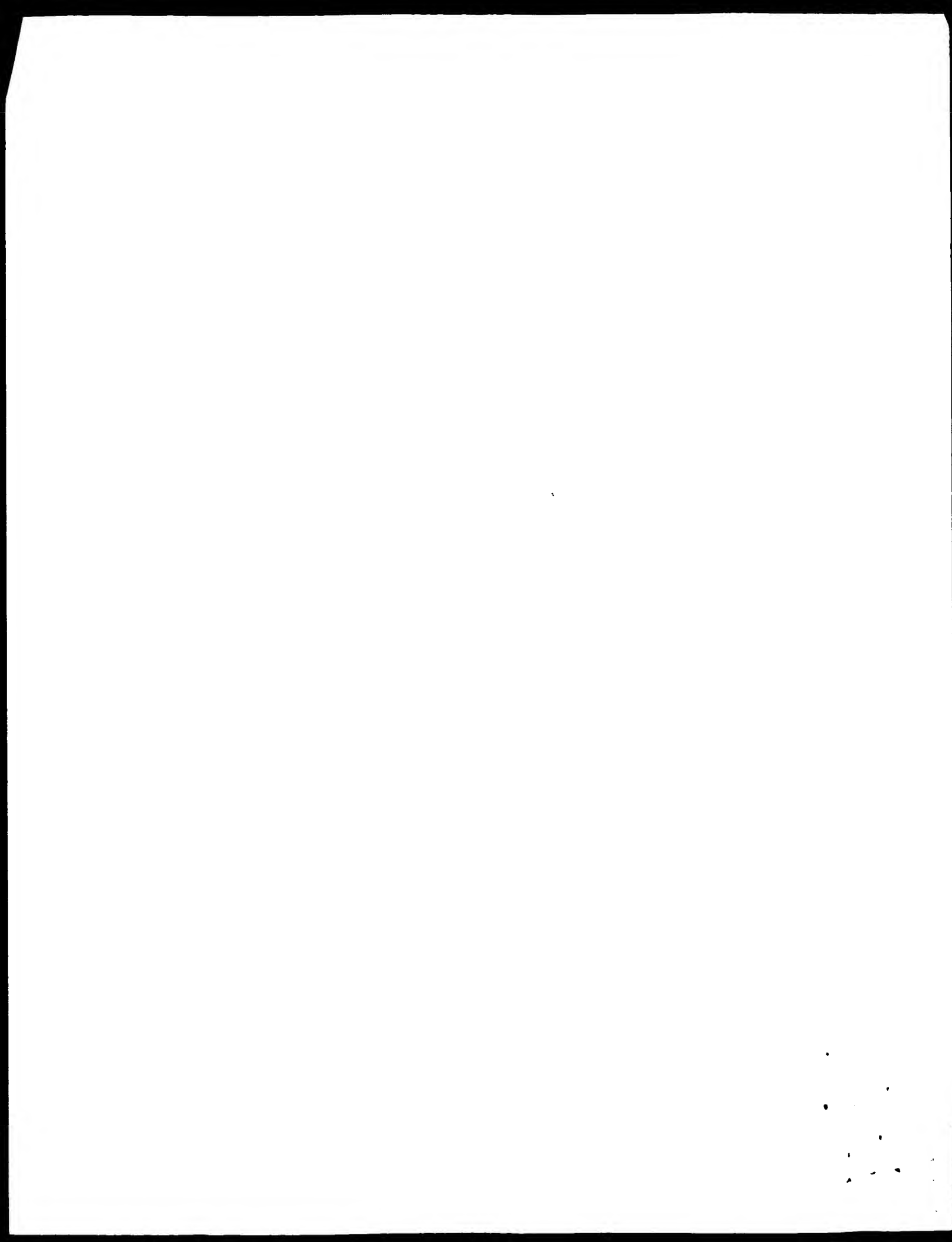
FT CHAIN 1 20
FT DOMAIN 21 >115 IG KAPPA CHAIN V-III REGION (V5).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 37E182FC CRC32.

Query Match 70.5%; Score 542; DB 5; Length 115.
Best Local Similarity 86.4%; Pred. No. 1.50e-99;
Matches 76; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

Db 24 ltqspatlsipgeratlnckssqv-ssylawyyqkpaqpklliydsnratqipaif 82
QY 3 LTQSPGTLISVSGEPATLSCPASQNTYSGYLGMWYCKPGCPPPELLIYGASNRATGIPLF 62

Db 83 sgsqsgtdftltisslpedafayyccq 110
QY 63 SSGSGGDTLTISRLESEDFAVYCOQ 90

Search completed: Tue Feb 24 07:25:27 1998
Job time : 18 secs.



ID US-07-634-278-86 STANDARD: PPT: 108 AA.
XX
AC
XX
XX
DT 01-JAN-1900
XX
DE Sequence 86, Application US/07634278.
XX
CC Sequence 86, Application US/07634278.
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO. 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN;

Query Match 87.4%; Score 672; DB 6; Length 108;
Best Local Similarity 90.5%; Pred. No. 2,76e-47;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 4 LTQSPGTLSSGGERATLSCRASQSVSSGYLWYQKQPGQAPPLLIYASSPAIGIPIWPF 63
QY 3 LTQSPGTLSSGGERATLSCRASQSVSSGYLWYQKQPGQAPPLLIYASSPAIGIPIWPF 62
Db 64 SSGSGTDFTLTISRLPEDFAVYVCCQYGSGRFTFGGKTKVEIK 108
QY 63 SSGSGTDFTLTISRLPEDFAVYVCCQYGSGRFTFGGKTKVEIK 107

RESULT 5
ID US-08-474-040-86 STANDARD: PPT: 108 AA.
XX
AC
XX
XX
DT 01-JAN-1900
XX
DE Sequence 86, Application US/08474040.
XX
CC Sequence 86, Application US/08474040.
CC Patent No. 5693761
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,040
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO. 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN;

Query Match 87.4%; Score 672; DB 7; Length 108;
Best Local Similarity 90.5%; Pred. No. 2,76e-47;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 4 LTQSPGTLSSGGERATLSCRASQSVSSGYLWYQKQPGQAPPLLIYASSPAIGIPIWPF 63
QY 3 LTQSPGTLSSGGERATLSCRASQSVSSGYLWYQKQPGQAPPLLIYASSPAIGIPIWPF 62
Db 64 SSGSGTDFTLTISRLPEDFAVYVCCQYGSGRFTFGGKTKVEIK 108

QY 63 SGGSGTDLTISPLEDEFAVYCCQYGSPPYIPGSGTKVEIK 107

RESULT 6

ID US-08-487-200-86 STANDARD: PRT: 108 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 86, Application US/08487200.

XX Sequence 86, Application US/08487200

CC Patent No. 5693762

CC GENERAL INFORMATION:

CC APPLICANT: QUEEN, Cary L.

CC APPLICANT: CO, Man Sung

CC APPLICANT: SCHNEIDER, William P.

CC APPLICANT: LANDOLEI, Nicholas F.

CC APPLICANT: COELINGH, Kathleen L.

CC APPLICANT: SELICK, Harold E.

CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

CC NUMBER OF SEQUENCES: 113

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend and Crew

CC STREET: 379 Lytton Avenue

CC CITY: Palo Alto

CC STATE: California

CC COUNTRY: US

CC ZIP: 94301

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1 25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/487,200

CC FILING DATE: 7-JUN-1995

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION NUMBER: US 07/634,278

CC FILING DATE: 19-DEC-1990

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/590,274

CC FILING DATE: 28-SEP-1990

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/310,252

CC FILING DATE: 13-FEB-1989

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/290,975

CC FILING DATE: 28-DEC-1988

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Smith, William M.

CC REGISTRATION NUMBER: 30,223

CC REFERENCE/DOCKET NUMBER: 11823-002610

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 326-2400

CC TELEFAX: (415) 326-2422

CC INFORMATION FOR SEQ ID NO: 86:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 108 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 87.4%: Score 672; DB 7; Length 108;

Best-Local Similarity 90.5%: Pred No 2 76e-47;

Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 4 LTQSPGTLISLSPGERATISCPASQSSVSSYGLGWYQKPGAPPLIYGASNPATIPDPF 63

|||||

QY 3 LTQSPGTLISLSPGERATISCPASQSSVSSYGLGWYQKPGAPPLIYGASNPATIPDPF 62

DB 64 SGGSGTDLTISPLEDEFAVYCCQYGSPPYIPGSGTKVEIK 108

QY 63 SGGSGTDLTISPLEDEFAVYCCQYGSPPYIPGSGTKVEIK 107

RESULT 7

ID PCT-US93-08786-23 STANDARD: PRT: 109 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 23, Application PC/TUS9308786.

XX Sequence 23, Application PC/TUS9308786

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R.

CC APPLICANT: Barbas, III, Carlos F.

CC APPLICANT: Chaddock, Robert M.

CC APPLICANT: Murphy, Brian F.

CC APPLICANT: Crowe, Jr., James E.

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC NUMBER OF SEQUENCES: 29

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Spensley Horn Jubas & Lubitz

CC STREET: 1880 Century Park East, Suite 500

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90067

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/08786

CC FILING DATE: 16-SEP-1993

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Wetherell, Jr., Ph.D., John P.

CC REGISTRATION NUMBER: 31,678

CC REFERENCE/DOCKET NUMBER: FD-2791

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 455-5100

CC TELEFAX: (619) 455-5110

CC INFORMATION FOR SEQ ID NO: 23:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 109 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC IMMEDIATE SOURCE:

CC CLONE: rsv 6L; 11L; 21L; anad 22L

CC FEATURE:

CC NAME/KEY: Peptide

CC LOCATION: 1..109

CC SEQUENCE 109 AA: 12099 MW: 62556 CN:

Query Match 87.4%: Score 672; DB 11; Length 109;

Best-Local Similarity 86.0%: Pred No 2 76e-47;

Matches 92; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

DB 2 AELTQSPGTLISLSPGERATISCPATSSISNLYAWYQKPGAPPLIYGASNPATIPDP 61

QY 1 AELTQSPGTLISLSPGERATISCPATSSISNLYAWYQKPGAPPLIYGASNPATIPDP 60

DB 62 RFSGSGSTDLTISPLEDEFAVYCCQYGSPPYIPGSGTKVEIK 108

|||||

QY * 61 FSGSGGDTFTLISPLESEDFAVYQQYSGSPPTFGGKVEIK 107

RESULT 8
ID PCT-US95-08743-86 STANDARD: PPT: 108 AA.

XX xxxxxx

DT 01-JAN-1900

XX Sequence 86, Application PC/TUS9508743

XX Sequence 86, Application PC/TUS9508743

XX GENERAL INFORMATION:

CC APPLICANT: FLOPPY DISK

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC COMPUTER PEADABLE FORM:

CC MEDIUM TYPE: FLOPPY DISK

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1 0, Version #1 25 (EPO)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US95/08743

CC FILING DATE: 11-JUL-1995

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/276,852

CC FILING DATE: 18-JUL-1994

CC INFORMATION FOR SEQ ID NO: 86:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 108 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 108 AA; 11769 MW; 65957 CN;

Query Match 87.1%; Score 670; DB 13; Length 108;

Best Local Similarity 87.7%; Pred. No. 4.09e-47;

Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGERATLSRLESEDFAVYQQYSGSPPTFGGKVEIK 106

QY 2 ELTQSPGTLSPGERATLSRLESEDFAVYQQYSGSPPTFGGKVEIK 107

Db 61 FSGSGGDTFTLISPLESEDFAVYQQYSGSPPTFGGKVEIK 106

QY 62 FSGSGGDTFTLISPLESEDFAVYQQYSGSPPTFGGKVEIK 107

RESULT 9

ID US-08-276-852-86 STANDARD: PPT: 108 AA.

XX xxxxxx

DT 01-JAN-1900

XX Sequence 86, Application US/08276852.

XX Sequence 86, Application US/08276852

XX GENERAL INFORMATION:

XX APPLICANT: Burton, Dennis R

XX APPLICANT: Barbas, Carlos F

XX APPLICANT: Lerner, Richard A

XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

XX NUMBER OF SEQUENCES: 170

XX CORRESPONDENCE ADDRESS:

XX ADDRESSEE: The Scripps Research Institute, Office of

XX ADDRESSEE: Patent Counsel

XX STREET: 10666 N. 555238th Torrey Pines Road, Suite 220,

XX STREET: Mail Drop 10C8

XX CITY: La Jolla

XX STATE: CA

XX COUNTRY: USA

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276,852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SC1452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 86:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 108 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 108 AA; 11769 MW; 65957 CN;

Query Match 87.1%; Score 670; DB 7; Length 108;

Best Local Similarity 87.7%; Pred. No. 4.09e-47;

Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGERATLSRLESEDFAVYQQYSGSPPTFGGKVEIK 106

QY 2 ELTQSPGTLSPGERATLSRLESEDFAVYQQYSGSPPTFGGKVEIK 107

Db 61 FSGSGGDTFTLISPLESEDFAVYQQYSGSPPTFGGKVEIK 106

QY 62 FSGSGGDTFTLISPLESEDFAVYQQYSGSPPTFGGKVEIK 107

RESULT 10

ID US-08-276-852-90 STANDARD: PPT: 107 AA.

XX xxxxxx

DT 01-JAN-1900

XX Sequence 90, Application US/08276852.

XX Sequence 90, Application US/08276852

XX Patent No. 5652138

XX GENERAL INFORMATION:

XX APPLICANT: Burton, Dennis R

XX APPLICANT: Barbas, Carlos F

XX APPLICANT: Lerner, Richard A

XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

XX NUMBER OF SEQUENCES: 170

XX CORRESPONDENCE ADDRESS:

XX ADDRESSEE: The Scripps Research Institute, Office of

XX ADDRESSEE: Patent Counsel

XX STREET: 10666 N. 5552138th Torrey Pines Road, Suite 220,

XX STREET: Mail Drop 10C8

XX CITY: La Jolla

XX STATE: CA

XX COUNTRY: USA


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XX Sequence 147, Application US/98/2682
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10556 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 147:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 109 AA: 11779 MW: 55550 CN:

Query Match 85.6%; Score 658; DB 7; Length 109;
Best Local Similarity 85.9%; Pred. No. 4,31e-46;
Matches 93; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Db 2 AELTQSPGILSLSPGEPAITLSCPASQVNSNYLAWYQKPGQCAPPLLYGASNPATGIPD 61
QY 1 AELTQSPGILSLSPGEPAITLSCPASQVNSNYLAWYQKPGQCAPPLLYGASNPATGIPD 60
Db 62 PFSGSGSGDTLTISPLPEPFANVYCOQYGGSSG-IFGQTKIEK 107
QY 61 RFSGSGSGDTLTISPLPEPFANVYCOQYGGSPPTFGQTKIEK 107

RESULT 14
ID PCI-US95-08743-110 STANDARD: PRT: 108 AA
XX
XX
XX
XX 01-JAN-1900
XX Sequence 110, Application PC/TUS9508743
XX Sequence 110, Application PC/TUS9508743
XX GENERAL INFORMATION:
XX APPLICANT: Burton, Dennis R
XX APPLICANT: Barbas, Carlos F
XX APPLICANT: Lerner, Richard A
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX NUMBER OF SEQUENCES: 170
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: The Scripps Research Institute, Office of
XX ADDRESSEE: Patent Counsel
XX STREET: 10556 No. 5652138th Torrey Pines Road, Suite 220,
XX CITY: La Jolla
XX STATE: CA
XX COUNTRY: USA
XX ZIP: 92037
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: Patentin Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/276,852
XX FILING DATE: 18-JUL-1994
XX CLASSIFICATION: 514
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 08/276,852
XX FILING DATE: 18-JUL-1994
XX INFORMATION FOR SEQ ID NO: 110:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 108 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
XX MOLECULE TYPE: protein
XX SEQUENCE 108 AA: 11981 MW: 63187 CN:

Query Match 84.4%; Score 649; DB 13; Length 108;
Best Local Similarity 92.1%; Pred. No. 2,53e-45;
Matches 87; Conservative 11; Mismatches 8; Indels 3; Gaps 0;

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CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPC)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PC/TUS95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 110:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11981 MW: 63187 CN:

Query Match 84.4%; Score 649; DB 13; Length 108;
Best Local Similarity 92.1%; Pred. No. 2,53e-45;
Matches 87; Conservative 11; Mismatches 8; Indels 3; Gaps 0;

Db 1 ELTQSPGILSLSPGEPAITLSCPASQVNSNYLAWYQKPGQCAPPLLYGASNPATGIPD 61
QY 2 ELTQSPGILSLSPGEPAITLSCPASQVNSNYLAWYQKPGQCAPPLLYGASNPATGIPD 61
Db 61 PFSGSGSGDTLTISPLPEPFANVYCOQYGGSSG-IFGQTKIEK 105
QY 62 PFSGSGSGDTLTISPLPEPFANVYCOQYGGSPPTFGQTKIEK 107

RESULT 15
ID US-08-276-852-110 STANDARD: PRT: 108 AA
XX
XX
XX
XX 01-JAN-1900
XX Sequence 110, Application US/08276852
XX Sequence 110, Application US/08276852
XX Patent No. 5652138
XX GENERAL INFORMATION:
XX APPLICANT: Burton, Dennis R
XX APPLICANT: Barbas, Carlos F
XX APPLICANT: Lerner, Richard A
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX NUMBER OF SEQUENCES: 170
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: The Scripps Research Institute, Office of
XX ADDRESSEE: Patent Counsel
XX STREET: 10556 No. 5652138th Torrey Pines Road, Suite 220,
XX CITY: La Jolla
XX STATE: CA
XX COUNTRY: USA
XX ZIP: 92037
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: Patentin Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/276,852
XX FILING DATE: 18-JUL-1994
XX CLASSIFICATION: 514
XX PRIOR APPLICATION DATA:

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WIPSEREA

(TW)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:26:26 1998; MasPar time 6.55 Seconds
Tabular output not generated. 226,930 Million cell updates/sec
Title: >US-08-844-215-12
Description: (1-107) from US08844215.pep
Perfect Score: 769
Sequence: 1 AELTOSPTLSLVSGERATL ... CQYGSPPYTFGGQIKVEIK 107

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13889129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq30
1:part1 2:part3 3:part4 4:part5 5:part6 6:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 29.627; Variance 158.010; scale 0.187
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	588	89.5	129	7	R38672	7,87e-44	
2	583	88.8	108	9	R54316	1.94e-43	
3	583	88.8	108	9	W01278	1.94e-43	
4	572	87.4	109	9	P50217	1.42e-42	
5	570	87.1	108	10	P54307	2.04e-42	
6	570	87.1	108	19	W01265	2.04e-42	
7	561	86.0	107	10	P54311	1.04e-41	
8	561	86.0	107	19	W01269	1.04e-41	
9	560	85.8	107	19	R38593	1.24e-41	
10	558	85.6	109	19	W01320	1.78e-41	
11	558	85.6	109	19	P54275	1.78e-41	
12	549	84.4	108	19	W01289	9.06e-41	
13	548	84.3	104	19	W01370	1.09e-40	
14	548	84.3	104	9	R54317	1.09e-40	
15	547	84.1	111	19	W01322	1.09e-40	
16	547	84.1	111	10	P54277	1.30e-40	
17	545	83.9	109	9	P50218	1.87e-40	
18	545	83.9	129	7	R38673	2.24e-40	
19	544	83.7	107	19	W01266	2.24e-40	
20	544	83.7	107	10	P54308	2.24e-40	

21	644	83.7	124	22	W04539	Immunoglobulin F101.2	2.24e-40
22	644	83.7	123	7	R41286	F105 rearranged vari	2.24e-40
23	643	83.6	215	19	W05216	Ulcerative colitis-as	2.58e-40
24	642	83.5	108	10	P54263	Anti-HIV gp120 immuno	2.21e-40
25	640	83.2	134	20	W11155	Anti-lung tumour anti	4.60e-40
26	637	82.8	112	10	W01324	VL of Fab, SS 41 R, b	7.91e-40
27	637	82.8	112	10	P54279	Anti-HIV gp41 immuno	7.91e-40
28	630	81.9	109	10	P56286	light chain of Ab 31	2.79e-39
29	630	81.9	214	19	W05215	Ulcerative colitis-as	2.79e-39
30	628	81.7	108	19	W01267	VL region of HIV neut	4.01e-39
31	625	81.3	108	10	P54255	Anti-HIV gp120 immuno	5.89e-39
32	625	81.3	108	19	W01275	VL region of HIV neut	5.89e-39
33	620	80.6	107	19	W01295	VL region of HIV neut	1.69e-38
34	620	80.6	107	19	W01294	VL region of HIV neut	1.69e-38
35	620	80.6	107	9	R54325	Anti-HIV gp120 immuno	1.69e-38
36	616	80.1	107	19	W01297	VL region of HIV neut	3.48e-38
37	616	80.1	107	10	R54265	Anti-HIV gp120 immuno	3.48e-38
38	615	80.0	108	10	P54309	Anti-HIV gp120 immuno	4.17e-38
39	613	79.7	107	9	R54326	Anti-HIV gp120 immuno	5.98e-38
40	613	79.7	107	19	W01296	VL region of HIV neut	5.98e-38
41	610	79.3	105	9	R54314	Anti-HIV gp120 immuno	1.03e-37
42	510	79.3	105	19	W01272	VL region of HIV neut	1.03e-37
43	606	78.8	116	7	R38650	Human V-kappa fragmen	2.11e-37
44	606	78.8	116	11	P52930	Human V-kappa vk65.8	2.11e-37
45	606	78.8	116	20	W03048	DNA fragment vk65.8,	2.11e-37

ALIGNMENTS

RESULT 1
ID R38672 standard; Protein: 129 AA.
AC R38672;
DE 01-NOV-1993 (first entry)
DT vk325-JK2.
KW Monoclonal antibody, MAB, envelope, glycoprotein, gp120, HIV; AIDS;
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide
FT Protein 21..129
FT /label= mat_protein
FT Region 1..115
FT /label= vk325
FT Region 117..129
FT /label= Jk2
FT Region 44..55
FT /label= CDR1
FT Region 71..77
FT /label= CDR2
FT Region 110..117
FT /label= CDR3
FT Misc.difference 1
FT /note= Met encoded by ATC (sic)
FT Misc.difference 35
FT /note= "FRC encoded by GCA (sic)"
FT Misc.difference 99
FT /note= "Leu encoded by GTG (sic)"
FT Misc.difference 113
FT /note= "Gly encoded by GAT (sic)"
FT Misc.difference 114
FT /note= "Ser encoded by AAC (sic)"
FT Misc.difference 116
FT /note= "Pro encoded by GTT (sic)"
PN W09312232-A.
PD 24-JUN-1993.
PF 10-DEC-1992; U10298.
PP 10-DEC-1991; US-904652.
PA (DAND) DANA FABER CANCER INST INC.
PA (NEWB-) NEW ENGLAND DEACONESS HOSPITAL CORP.
PI Resolving WA, KARASC WA, POSENY MP, SODICKSI JG;
DE WFI: 93-214174/26.

DR N-PSDB; Q42706.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection
PS Disclosure: Page 74-75; 109pp; English
CC The nucleotide sequence of F105 Vx (Q42707 - sequence differs from
CC other F105 Vx sequences given elsewhere in the specification) was
CC compared with germline gene Humv325 (Q42706), showing 97.7%
CC similarity. By nucleotide sequence analysis, F105 appears to
CC be derived from a member of the Vx III subgroup gene family.
SQ Sequence 129 AA;

Query Match 89.5%; Score 688; DB 7; Length 129;
Best Local Similarity 89.5%; Pred. No. 7.87e-44;
Matches 94; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Db 24 ltqspgtlslspgeratiscragssvssylawyqkpgqaprllygssratgipdrf 83
QY 3 LTQSPGTLSLSVGERATLSGPRATLSGASQNIYSGYLGWYQKPGQPPPLLYGASNPATGIPDRF 62

Db 84 sgsdsgtdftltisrlpepfavyyccqygsspytfqgqtkleik 128
QY 63 SSGSGGTDFTLTISRLESEDFAVYYCQYGGSPPYTFQGQTKVEIK 107

RESULT 2 Location/Qualifiers
ID F54316 standard; protein: 108 AA
AC R54316;
DE 10-NOV-1994 (first entry)
DT Anti-HIV gp120 immunoglobulin light chain variable region b6.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
PN WO960273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U0874?
PR 18-JUL-1994; US-276852.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English
CC The sequences given in W01361-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAb's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the Jk2
CC gene clone, b6. A MAb containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml and
CC binds mature gp120 preferentially over the precursor gp160. The MAb
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;

Query Match 88.8%; Score 683; DB 9; Length 108;
Best Local Similarity 86.8%; Pred. No. 1.94e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratiscragssvssylawyqkpgqaprllygssratgipdr b0
QY 2 ELTQSPGTLSLSVGERATLSGPRATLSGASQNIYSGYLGWYQKPGQPPPLLYGASNPATGIPDR 61

Db 61 fsgsgsgtdftltisrlpepfavyyccqygsspytfqgqtkleik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYYCQYGGSPPYTFQGQTKVEIK 107

RESULT 4
ID P50217 standard; protein: 109 AA.

Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratiscragssvssylawyqkpgqaprllygssratgipdr 60
QY 2 ELTQSPGTLSLSVGERATLSGPRATLSGASQNIYSGYLGWYQKPGQPPPLLYGASNPATGIPDR 61

Db 61 fsgsgsgtdftltisrlpepfavyyccqygsspytfqgqtkleik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYYCQYGGSPPYTFQGQTKVEIK 107

RESULT 3
ID W01278 standard; protein: 108 AA.
AC W01278;
DE 29-JAN-1997 (first entry)
DT VL region of HIV neutralising MAB, clone b6.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
PN WO960273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U0874?
PR 18-JUL-1994; US-276852.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English
CC The sequences given in W01361-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAb's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the Jk2
CC gene clone, b6. A MAb containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;

Query Match 88.8%; Score 683; DB 19; Length 108;
Best Local Similarity 86.8%; Pred. No. 1.94e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratiscragssvssylawyqkpgqaprllygssratgipdr b0
QY 2 ELTQSPGTLSLSVGERATLSGPRATLSGASQNIYSGYLGWYQKPGQPPPLLYGASNPATGIPDR 61

Db 61 fsgsgsgtdftltisrlpepfavyyccqygsspytfqgqtkleik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYYCQYGGSPPYTFQGQTKVEIK 107

RESULT 4
ID P50217 standard; protein: 109 AA.

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FT /label= FR2          49..55
FT Region              49..55
FT /label= CDP2
FT Region              56..87
FT /label= FR3
FT Region              88..96
FT /label= CDR3
FT Region              97..108
FT /label= FR4
FT WO9407922-A.
PN 14-APR-1994.
PD 30-SEP-1993: U09328.
PP 30-SEP-1992: US-954148.
PR (SBL) SCPIPS RES INST
PA Barbas CF, Burton DR, Lerner RA;
PI WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 177-178; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC diastronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence #54307 is from a gp120-
CC specific clone. AA:
SQ Sequence 108 AA;

Query Match      87.1%   Score 670; DB 10; Length 108;
Best Local Similarity 87.7% Prod. No. 2,04c-42;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps

Db 1 elttqpgtlslspertatlsccragswisnylawyqgkdqagcrlllyqvsnratqidr 60
    |||||
Cv 2 ELTTQPGTSLSSVSEKATLSCKRASNIYISYELWYCKRGJFPFLLIYKASNAHGIIFER 61
    |||||

Db 61 fggsgsrtdftltisrlcpedafayvsqqqwtspwifgaqtakvek 106
    |||||
Cv 62 FGGSGSRDFTLTISPLESFFAVYGLAYGSPVFEGACTKVEIK 107
    |||||

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RESULT	6	
ID	W01265	standard; Protein; 108 AA.
AC	W01265;	
DE	28-JAN-1997	(first entry)
DT	VL region of HIV neutralising MAB, clone b24.	
DD	Heavy chain, light chain, variable region, VH; monoclonal antibody;	
KW	MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;	
KK	virus infectivity assay; precursor p24; immunoprecipitate; human;	
KW	anti-HIV antibody; detection; HIV infection.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Region	1...21
FT	/label= FR1	
FT	Region	22..33
FT	/label= CDR1	
FT	Region	34..48
FT	/label= FR2	
FT	Region	49..55
FT	/label= CDR2	
FT	Region	56..87
FT	/label= FR3	
FT	Region	88..96
FT	/label= CDR3	
FT	Region	97..108
FT	/label= FR4	
PN	W09502273-A1.	
PD	01-FEB-1995.	
PF	11-JUL-1995;	U08743.
PR	18-JUL-1994;	US-276952.

```

PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK1
CC gene clone, b44. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

Query Match 87.1%; Score 670; DB 19; Length 108;
Best Local Similarity 87.7%; Pred. No. 2.04e-42;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratlscrasqslsnnylawyqkpgqaprllygsstrgtgipdr 60
QY 2 ELTQSPGTLSLSVGERATLSRASQNIYSGYLGWYQKPGQPPRLIYGASNPATGIPDR 61
Db 61 fsgsgsgtdftltisrlepefavyycqyqgtsptwtfgggtkveik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYCYQYQYSPPTFGQGTKEIK 107

RESULT 7
ID R54311 standard; protein; 107 AA.
AC R54311;
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107
FT /label= FR4
FT W09407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 180: 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC distrophic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive

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CC clones. The light chain VK region sequence R54311 is from a gp120-
CC specific clone.
SQ Sequence 107 AA;

Query Match 86.0%; Score 661; DB 10; Length 107;
Best Local Similarity 83.0%; Pred. No. 1.04e-41;
Matches 88; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratlscrasqslsnnylawyqkpgqaprllygsstrgtgipdr 60
QY 2 ELTQSPGTLSLSVGERATLSRASQNIYSGYLGWYQKPGQPPRLIYGASNPATGIPDR 61
Db 61 fsgsgsgtdftltisrlepefavyycqyqgtsptwtfgggtkveik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYCYQYQYSPPTFGQGTKEIK 107

RESULT 8
ID W01269 standard; Protein; 107 AA.
AC W01269;
DT 28-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone B20.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 98..107
FT /label= FR4
FT W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, B20. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

Query Match 86.0%; Score 661; DB 19; Length 107;
Best Local Similarity 83.0%; Pred. No. 1.04e-41;
Matches 88; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratlscrasqslsnnylawyqkpgqaprllygsstrgtgipdr 60
QY 2 ELTQSPGTLSLSVGERATLSRASQNIYSGYLGWYQKPGQPPRLIYGASNPATGIPDR 61
Db 61 fsgsgsgtdftltisrlepefavyycqyqgtsptwtfgggtkveik 106

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QY 62 FSSGSGIDFTLIISRLSESEDFAVYCCYGGSPPTIFGGIKVEIK 107
|||||

RESULT 9
ID R38593 standard: peptide; 107 AA.
AC R38593.
DT 28-OCT-1993 (first entry)
DE Human lambda light chain subgroup 3 (HL3).
KW Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
EH Key Location/Qualifiers
FT Misc.diffence 96
FT /note- residue conserved in less than 50% of the
FT known sequences of HL3*
PN WC9411794-A.
PD 24-JUN-1993.
PF 14-DEC-1993: U10904
PF 13-DEC-1991: US-908464
PA (XOMA) XOMA CORP.
PI Fishwild DM, Kahn PP, Little PG, Studnicka GM.
DI WPI: 93-213827/26.
PT Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc
PS Claim 2: Page 93-94: 150pp. English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (hk1 - R38590, hk3 - NCK, hk2 - GST, hL1 - R38591, hL2 -
CC R38592, hL3 - R38593, hL6 - R38594, hK4 - R38595, hL4 - R38596,
CC and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
CC hH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 107 AA:

Query Match 85.8%; Score 650; DB 7; Length 107;
Best Local Similarity 87.6%; Prod. No. 1.24e-41;
Matches 92: Conservative 8; Mismatches 4; Indels 1; Gaps 1;
Db 4 ltqspstlslspgervivscrasqsvssylawgqkpgqprlllygssratgipdrf 62
|||||
QY 3 LTQSPSTLSLVGERATISCPASQNIYSGYLGWYCCQKPGGTPPLIYGCASNPATGIPDPF 62
|||||
Db 63 sqsgsgtdftlslslpqrdfavycgqgsspxtfqgtdveik 107
|||||
QY 63 SSGSGSIDFTLIISRLSESEDFAVYCCYGGSPPTIFGGIKVEIK 107
|||||

RESULT 10
ID W01320 standard: Protein; 109 AA.
AC W01320.
DT 29-JAN-1997 (first entry)
DE VL of Fab, DL 4119, binds to HIV gp41.
KW Heavy chain, light chain, variable region, VH monoclonal antibody;
KW MAb: HIV; human immunodeficiency virus; glycoprotein gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
EH Key Location/Qualifiers
FT Region
FT /label- FR1
FT Region
FT /label- CDR1
FT /label- CDR2
FT /label- CDR3
FT /label- FR4

FT Region 51..57
FT /label- CDR2
FT Region 58..89
FT /label- FR3
FT Region 90..97
FT /label- CDR3
FT Region 98..109
FT /label- FR4
PN W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995: U08743.
PF 18-JUL-1994: US-276852.
PA (SCPI) SCRIpps RES INST.
PI Barbas CF, Burton DR, Lerner RA.
DI WPI: 96-179601/1R
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example 3, Fig 19, 36pp. English.
CC The sequences given in W01320-24 represent the light chain variable
CC regions (VH) of a series of antibody fragments (FAB's) which are
CC immunoreactive with HIV glycoprotein gp41. This sequence represents
CC the sequence of the clone, DL 4119. These sequences represent light
CC chains which bind to the heavy light chain clones given in W01315-19. A
CC monoclonal antibody containing one of these Fab sequences may have the
CC capacity to reduce HIV infectivity titre in an *in vivo* virus infectivity
CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
CC The MAb may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 109 AA:

Query Match 85.6%; Score 658; DB 19; Length 109;
Best Local Similarity 86.9%; Prod. No. 1.78e-41;
Matches 93: Conservative 7; Mismatches 6; Indels 1; Gaps 1;
Db 2 aeltqspstlslspgervivscrasqsvssylawgqkpgqprlllygssratgipdrf 61
|||||
QY 1 AELTQSPSTLSLVGERATISCPASQNIYSGYLGWYCCQKPGGTPPLIYGCASNPATGIPDPF 66
|||||
Db 62 rfsqsgsgtdftlslslpqrdfavycgqgsspxtfqgtdveik 107
|||||
QY 61 RFSGSGSIDFTLIISRLSESEDFAVYCCYGGSPPTIFGGIKVEIK 107
|||||

RESULT 11
ID R54275 standard: protein, 109 AA.
AC R54275.
DI 10-NOV-1994 (first entry)
DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 4119.
KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
KW neutralisation; monoclonal antibody; light chain; variable region;
KW framework region; complementarity determining region.
OS Homo sapiens.
EH Key Location/Qualifiers
FT Region
FT /label- FR1
FT Region 24..35
FT /label- CDR1
FT Region 36..50
FT /label- FR2
FT Region 51..57
FT /label- CDR2
FT Region 58..89
FT /label- FR3
FT Region 90..97
FT /label- CDR3
FT Region 98..109
FT /label- FR4
PN W09407923-A.
PD 14-APR-1994.
PF 30-SEP-1993: U09328.
PF 30-SEP-1992: US-954148.
PA (SCRI) SCRIpps RES INST.
PI Barbas CF, Burton DR, Lerner RA.

WPI; 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Claim 11, Page 215-216, 248pp, English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive HIV
 CC clones. The light chain VL region sequence R54275 neutralises HIV1
 CC gp41.
 SQ Sequence 109 AA:

Query Match 85.6%; Score 658; DB 10; Length 109;
 Best Local Similarity 86.9%; Pred No. 1.78e-41;
 Matches 93; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
 Db 2 aeltspgtlslspqervivscrasqsvssnylawyqgkpgqgprlliygasmratgipd 61
 QY 1 AELTSPGTLSLSVGERATLSPASQNIYSGYLGWYQKPGQPPPELLIYGASNRATGIPD 60
 Db 62 rfsgsgsgtdftltisrlepedfavyycqygssg-tfgggtkveik 107
 QY 61 RFSGSGSGTDFTLTISRLESEDFAVYCYQYGSPPYTFGGGTKEIK 107

RESULT 12
 ID W01289 standard; Protein; 108 AA.
 AC W01289;
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b11.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB, HIV, human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence, human.
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIpps RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.

CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC clone, b11. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV

CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 84.4%; Score 649; DB 19; Length 108;
 Best Local Similarity 82.1%; Pred No. 9.06e-41;
 Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
 Db 1 eltsptslsperatlsqrasqsvssnylawyqgkpgqgprlliystratgipdr 60
 QY 2 ELTSPGTLSLSVGERATLSPASQNIYSGYLGWYQKPGQPPPELLIYGASNRATGIPDR 61
 Db 61 fsgsgsgtdftltisrlepedfavyycqygfgdaqytfgggtkveik 106
 QY 62 FSGSGSGTDFTLTISRLESEDFAVYCYQYGSPPYTFGGGTKEIK 107

RESULT 13
 ID W01279 standard; Protein; 104 AA.
 AC W01279;
 DT 29-JAN-1997 (first entry)

DE VL region of HIV neutralising MAB, clone s6.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB, HIV, human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.

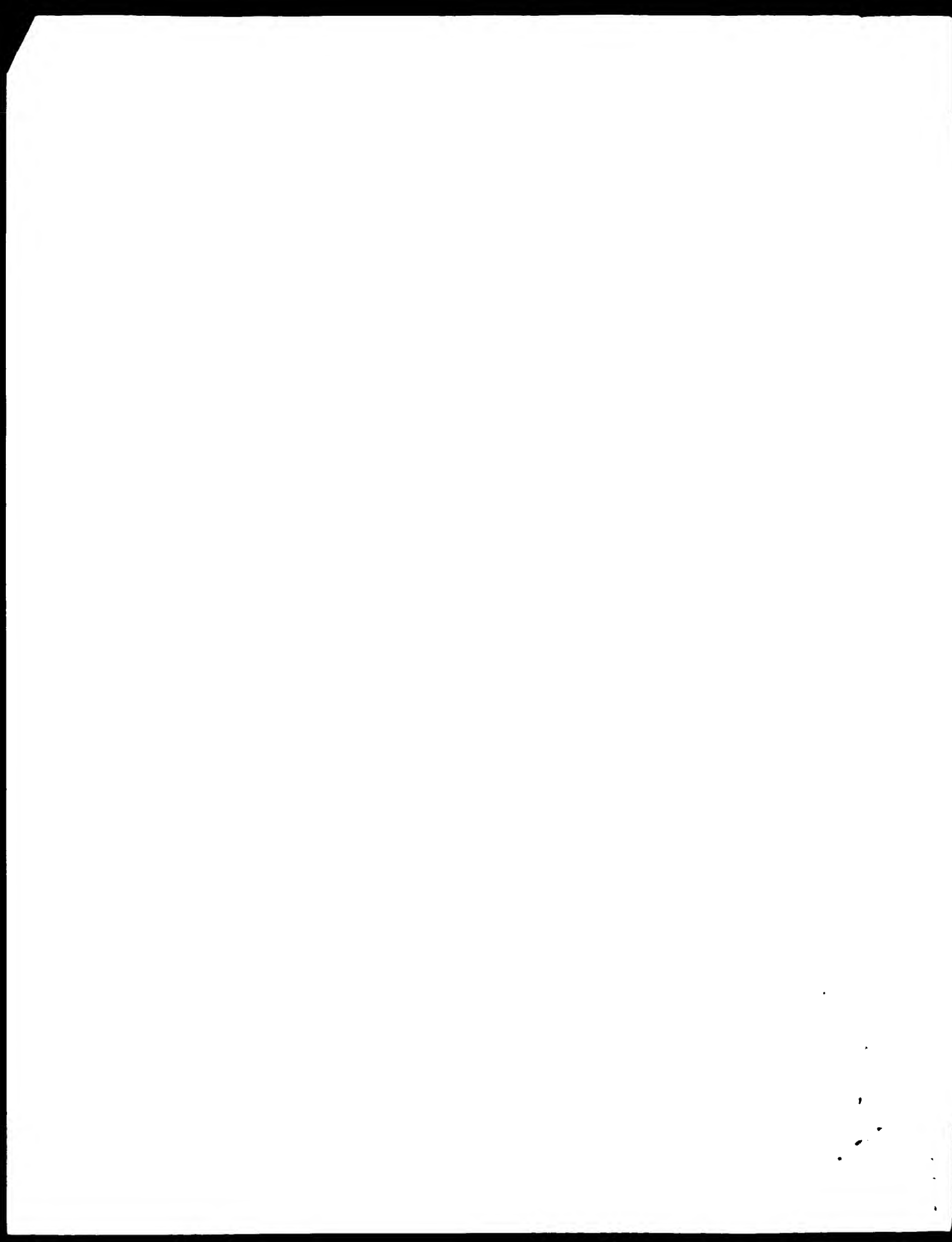
FH Key Location/Qualifiers
 FT Region 1..18
 FT /label= FR1
 FT Region 19..30
 FT /label= CDR1
 FT Region 31..45
 FT /label= FR2
 FT Region 46..52
 FT /label= CDR2
 FT Region 53..84
 FT /label= FR3
 FT Region 85..93
 FT /label= CDR3
 FT Region 94..104
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIpps RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.

CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, s6. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 104 AA;

Query Match 84.3%; Score 648; DB 19; Length 104;
 Best Local Similarity 84.5%; Pred No. 1.04e-40;
 Matches 87; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Db 1 qspgtlslsperatlsqrasqsvssnylawyqgkpgqgprlliystratgipdrfsq 60
 QY 5 QSPGTLSLSVGERATLSQASQNIYSGYLGWYQKPGQPPPELLIYGASNRATGIPDRFSQ 64
 Db 61 gsgsgtdftltisrlepedfavyycqygsgsvytfgggtkveik 103
 QY 62 FSGSGSGTDFTLTISRLESEDFAVYCYQYGSPPYTFGGGTKEIK 107

RESULT	15
IC	W01322 standard: Protein: 111 AA.
AC	W01322:
DI	29-JAN-1997 (first entry)
DE	VL of Fab, GL 41.1. binds to HIV gp41.
KE	Heavy chain: light chain: variable region: VH; monoclonal antibody:
MD	MAD: HIV; human immunodeficiency virus; glycoprotein: gp120; clone;
KW	virus infectivity assay: precursor gp160, immunocompetence; human;
KW	anti-HIV antibody: detection; HIV infection.
OS	Homo sapiens.
PH	Key
	Location/Qualifiers



 W O R L D

 (TM)

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MParch.pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:23:21 1998; MaxPar time 7.30 Seconds
 442,233 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-844-215-11
 Description: (1-106) from US08844215.pep
 Perfect Score: 746
 Sequence: 1 AELQSPATLSVSPGEASL ..COHSTWPLTFGGGKVEFK 106

Scoring Table: PAM 150
 Gap 11

Searched: 95051 seqs, 30459580 residues

Post-processing: Minimum Match 48
 Listing first 45 summaries

Database: pif53
 1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:unann2 7:unann3
 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
 13:unann9 14:unann10 15:unann11 16:unann12 17:unann
 18:unrev

Statistics: Mean 39.648; Variance 128.596; scale 0.308

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description	Pred No
1	672	90.1	117	7 S40362	Ig kappa chain - hum	1.52e-67
2	647	86.7	127	7 S34005	Ig kappa chain V reg	2.21e-64
3	627	84.0	124	7 S40343	Ig kappa chain V reg	7.42e-62
4	624	83.6	144	7 PLO106	Ig kappa chain V reg	1.77e-61
5	622	83.4	108	7 G44151	Ig kappa chain V reg	3.17e-61
6	614	82.3	108	7 H44151	Ig kappa chain V reg	3.23e-60
7	613	82.2	109	7 K30601	Ig kappa chain V-III	4.32e-60
8	612	82.0	109	2 K3HUPM	Ig kappa chain V-III	5.78e-60
9	611	81.9	108	7 B30608	Ig kappa chain V-III	7.72e-60
10	610	81.8	109	7 G30601	Ig kappa chain V-III	1.03e-59
11	610	81.8	114	7 S54905	Ig kappa chain V reg	1.03e-59
12	610	81.8	131	7 S40328	Ig kappa chain - hum	1.03e-59
13	609	81.6	109	7 G30607	Ig kappa chain V-III	1.38e-59
14	609	81.6	109	7 G30607	Ig kappa chain V-III	1.38e-59
15	606	81.2	115	7 B26555	Ig kappa chain V-III	3.22e-59
16	605	81.1	109	7 F44151	Ig kappa chain V reg	4.40e-59
17	604	81.0	111	7 S23628	Ig kappa chain V reg	5.88e-59
18	603	80.8	129	2 K3HUBA	Ig kappa chain V reg	7.85e-59
19	602	80.7	129	2 K3HUBA	Ig kappa chain V-III	1.05e-58
20	601	80.6	128	7 A56701	Ig kappa chain V reg	1.40e-58

21	600	80.4	109	7 D30601	Ig kappa chain V-III	1.47e-58
22	599	80.3	125	7 S43344	Ig kappa light chain	2.50e-58
23	599	80.2	109	7 PH0963	Ig kappa chain V reg	3.34e-58
24	596	79.9	109	7 F30607	Ig kappa chain V-III	5.97e-58
25	595	79.9	109	7 H30601	Ig kappa chain V-III	5.97e-58
26	595	79.8	130	7 S40360	Ig kappa chain - hum	7.47e-58
27	594	79.6	108	7 C30608	Ig kappa chain V-III	1.06e-57
28	594	79.6	109	2 K3HUT1	Ig kappa chain V-III	1.06e-57
29	594	79.5	129	2 K3HUB1	Ig kappa chain V reg	1.06e-57
30	594	79.6	109	7 S40325	Ig kappa chain - hum	1.06e-57
31	593	79.5	127	7 PH0965	Ig kappa chain V reg	1.42e-57
32	592	79.4	129	7 S43369	Ig light chain varia	1.90e-57
33	592	79.4	134	7 S38643	Ig kappa chain V reg	1.90e-57
34	591	79.2	91	7 S37525	Ig kappa chain V reg	2.54e-57
35	591	79.2	104	7 G30601	Ig kappa chain V-III	2.54e-57
36	591	79.2	128	7 S43379	Ig kappa light chain	2.54e-57
37	590	79.1	108	2 K3HUB6	Ig kappa chain V-III	3.39e-57
38	590	79.1	115	2 K3HUC1	Ig kappa chain V reg	3.39e-57
39	590	79.1	128	7 S20636	Ig kappa chain V reg	4.53e-57
40	589	79.0	129	7 S29627	Ig kappa chain V reg	4.53e-57
41	587	78.7	110	7 S20635	Ig kappa chain V reg	8.07e-57
42	587	78.7	115	7 A30553	Ig kappa chain V reg	8.07e-57
43	586	78.6	128	7 S40345	Ig kappa light chain	1.08e-56
44	586	78.6	129	7 S45832	anti-Sm antibody V1	1.08e-56
45	585	78.4	108	7 E30609	Ig kappa chain V-III	1.44e-56

ALIGNMENTS

RESULT 1
 ENTRY S40362 #type complete
 TITLE Ig kappa chain - human
 ORGANISM Homo sapiens #common_name man
 DATE 06-Mar-1994 #sequence_revision 26-May-1996 #text_change 16-Aug-1996

ACCESSIONS S40362
 REFERENCE S40312
 #authors Klein, R.; Juenichen, R.; Zachau, H.G.
 #journal Eur. J. Immunol. (1993) 23:3249-3271
 #title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40362
 #status preliminary; translation not shown
 ##molecule_type mRNA
 ##residues 1-117 #label KLE
 ##cross-references EMBL:X72472
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 117 #molecular-weight 12613 #checksum 8309

Query Match 90.1% Score 672; DB 7; Length 117;
 Best Local Similarity 87.5% Pred. No 1.52e-67;
 Matches 91; Conservative 10; Mismatches 3; Indels 3; Gaps 1;

Db 14 mtspstlsvspgprtltscragssslawyyqyqpgpprtlllygstratcpafis 73
 QY 3 ITSPATLSVSPGEASLSCASQSGVNNLAWYQKPSAPPELLYNGNTPAISDPHFS 62

Db 74 qsgsgteftltsslsgsfavyyqggnwplttfggqtkveik 117
 QY 63 GSGSGTEFTLTSSLSGSEFAFYFCWHYSTWELTFGGGKVEFK 106

RESULT 2
 ENTRY S34005 #type complete
 TITLE Ig kappa chain V region - human
 ORGANISM Homo sapiens #common_name man
 DATE 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

ACCESSIONS S34005; S30524
 REFERENCE S34001
 #authors Mariette, X.; Tsapis, A.; Brouet, J.C.
 #journal Eur. J. Immunol. (1993) 23:846-851

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#title      Nucleotide sequence analysis of the variable domains of four
#accession  S34005
#status     preliminary
#molecule_type mRNA
#residues   1-107 #label MAR
#cross-references EMBL:Z18330
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer: immunoglobulin
SUMMARY       #length 107 #molecular-weight 11659 #checksum 7893

Query Match      86.7% Score 647 DB 7 Length 107
Best Local Similarity 85.6% Pred No 2 21e-64
Matches 89; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 4 mtgspatlsppgeratlsrscrasgsvsnlwygqkpgqaprtliygasttratgiparfs 63
QY 3 LTQSPATLSVSGEPASLSRSCASOSVGNLAWYQKQPGQAPRLIYGGNTRATGTPDRFS 62

Db 64 gsgsgtftltisslqsdafvvyccqyrnwprrtfggktkveik 107
QY 63 GSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 3
ENTRY   S40343 #type complete
TITLE   Ig kappa light chain (VJ) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     19-May-1994 #sequence_revision 26-May-1995 #text_change
16-Aug-1996
ACCESSIONS S40343
REFERENCE S40312
#authors Klein, P.; Jaenichen, P.; Zachau, H.G
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their
hypermutation.
#accession S40343
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-128 #label KLE
#cross-references EMBL:X72453
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer: immunoglobulin
SUMMARY       #length 128 #molecular-weight 13950 #checksum 6935

Query Match      84.0% Score 627 DB 7 Length 128
Best Local Similarity 82.7% Pred. No. 7.42e-62
Matches 86; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 24 mtgspatlsppgeratlsrscrasgsvsnlwygqkpgqaprtliygasttratgiparfs 83
QY 3 LTQSPATLSVSGEPASLSRSCASOSVGNLAWYQKQPGQAPRLIYGGNTRATGTPDRFS 62

Db 84 gsgsgtftltisslqsdafvvyccqyrnwprrtfggktkveik 127
QY 63 GSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 4
ENTRY   PL0106 #type fragment
TITLE   Ig kappa chain in precursor V-J-C region (LS1) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
16-Aug-1996
ACCESSIONS PL0106
REFERENCE PL0106
#authors Silberstein, L.E.; Litwin, S.; Carmack, C.E
#journal J. Exp. Med. (1989) 169:1631-1643
#title Relationship of variable region genes expressed by a human B
cell lymphoma secreting pathologic anti-pr-2 erythrocyte
autoantibodies

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#cross-references MUID:89235583
#accession PL0106
#molecule_type mRNA
#residues 1-144 #label SIL
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer: immunoglobulin
FEATURE       #domain signal sequence #status predicted #label SIG
1-20          #domain V region #label VREN
21-115        #region complementarity-determining 1\
44-54         #region complementarity-determining 2\
70-76         #region complementarity-determining 3\
109-115       #domain J region #label JRG
116-127       #domain C region (fragment) #label CPE
128-144       #length 144 #checksum 3623
SUMMARY

Query Match      83.6% Score 624 DB 7 Length 144
Best Local Similarity 80.8% Pred. No. 1.77e-61
Matches 84; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Db 24 ltgspatlsppgeratlsrscrasgsvsnlwygqkpgqaprtliygasttratgiparfs 83
QY 3 LTQSPATLSVSGEPASLSRSCASOSVGNLAWYQKQPGQAPRLIYGGNTRATGTPDRFS 62

Db 84 gsgsgtftltisslqsdafvvyccqyrnwprrtfggktkveik 127
QY 63 GSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 5
ENTRY   G44151 #type fragment
TITLE   Ig kappa chain V region (JM-10) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS G44151
REFERENCE G44151
#authors Zehedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.;
Griff, R.; DeGraw, J.; Pyati, J.; LaPolla, R.; Burton,
D.R.; Lerner, P.A.; Thornton, G.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
#title Human combinatorial antibody libraries to hepatitis B surface
antigen.
#accession G44151
#status Preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-108 #label ZEB
#note nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer: immunoglobulin
SUMMARY       #length 108 #checksum 770

Query Match      81.4% Score 622 DB 7 Length 108
Best Local Similarity 80.2% Pred. No. 3.17e-61
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Db 1 aeltgspatlsppgeratlsrscrasgsvsnlwygqkpgqaprtliygasttratgipar 60
QY 1 AELTQSPATLSVSGEPASLSRSCASOSVGNLAWYQKQPGQAPRLIYGGNTRATGTPDRFS 60

Db 61 fsgsgtftltisslqsdafvvyccqyrnwprrtfggktkveik 106
QY 61 FSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 6
ENTRY   H44151 #type fragment
TITLE   Ig kappa chain V region (JM-15) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS H44151
REFERENCE A44151

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ENTRY          C30601      #type fragment
TITLE          Ig kappa chain V-III region (Pay) - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
ACCESSIONS     16-Aug-1996
REFERENCE      C30601
#authors       Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
                Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
                Frangione, B.
#journal       J. Immunol. (1989) 142:3158-3163
#title        Structural and idiotypic characterization of the L chains of
                human IgM autoantibodies with different specificities.
#cross-references EMBL:X82934
#accession     C30601
#status       preliminary
#molecule_type protein
#residues      1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 109 #checksum 6191

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Best Local Similarity 78.1%; Pred. No. 1.03e-59;
Matches 82; Conservative 18; Mismatches 4; Indels 1; Gaps 1;

Db 4 4tspgtlspgeratlsrasqssvssylawygqpgqaprllygassratgipdrf 63
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QY 3 LTQSPATLSVSPGERASLSRASQSGVGN-LAWYQKPGQAPRLIYGGNTPATGTDPDF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 64 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 SGSGSGTEFTLTSSLOSEDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 11
ENTRY      S54905      #type fragment
TITLE      Ig kappa chain V region - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
ACCESSIONS 16-Aug-1996
REFERENCE   S54905
#authors    Esposito, G.; Traboni, C.
#submission submitted to the EMBL Data Library, November 1994
#description Cloning and sequencing of cDNA coding for the variable
                domains of a human antibody against Hepatitis C virus
                helicase.
#accession  S54905
#status     preliminary
#molecule_type mRNA
#residues   1-114 #label ESP
#cross-references EMBL:X82934
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 114 #checksum 5831

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Best Local Similarity 80.0%; Pred. No. 1.03e-59;
Matches 84; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 4 4tspgtlspgeratlsrasqssvssylawygqpgqaprllydsrratgiparfs 63
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QY 3 LTQSPATLSVSPGERASLSRASQSGVGN-LAWYQKPGQAPRLIYGGNTPATGTDPDF 62
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Db 64 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 108
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QY -63 SGSGSGTEFTLTSSLOSEDFAVYFCQHYSTWPL-LTFGGGKVEFK 106

RESULT 12
ENTRY      S40328      #type complete
TITLE      Ig kappa chain - human

```

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ORGANISM       #formal_name Homo sapiens #common_name man
DATE           06-Mar-1994 #sequence_revision 26-May-1995 #text_change
ACCESSIONS     16-Aug-1996
REFERENCE      S40328
#authors       Klein, R.; Jaenichen, P.; Zachau, H.G.
                Eur. J. Immunol. (1993) 23:3248-3271
#title        Expressed human immunoglobulin chi genes and their
                hypermutation.
#accession     S40328
#status       preliminary; translation not shown
#molecule_type mRNA
#residues      1-131 #label KLE
#cross-references EMBL:X72438
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 131 #molecular-weight 14270 #che-ksun 0795

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Best Local Similarity 81.4%; Pred. No. 1.03e-59;
Matches 86; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Db 23 mtgspatlsipgeratlsrasqssvssylawygqpgqaprllygassratgipdrfs 82
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QY 3 LTQSPATLSVSPGERASLSRASQSGVGN-LAWYQKPGQAPRLIYGGNTPATGTDPDF 82
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Db 83 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 127
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RESULT 13
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TITLE      Ig kappa chain V-III region (Kas) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
ACCESSIONS     16-Aug-1996
REFERENCE      G30607
#authors       Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
                Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
                Frangione, B.
#journal       J. Immunol. (1989) 142:3158-3163
#title        Structural and idiotypic characterization of the L chains of
                human IgM autoantibodies with different specificities.
#cross-references EMBL:X8215279
#accession     G30607
#status       preliminary
#molecule_type protein
#residues      1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 109 #checksum 4998

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Best Local Similarity 78.1%; Pred. No. 1.03e-59;
Matches 82; Conservative 18; Mismatches 4; Indels 1; Gaps 1;

Db 4 4tspgtlspgeratlsrasqssvssylawygqpgqaprllygassratgipdrf 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPATLSVSPGERASLSRASQSGVGN-LAWYQKPGQAPRLIYGGNTPATGTDPDF 61
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Db 64 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 SGSGSGTEFTLTSSLOSEDFAVYFCQHYSTWPL-LTFGGGKVEFK 106

RESULT 14
ENTRY      A30608      #type fragment
TITLE      Ig kappa chain V-III region (Son) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change

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QY 301 COTCCAGATATTCAGTGGTGGTAGAGTGTAC 333
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RESULT 12
LOCUS HS20364 525 bp RNA PRI 03-AUG-1995
DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 203-64)
ACCESSION Z47271
NID g619482
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 525)
REFERENCE Lebecque, S.
AUTHORS Direct Submission
TITLE Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
JOURNAL Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, France, 69572, FRANCE
2 (bases 1 to 525)
REFERENCE Galibert, L., van Dooren, J., Durand, I., Pousset, F., Jefferis, P.,
AUTHORS Bancheureau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
FEATURES
source Location/Qualifiers
1..525
/organism="Homo sapiens"
/clone="203-G4"
/tissue_type="blood"
/cell_type="B-lymphocyte"
BASE COUNT 99 a 144 c 173 g 109 t
ORIGIN
Query Match 43.5%; Score 167; DB 87; Length 525;
Best Local Similarity 80.8%; Pred. No. 7.02e-120;
Matches 311; Conservative 0; Mismatches 60; Indels 14; Gaps 6;
Db 67 ctatgagctctgggtgagctgaagaagcctgggtctctctggtgaggtctctctgcaag 126
QY 1 CTCGAGCAGTCTGGGGTCTGAGGTAAGAGAGGCTGGGTCTGTTGAGTCTGAGGCTGAGG 60
Db 127 gcttctgagagcacttcagagctatctatcagctgggtgggtggcagagccctgacaa 186
QY 61 GTTCTGGAGGACCTTCAGGGGCTATGTTATCAGCTGGGTGGTGGAGAGGCGCTGGACAA 120
Db 187 ggccttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 234
QY 121 GGACTTCAGTCTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 235 tacacacagaagttccagagcagagctacagctacagctacagctacagctacagctacagc 294
QY 181 TACGTCACAAATTCGGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 295 tacatggagctgagcagctgagctgagctgagctgagctgagctgagctgagctgagctgag 354
QY 241 TTCAATTGAGCTGAGTAACCTGAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 355 ggggcta-aggtcgaaattttggagtggtttcagtggttggttggttggttggttggttggt 413
QY 301 COTCCAGATATTCAGTGGTGGTAGAGTGTAC 333
|||||
Db 414 ggggaaccttggtcacctctctcctca 438
QY 360 GGGCACCCTCTGTCAGCGTCTCTCTCA 384
|||||
RESULT 14
LOCUS HUMIGHVAN 421 bp mRNA PPI 06-NOV-1994
DEFINITION Human (fetal) Ig rearranged H-chain VDJ-region mRNA, clone 51P1.
ACCESSION M18516
NID g185545
KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
immunoglobulin mu-chain; processed gene; variable region subregion
VH-1.
SOURCE Homo sapiens foetus liver cDNA to mRNA.
ORGANISM Homo sapiens

```



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Db 391 tacatgaagcagcctgaatctaaagacacagcgcgtatattactgtgcgaagg 450
QY 241 TCAATGAGTGAAGCTGAGATCTGAGACAGGAGGCTGCTACATCTGCGAGAGAC 300
Db 451 guraaggaattactatgaacttcttactgaactactgaagctgtggggccaa 510
QY 301 CCTCAAGATATGAGAGCTGGTATCTATCTGAGATCTGAGAGAG 360
Db 511 ggaacacaggtcacctctctca 534
QY 361 GGCACCTCTGTCACCGTCTCTCA 384

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Search completed: Tue Feb 24 09:37:00 1998
 Job time : 511 secs.



MISCELL

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit
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MParch_Rn a.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 09:25:54 1998 Master file 112 78 Records
669 785 Million cell updates/sec

Tabular output not generated.

Title: NUS-08-844-215-21
Description: (1-219) from US08844215.scq
Perfect Score: 317
N.A. Sequence: 1 GCGGACGTCAGGACATGTC
Comp: GCGGTCGAGTCGTCGAGAGG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 33433 seqs, 126143548 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19
20:STS20 21:STS21 22:STS22 23:STS23 24:STS24
25:STS25 26:STS26 27:STS27 28:STS28 29:STS29
30:STS30 31:STS31 32:STS32 33:STS33 34:STS34
35:STS35 36:STS36 37:STS37 38:STS38 39:STS39
40:STS40 41:STS41 42:STS42 43:STS43 44:STS44
45:STS45 46:STS46 47:STS47 48:STS48 49:STS49
50:STS50 51:STS51 52:STS52 53:STS53 54:STS54
55:STS55 56:STS56 57:STS57 58:STS58 59:STS59
60:STS60 61:STS61 62:STS62 63:STS63 64:STS64
65:STS65 66:STS66 67:STS67 68:STS68 69:STS69
70:STS70 71:STS71 72:STS72 73:STS73 74:STS74
75:STS75 76:STS76 77:STS77 78:STS78 79:STS79
80:STS80 81:STS81 82:STS82 83:STS83 84:STS84
85:STS85 86:STS86 87:STS87 88:STS88 89:STS89
90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95 96:STS96

Statistics: Mean 9.406; Variance 1.929; scale 5.136

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	240	75	400	60 HSI244850	242711
2	211	66	478	19 AAC55239	6660-07

3	211	66	6	HSI308877	418	71	HSI308877	6660-07	SI	NCL_GCAP_L	0.00e+00
4	181	57	1	HSI28912	242	64	HSI28912	Soares	ova	0.00e+00	
5	181	57	1	AA479857	242	25	AA479857	Soares	ova	0.00e+00	
6	156	49	2	HSI246790	242	59	HSI246790	Soares	ova	2.82e-262	
7	149	47	0	AA476303	171	26	AA476303	Soares	ova	1.17e-247	
8	149	47	0	HSI267793	171	63	HSI267793	Soares	ova	1.17e-247	
9	145	45	7	AA464224	242	16	AA464224	Soares	ova	2.63e-249	
10	145	45	7	HSI28064	324	63	HSI28064	Soares	ova	2.63e-249	
11	138	43	5	AA494354	217	38	AA494354	NCL_GCAP_L	0.00e+00		
12	138	43	5	HSI284559	217	67	HSI284559	NCL_GCAP_L	0.00e+00		
13	136	42	0	HSI145281	260	40	HSI145281	NCL_GCAP_L	0.00e+00		
14	136	42	0	AA4225858	260	27	AA4225858	NCL_GCAP_L	0.00e+00		
15	131	41	3	AA492331	262	38	AA492331	NCL_GCAP_L	0.00e+00		
16	131	41	3	HSI290157	262	68	HSI290157	NCL_GCAP_L	0.00e+00		
17	129	40	7	HSI236269	230	58	HSI236269	Soares	ova	2.65e-206	
18	129	40	7	HSI188008	243	52	HSI188008	Soares	ova	3.65e-206	
19	129	40	7	AA481842	243	28	AA481842	Soares	ova	3.65e-206	
20	129	40	7	HSI272128	243	55	HSI272128	Soares	ova	3.65e-206	
21	127	40	1	HSI188096	255	52	HSI188096	Soares	ova	4.95e-202	
22	117	38	8	AA495616	240	29	AA495616	Soares	ova	8.24e-194	
23	113	38	8	HSI280478	240	56	HSI280478	Soares	ova	8.24e-194	
24	110	37	5	HSI227532	244	57	HSI227532	Soares	ova	1.38e-185	
25	117	36	9	AA464451	242	16	AA464451	Soares	ova	1.65e-181	
26	117	36	9	HSI258291	242	53	HSI258291	Soares	ova	1.65e-181	
27	117	36	9	AA482641	242	29	AA482641	Soares	ova	2.02e-177	
28	115	36	3	HSI272927	242	55	HSI272927	Soares	ova	2.02e-177	
29	110	34	7	AA454547	251	63	AA454547	Soares	ova	3.14e-167	
30	110	34	7	HSI212377	240	55	HSI212377	Soares	ova	3.14e-167	
31	110	34	7	AA464213	363	16	AA464213	Soares	ova	4.15e-159	
32	106	33	4	HSI227505	248	57	HSI227505	Soares	ova	4.15e-159	
33	106	33	4	HSI145677	219	50	HSI145677	NCL_GCAP_P	5.69e-145		
34	99	31	2	AA330271	239	36	AA330271	Soares	ova	5.74e-125	
35	99	31	2	HSAA54151	442	78	HSAA54151	Soares	ova	5.74e-125	
36	89	28	1	AA496610	287	33	AA496610	Soares	ova	5.56e-123	
37	88	27	8	HSI291552	287	68	HSI291552	Soares	ova	5.56e-123	
38	88	27	8	AA464213	363	16	AA464213	Soares	ova	5.12e-119	
39	86	27	1	HSI258153	363	63	HSI258153	Soares	ova	5.12e-119	
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41	82	25	9	HSI268888	242	64	HSI268888	Soares	ova	4.00e-111	
42	82	25	9	HSI220206	171	54	HSI220206	Soares	ova	2.10e-99	
43	76	24	0	HSI201913	335	54	HSI201913	Soares	ova	1.95e-74	
44	73	19	9	AA479195	129	25	AA479195	Soares	ova	1.50e-72	
45	62	19	6	AA479195	129	25	AA479195	Soares	ova	1.50e-72	

ALIGNMENTS

RESULT 1
ID HSI244850 standard, RNA, EST, 430 BP.
AC AA456778;
NI 92177199
DT 07-JUN-1997 (rel. 52, Created)
DT 07-JUN-1997 (rel. 52, last updated, Version 1)
DE 242711 r1 Soares (ovary tumor NHCT) Homo sapiens (HSA) chr24:779541
DE 5: similar to gb:X06764 IG KAPPA CHAIN PHCOPROTOR V-III REGION
DE (HUMAN):
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-400

PA Hillier L., Allen M., Bowles L., Dubouche P., Giesel G., Jost S.,
PA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
PA Moore B., Schellenberg K., Steptoe M., Tan F., Theising R.,
PA White V., Wyllie T., Waterston R., Wilson R.,
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel.: 314 286 1909 Fax: 314 286 1810 Email:
CC est@wustl.wustl.edu This clone is available royalty-free through
CC EMBL. Contact the IMAG Consortium (info@imagedb.llnwd.net) for

RESULT	5	
ID	HS1236090	standard: RNA; EST: 269 BP.
AC	AA434001;	
NI	g2138915	
DT	01-JUN-1997	(Rel. 52, Created)
DT	01-JUN-1997	(Rel. 52, Last updated, Version 1)
DE	zw25f01.r1	Soares ovary tumor NBH07 Homo sapiens
DE	5	similar to gb:211894 U5 RABPA CHAIN PRP230P V-III PERSON
DE	(HUMAN)??	
DE	KW	EST.
OS	Homo sapiens (human)	
OC	Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;	

ESL.
SOURCE
ORGANISM
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata, Mammalia; Eutheria, Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 171)
Hillier, L., Allen, M., Boules, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lary, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Thaising, B., White, Y., Wylie, T., Waterston, P. and Wilson, R.
WASHU-NCI human EST Project
Unpublished (1997)

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham.
Location/Qualifiers
1..171
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Ronaldo.
/clone="770705"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
complement(<1..>171)
/db_xref="GDB:594057a" 32 t

FEATURES

source

mrna

Query Match 47.0%; Score 149; DB 26; Length 171;
Best Local Similarity 94.7%; Pred. No. 1.17e-247;
Matches 162; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
BASE COUNT 36 a 58 c 45 g 32 t
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||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 10 ACCGAGTCTCCAGGACCCCTGCTTTCTCCAGGAGGAGAGGACCCCTCTCTCAGG 69
Db 61 gccatcagaagttagcagcactacttagcttagtaccagcagaacccctgacagct 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 70 GCGAGTCAAGTCTTAGAGCAAAATAGTATAGTNTGATGACAAAGAAACCGTCAAGCT 129
Db 121 cccagctcagc 171
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QY 130 CCCAGGCTCTTATTATGATGATCCAGCAGGCGCACTGGCATCCCGAGAC 180

RESULT

ID HS1267683 standard: RNA: EST: 171 BP.
AC AA476303.
NI Q2204514
DT 23-JUN-1997 (Rel. 52, Created)
DE ZW2904 s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770705
DE 3' similar to gb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION
DE (HUMAN)..
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-171
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kriman D., Kucaba L., Lacy M., Le N., Lennon G., Marra M.,
RA Martin J., Moore R., Schellenberg K., Steptoe M., Tan F.,
RA Theising B., White Y., Wylie T., Waterston R., Wilson R.,
RT "WashU-NCI human EST Project";
RL Unpublished.
CC Contact: Wilson RK Washington University School of Medicine 4444
CC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
CC 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is

CC available royalty-free through LLNL : contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information Seq primer: -41m13
CC fwd. ET from Amersham.
FH Key Location/Qualifiers
FH source 1 171
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5'
FT TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3']
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M. Fatima Ronaldo.
FT /clone="770705"
FT /sex="Female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT complement(<1..>171)
FT mrna
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Query Match 47.0%; Score 149; DB 63; Length 171;
Best Local Similarity 94.7%; Pred. No. 1.17e-247;
Matches 162; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Db 2 accagat-tccaggacccctgtcttctccaggaggaagacacccctctctcagg 60
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QY 10 ACCGAGTCTCCAGGACCCCTGCTTTCTCCAGGAGGAGAGGACCCCTCTCTCAGG 69
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QY 70 GCGAGTCAAGTCTTAGAGCAAAATAGTATAGTNTGATGACAAAGAAACCGTCAAGCT 129
Db 121 cccagctcagc 171
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QY 130 CCCAGGCTCTTATTATGATGATCCAGCAGGCGCACTGGCATCCCGAGAC 180
RESULT 9
LOCUS AA454224 324 bp mRNA EST 10-JUN-1997
DEFINITION ZW2904 s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770705
5' similar to gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION
(HUMAN)..
ACCESSION AA454224
NID G2189108
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Kucaba L., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
White Y., Wylie T., Waterston R. and Wilson R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 161.

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TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not 1 and cloned into
the Not 1 and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/cclone="810346"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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Matches 190; Conservative 0; Mismatches 16; Indels 5; Gaps 3;
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QY 70 GCCAGTCACAGCTTTAGTACCAAACTATTAGCTGTAGTGTACCAAGAACTCTGCTGTATAG 129
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QY 130 CCCAGGCTCTTCATTTATCATGATCCAGCAGGCGCACTGGCATCCACAGACAGGTTTCAG- 188
Db 257 tggcagtgaggtctaggacagagttcactct 287
QY 189 TGGCAGTGGGTCT-TGGACAGACTTCACCTCT 218
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AC AA464224;
NI 92189108
DT 13-JUN-1997 (Rel 52, Created)
DE zx83c06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810346
DE 5' similar to gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION
DE (HUMAN);.
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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RP 1-324
RA Hillier L., Allen M., Bowles L., Dubouque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore R., Schellenberg K., Steptoe M., Tan F., Theising R.,
RA White Y., Wyllie T., Waterston P., Wilson P.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilton RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC estw@wustl.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28m13 rev2 ET from Amersham High
CC quality sequence stop 161
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FH Location/Qualifiers
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/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
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strand cDNA was primed with a Not 1 - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not 1 and cloned into
the Not 1 and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/cclone="810346"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:6040648"
BASE COUNT 68 a 102 c 82 g 72 t
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Query Match 45.7%; Score 145; DB 16; Length 324;
Best Local Similarity 90.0%; Pred. No. 2,53e-239;
Matches 190; Conservative 0; Mismatches 16; Indels 5; Gaps 3;
Db 80 acgagctccagcaccctctgtgtatccgggggaaagcaccctctctgcagg 139
QY 10 ACGCAGTCTCCAGCGCACCTGTCTGTCTCCAGGGGAAGAGCCCTCTCTCGAGG 69
Db 140 gccagtcagagtttagcagcaa---cttagcctgtaccagcagattcctggccagct 196
QY 70 GCCAGTCACAGCTTTAGTACCAAACTATTAGCTGTAGTGTACCAAGAACTCTGCTGTATAG 129
Db 197 cccaggtcctcatctatgtgtatccaccagggcgcacttggtatccagcagattcaga 256
QY 130 CCCAGGCTCTTCATTTATCATGATCCAGCAGGCGCACTGGCATCCACAGACAGGTTTCAG- 188
Db 257 tggcagtgaggtctaggacagagttcactct 287
QY 189 TGGCAGTGGGTCT-TGGACAGACTTCACCTCT 218
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LOCUS AA494059 217 bp mpNA EST 10-JUL-1997
DEFINITION ng61b01.s1 NCI-CCAP-Lip2 Homo sapiens cDNA clone 939241 similar to
gb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
ACCESSION AA494059
NID 92223900
KEYWORDS EST;
SOURCE human
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 217)
AUTHORS NCI-CCAP.
TITILE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/obrp/image/image.html
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Location/Qualifiers

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BASE COUNT
ORIGIN

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Best Local Similarity 90.1%: Pred. No. 8.85e-225:
Matches 154: Conservative 0: Mismatches 17: Indels 0: Gaps 0:

Db 47 acgacgtcgcagcaccctcttcttctcgaaggaacacacacccctctctcagg 106
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QY 10 ACCGAGTCTCCAGGACACCTCTCTCTCTCCAGGACCAAGGACCTCTCTCTCAGG 69
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QY 70 GCCAGTCAGAGCTTAGAGAGCAAAACATTAAGTCTCTCTCTCTCTCTCTCTCT 129
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Db 167 cccaggtctctctctctctctctctctctctctctctctctctctctctctct 217
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RESULT 12
ID HS1284569 standard: RNA: EST: 217 BP.
AC AA444039:
NI 92223900
DT 28-JUN-1997 (Rel. 52, Created)
DE nq61b01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 939241 similar to
DE qb:X06764 IG KAPPA CHAIN PREPROMOTER V-III REGION (HUMAN):
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
OC Homo.
RN [1]
RP 1-217
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,
CC M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation:
CC David B. Krizman, Ph.D. cDNA Library Arrayed by Greg Lennon, Ph.D.
CC DNA Sequencing by: Washington University Genome Sequencing Center
CC Clone distribution: NCI-CGAP clone distribution information can be
CC found through the I.M.A.G.E. Consortium/LLNL at:
CC www.bio.llnl.gov/bbrp/image/image.html Insert Length: 922 Std
CC Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham.
CC Location/Qualifiers
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FH source
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44 a 75 c 55 g 43 t
BASE COUNT
ORIGIN

Query Match 43.5% Score 138: DB 38: Length 217:
Best Local Similarity 90.1%: Pred. No. 8.85e-225:
Matches 154: Conservative 0: Mismatches 17: Indels 0: Gaps 0:

Db 47 acgacgtcgcagcaccctcttcttctcgaaggaacacacacccctctctcagg 106
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QY 10 ACCGAGTCTCCAGGACACCTCTCTCTCTCCAGGACCAAGGACCTCTCTCTCAGG 69
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Db 167 cccaggtctctctctctctctctctctctctctctctctctctctctctctct 217
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QY 130 CCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
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RESULT 13
ID HS1145281 standard: PNA: EST: 260 BP.
AC AA225858:
NI 91847166
DT 23-FEB-1997 (Rel. 51, Created)
DE nq61b01.s1 NCI_CGAP_Pri Homo sapiens cDNA clone 1009353 similar to
DE qb:X11894 IG KAPPA CHAIN PREPROMOTER V-III REGION (HUMAN):
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
OC Homo.
RN [1]
RP 1-260
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: W. Marston Linehan,
CC M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA
CC Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed
CC by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by:
CC Washington University Genome Sequencing Center Clone distribution:
CC NCI-CGAP clone distribution information can be found through the
CC I.M.A.G.E. Consortium/LLNL at:
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Matches 154: Conservative 0: Mismatches 17: Indels 0: Gaps 0:

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QY 10 ACCGAGTCTCCAGGACACCTCTCTCTCTCCAGGACCAAGGACCTCTCTCTCAGG 69
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Db 167 cccaggtctctctctctctctctctctctctctctctctctctctctctctct 217
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QY 130 CCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
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adaptors, 5 cycles of PCR applied to the cDNA with an
adaptor-specific primer, and the resulting PCR product
subcloned into pAMP10 by the ligation cloning method (Life
Technologies). Average insert size is 600 bp. NCI: Not
directionally cloned. This library was constructed by David
Krizman."
/clone="1009353"
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ACCESSION AA225858
NID 91847166
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes, Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria, Primates, Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS NCI-CGAP.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph D
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,
M D, Michael Emmert-Buck, M D, Ph D
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

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High quality sequence stop: 250
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/notes="vector: pAMP10; Site_1: NotI, Site_2: EcoRI, 1st
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5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
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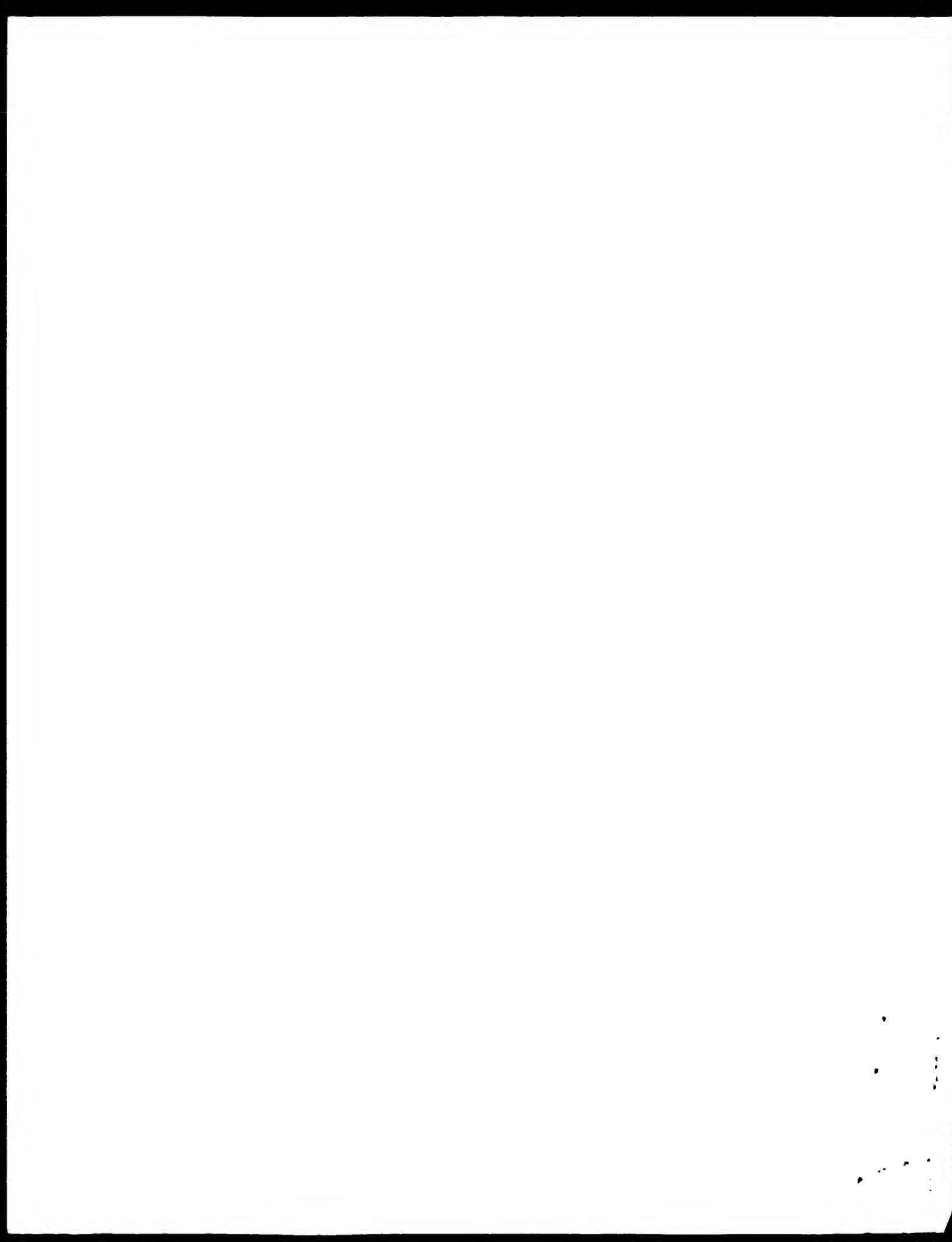
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QY 70 GGCAGTCAGAGCTTAGGAGGAAATAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129
DB 213 cccattcctcctcctatctatagcagcagcagcagcagcagcagcagcagcagcagcagc 252
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 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
 REFERENCE 1 (bases 1 to 370)

REFERENCE
AUTHORS

1 (bases 1 to 370)
Adams, M. D., Karlavagne, A. P., Fleischmann, P. D., Fuldner, P. A., Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Well, C., Clayton, P. A., Cline, T. P., Cotton, M. D., Parle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geochagen, N. S., Glodak, A., Gnehm, G. L., Hanna, M. C., Hedblom, E., Hinkle, S. J., Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Mertlich, J. M., Moreno-Palanco, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, P., Small, K. V., Spraggs, T. A., Unterback, T. P., Weidman, J. F., White, D., Benard, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dunke, D. L., Feng, D. F., Fertile, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, T., Hudson, P., Kim, A. K., Kozak, D. L., Kunsch, C., HungJun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J. X., Yu, G. L., Yuen, S. M., Dillion, P. J., Fannon, M. P., Posen, C. A., Haseltine, W. A., Fields, C. C., Fraser, C. M., and Venter, J. C.

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100	1000	1000

Rest. local	Matches
Db	59
Qy	10
Db	119
Qy	70
Db	176

Db	296	gc
Qy	250	gc

RESULT	8
LOCUS	
DEFINITION	

DEFINITION
ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

QY	275	GAA-CACCTC-GC-ACCTCGGCGGAGGACCAAGGTGGAAATCAAA	318
RESULT	13		
LOCUS		AA434001	269 bp mpNA
DEFINITION		AA425f01.v1 Soares ovary; tumor NDH01 Homo sapiens cDNA clone 770329	29-MAY-1997
		5' similar to gb:211894 IG KAPPA CHAIN PRECURSOR V-III REGION	
ACCESSION		(HUMAN):	
		AA434001	
KEYWORDS		g2138915	
SOURCE		EST.	
ORGANISM		human.	
		Homo sapiens	
		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	
		Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae;	
		Homo.	
REFERENCE		1 (bases 1 to 269)	
AUTHORS		Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,	
		Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,	
		Moore,B., Schellenberg,K., Stepec,M., Tan,F., Theising,B.,	
		White,Y., Wylie,T., Waterston,P. and Wilson.R.	
TITLE		WashU-Merck EST Project 1997	
JOURNAL		Unpublished (1997)	

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINK. Contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham.

```

FEATURES
source
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1..269
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer {5
TGTACCAATCTGAAGTGGAGGCGCGGTTTCTTTTCTTTT 3'},
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo."

```

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mRNA  
BASE COUNT      59 a    90 c   67 q   53 t
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/db_xref="GDB:5980203"
.l>269
/lab_host="DH10B (ampicillin resistant)"
/tissue_type="ovarian tumor"
/sex="Female"
/clone_lib="Soares ovary tumor NbHOT"

Query Match:	49.2%	Score 156;	DB 87;	Length 269;
Best Local Similarity	95.3%;	Pred. No. 1.16e-264;		
Matches	163;	Conservative	0;	Mismatches 8;
		Indels	0;	Gaps 0;

Db	99	acccagctccagcacccctctcttctccaggggaaagagccacccctctctccagc	158
QY	10	AGCCAGCTCTCCAGAGCACTCTCTCTTTTCTCTCTCAAGGGCAAAACACCTCACTCTCTCAAGG	69
Db	159	gccagctcagagtggttagcagcagctctattagctcttggtaccagcagaacacctgacccaggtc	218
QY	70	GCCAGCTCAGAGTCTCTAGCAGCAATACTATGCTNTGGTATCCAACTAAACAGAAATTTGGCTAGAGCT	129
Db	219	cccagagctccctcaactctatgttgctccctccagcagggccactgagcctccccagac	269
QY	130	CCGAGGCTCTCTATTATATGATGCTATCCATCCAGCAGAGGCCCATGGCATCTCCAGAC	180

Matches	177:	Conservative	0:	Mismatches	20:	Indels	3:	Gaps	2:
Db	87	ctccagccacctgtctgtntctccaggaggaaagagccaccctntcctgcagggccagtc							146
Qy	17	CTCCAGGCACCCCTGTCTTTTGTCTCCAGSGGAAAGAGACCCCTCTCTCTGCGAGGGCCAGTC							76
Db	147	agagtgttagcag--aa-acttagcctgggtccagcagaaacccctggccagcctcccaggc							203
Qy	77	AGAGTCTTAGCAGCAAAATACCTTAGCTGTGTACCAACAGAAACCTGGCCAGGCTCCACAGGC							136
Db	204	tectnttctatgggtgcctccaccagggccactgggtatcccagccaggttcaagtggcagtg							263
Qy	137	TCTTCATTATGATGTCATCCAGCAGGGCCACTGSCATCCACAGAGGTTDAGTGGCAGTG							196
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Qy	197	GGTCTGGGACAGACTTCACT							216

Search completed: Tue Feb 24 09:25:31 1998
 Job time : 130 secs.

[WATERMAN] (TM)

Release 2 ID John F. Collins, Biocomputing Research Unit.
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MPsrch_nnn a - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 09:19:27 1998 MasPar time 204.25 seconds
Tabular output not generated 768,844 Million cell updates/sec

Title: >US-08-844-215-21
Description: (1-118) from M80844215.seq
Perfect Score: 317
N.A. Sequence: 1 GCGCAGGTCACGGCAATGTCG
Comp: CGCTTCAGTCTGCTCAAGCG

Scoring table:
Gap 6
TABLE default

Nmatch STD : Dbase 0; Query 0
Searched: 565703 seqs, 246912800 bases x 2
Post-processing: Minimum Match 0
Listing first 45 summaries

Database:
EST-A
1-EST1 2-EST2 3-EST3 4-EST4 5-EST5 6-EST6 7-EST7 8-EST8
9-EST9 10-EST10 11-EST11 12-EST12 13-EST13 14-EST14
15-EST15 16-EST16 17-EST17 18-EST18 19-EST19 20-EST20
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184-EST184 185-EST185 186-EST186 187-EST187 188-EST188
189-EST189 190-EST190 191-EST191 192-EST192 193-EST193
194-EST194 195-EST195 196-EST196

Statistics: Mean 3.528; Variance 1.999; scale 5.202

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Prod. No.
1	228	71.9	381.58	T29114	EST69430 Homo sapiens	0.00e+00
2	217	68.5	383.59	T29145	EST99871 Homo sapiens	0.00e+00
3	211	66.6	383.58	T27870	EST19007 Homo sapiens	0.00e+00
4	192	60.6	570.34	P75233	Y38138 H1 Homo sapiens	0.00e+00
5	184	58.0	463.34	P65632	Y32086 H1 Homo sapiens	0.00e+00
6	183	57.7	389.69	H44798	YF4410 H1 Homo sapiens	0.00e+00
7	182	57.4	401.40	P10529	YF1406 H1 Homo sapiens	0.00e+00
8	181	57.1	332.58	T29342	EST77121 Homo sapiens	0.00e+00
9	180	56.8	359.64	H27642	Y16107 H1 Homo sapiens	0.00e+00
10	159	50.2	451.10	T90236	Y15d10 H1 Homo sapiens	1.38e-271
11	146	45.1	171.64	H26498	Y14706 H1 Homo sapiens	4.31e-274
12	143	45.1	385.64	H26475	Y15195 H1 Homo sapiens	9.20e-238
13	136	42.9	421.27	P48043	Y35501 H1 Homo sapiens	4.44e-223
14	127	40.1	360.37	P39907	Y35501 H1 Homo sapiens	3.12e-204
15	125	39.4	261.28	P51942	Y37167 H1 Homo sapiens	4.10e-200
16	124	39.1	438.23	R64693	Y122109 H1 Homo sapiens	5.58e-198
17	122	38.5	235.65	H28891	YP0311 H1 Homo sapiens	8.08e-194
18	115	36.3	232.63	H21646	Y33013 H1 Homo sapiens	2.65e-179
19	114	36.0	219.64	H27031	Y15501 H1 Homo sapiens	2.00e-177
20	109	34.4	201.64	H26206	Y13502 H1 Homo sapiens	5.22e-167
21	108	34.1	493.68	T27593	EST10654 Homo sapiens	7.21e-165
22	100	31.5	130.69	H44338	YP04110 H1 Homo sapiens	1.74e-148
23	97	30.6	176.81	H54909	Y35501 H1 Homo sapiens	2.22e-142
24	96	30.3	151.83	H22098	Y134305 H1 Homo sapiens	2.40e-140
25	96	30.3	364.68	T27593	EST10654 Homo sapiens	2.40e-140
26	93	29.3	470.81	H22117	Y34301 H1 Homo sapiens	2.89e-134
27	91	28.7	447.84	H26726	Y35501 H1 Homo sapiens	3.18e-130
28	87	27.4	516.23	P75559	Y14706 H1 Homo sapiens	3.55e-122
29	86	27.1	279.58	T29145	EST99871 Homo sapiens	3.61e-120
30	86	27.1	503.22	P28231	Y35501 H1 Homo sapiens	3.61e-120
31	85	26.8	295.58	T29114	EST69430 Homo sapiens	3.61e-118
32	85	26.8	433.11	T29114	EST69430 Homo sapiens	3.61e-118
33	84	26.5	393.41	H25942	Y34301 H1 Homo sapiens	3.62e-116
34	82	25.9	488.64	H25935	Y14706 H1 Homo sapiens	3.62e-112
35	79	24.9	457.64	H27034	Y15501 H1 Homo sapiens	2.22e-106
36	75	23.7	297.28	P49771	Y35501 H1 Homo sapiens	2.54e-98
37	74	23.3	261.27	P45879	Y15403 H1 Homo sapiens	2.94e-96
38	73	23.0	210.34	P58493	Y34301 H1 Homo sapiens	3.61e-94
39	71	22.4	288.58	T27731	EST13641 Homo sapiens	1.74e-90
40	71	22.4	359.58	T27593	EST10654 Homo sapiens	1.74e-90
41	70	22.1	203.68	H29743	Y34301 H1 Homo sapiens	1.54e-88
42	69	21.8	189.51	P29213	Y14706 H1 Homo sapiens	1.35e-86
43	69	21.8	248.24	P29535	Y34301 H1 Homo sapiens	1.35e-86
44	67	21.1	288.58	T27593	EST10654 Homo sapiens	1.35e-82
45	67	21.1	366.64	H27048	Y15501 H1 Homo sapiens	1.35e-82

ALIGNMENTS

RESULT 1 T29114 381 bp mRNA EST 06-SEP-1995
LOCUS EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light
DEFINITION chain V(LII).J(V) regions (GB:227170) (MT:3121).
ACCESSION T29114
NID d611212
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human Lymphoid tissue.

ORGANISM	Homo sapiens
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Osteichthyes; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota, Mammalia, Theria, Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 381)
AUTHORS	Adams,M.B., Lee,N., Kirkness,E.F., Weinstein,K.G., Gorsyne,J.D., Bult,C.J., Kerlan,G., Blake,J.A., Brandon,P.C., Chiu,M.-W., White,O., Sutton,G., Clontz,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Clayton,P.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.M., Glodak,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Pyder,S.E., Scott,B.L., Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Ytterback,T.P., Weidman,D.F., Willy,V., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrige,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,T.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Puben,S.M., Dillon,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL	Unpublished (1995)

NTD KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL
9612014	human primer=M13 Reverse library=Human Pancreas. EST. human sapiens Eukaryotae: Metazoa: Eumetazoa: Bilateria: Coelomata: Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes: Sarcopterygii: Chonata: Tetrapoda: Amniota: Mammalia: Theria: Eutheria: Archonta: Primates: Catarrhini: Hominiidae: Homo: 1 (bases 1 to 383)	ADAMS, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A., Bult, C. J., Lee, N., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, C. J., Sutton, G., Blake, J. A., Brandon, P. C., Chiu, M.-W., Clayton, R. A., Cline, P. T., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S. M., Glodek, A., Gnehm, C. T., Hanna, M. C., Hedblom, E., Hinkle, J. P. S., Kelley, J. M., Klemke, K. M., Kelley, J. C., Liu, L. I., Marmaro, S. M., Merrick, J. M., Moreno-Palauques, P. F., McDonald, L. A., Nguyen, D. T., Pellegrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, P., Small, K. V., Springs, T. A., Utterback, T. K., Weidman, J. F., Li, Y., Bednarek, D. P., Rao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, P., Ferrle, A., Fischer, C. A., Hastings, G. A., He, W.-W., Hu, L.-S., Greene, J. M., Gruber, J., Hudson, P., Kim, A., Kozak, D. I., Kunsch, C. J. H., Li, H., Lubliner, P. S., Olsen, H., Raymond, D. L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Rubin, S. M., Millon, P. J., Fannon, M. P., Posen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C.	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 42 Million Basepairs of cDNA Sequence Unpublished (1995)

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699356
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this Esf, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

[illegible]

qb:M12743_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN):.
 RS1922
 MID g813824
 KEYWORDS EST.
 SOURCE human clone-154165 library-Soares breast 2NBHst vector-pT73D
 (pharmacia) with a modified polylinker host-DH10B (ampicillin
 resistant) primer-M13RP1. Rsite1-Not I Rsite2-Eco RI Adult female.
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
 TGTTACCAATGTGAGTGGAGCGGCCCTTTTITTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned into the Not I and Eco RI sites of a
 modified p773 vector (Pharmacia). Library went through one round
 of normalization to a Cot - 230. Library constructed by Bento
 Soares and M.Fatima Bonaldo.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 361)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, I., Soares, M., Tan, F.,
 Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence stops: 308
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 FEATURES
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 /clone="154165"
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 Db 268 cagtgaggtctgggacacaggttcantttccacatcagacacacacacacacacacacacacac 327
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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 Db 328 tcaagctctattattgttcacagatcat 353
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Search completed: Tue Feb 24 09:23:01 1998
 Job time : 214 secs.



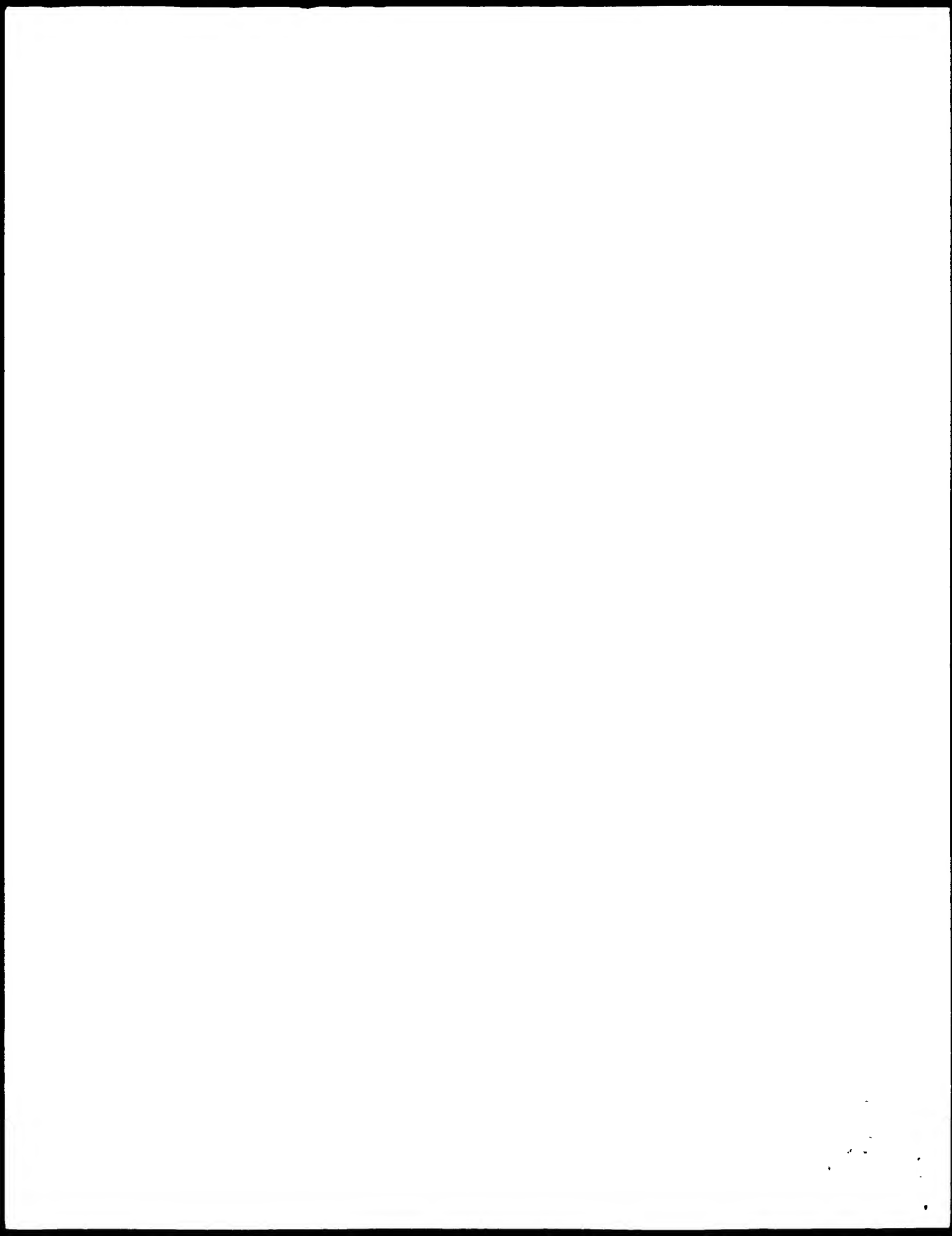
RESULT 14
 ID R41286 standard; Protein: 129 AA.
 AC R41286;
 DT 01-NOV-1993 (first entry)
 DE F105 rearranged variable region light chain.
 KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..129
 FT /label= mat_protein
 PN W09J12232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U10928.
 PP (DAND) DANA FARBER CANCER INST INC
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 DR WPI: 93-214174/26.
 DR N-PSDB: Q49155.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Claim 10; Page 79; 109pp; English.
 CC mpNA from the known hybridoma F105 was converted to cDNA and this
 CC subjected to PCR amplification using primers corresp. to appropriate
 CC parts of the heavy or light chains and having restriction sites to
 CC permit cloning. The extension prods. were isolated and sequenced.
 CC The recombinant human monoclonal antibody (MAB) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The MAB may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/kg.
 SQ Sequence 129 AA:

Query Match 87.5%; Score 561; DB 7; Length 129;
 Best Local Similarity 90.5%; Pred. No. 6.47e-39;
 Matches 95; Conservative 3; Mismatches 7; Indels 0; Gaps 0.
 Db 24 ltqspgtlslsageratlsrscasgsrsrylawyqkpgqaprllygassratgipdrf 83
 ||||||||||||||||||| ||||| ||||||||||||||||||| |||||||
 QY 3 LTQSPGTLSLSPGPATLSGASQSVPSNYLAWYQKPGQAPPLLYGVSSPATGIDPF 62
 ||||||||||||||||||| ||||| ||||||||||||||||||| |||||||
 Db 84 ssgsgtdftltisrvepedfavyycqgydbsvctfsggtkleik 128
 ||||||||||||||||||| ||||| ||||||||||||||||||| |||||||
 QY 53 SSGSGTDFTLTISRPEDEFAVYVCQYGSSPRTFGGKTLEIK 107

RESULT 15
 ID R38673 standard; Protein: 129 AA.
 AC R38673;
 DT 01-NOV-1993 (first entry)
 DE F105VK-F105JK.
 KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide
 FT Protein 21..129
 FT /label= mat_protein
 FT Region 1..116
 FT /label= F105VK
 FT Region 117..129
 FT /label= F105JK
 FT Region 44..55
 FT /label= CDR1

FT Region 71..77
 FT /label= CDR2
 FT Region 110..117
 FT /label= CDR3
 FT Misc_difference 1
 FT /note= "Met encoded by ATC (sic)"
 FT Misc_difference 35
 FT /note= "Pro encoded by GCA (sic)"
 FT Misc_difference 99
 FT /note= "Leu encoded by GTG (sic)"
 FT Misc_difference 113
 FT /note= "Gly encoded by GAT (sic)"
 FT Misc_difference 114
 FT /note= "Ser encoded by AAC (sic)"
 FT Misc_difference 116
 FT /note= "Pro encoded by GTT (sic)"
 FN W09J12232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U10928.
 PP (DAND) DANA FARBER CANCER INST INC.
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 DR WPI: 93-214174/26.
 DR N-PSDB: Q42706.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Disclosure: Page 74-75; 109pp; English.
 CC The nucleotide sequence of F105 V_K (Q42707 - sequence differs from
 CC other F105 V_K sequences given elsewhere in the specification) was
 CC compared with germline gene Humk325 (Q42706), showing 97.7%
 CC similarity. By nucleotide sequence analysis, F105 appears to
 CC be derived from a member of the V_K III subgroup gene family.
 SQ Sequence 129 AA:
 Query Match 87.2%; Score 658; DB 7; Length 129;
 Best Local Similarity 89.5%; Pred. No. 1.07e-38;
 Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0.
 Db 24 ltqspgtlslsageratlsrscasgsrsrylawyqkpgqaprllygassratgipdrf 83
 ||||||||||||||||||| ||||| ||||||||||||||||||| |||||||
 QY 3 LTQSPGTLSLSPGPATLSGASQSVPSNYLAWYQKPGQAPPLLYGVSSPATGIDPF 62
 ||||||||||||||||||| ||||| ||||||||||||||||||| |||||||
 Db 84 ssgsgtdftltisrvepedfavyycqgydbsvctfsggtkleik 128
 ||||||||||||||||||| ||||| ||||||||||||||||||| |||||||
 QY 53 SSGSGTDFTLTISRPEDEFAVYVCQYGSSPRTFGGKTLEIK 107

Search completed: Tue Feb 24 07:22:39 1998
 Job time : 29 secs.



CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/926,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: TSP1 409 1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 646 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ Sequence 546 BP: 162 A: 187 C: 170 G: 127 I: 0 Other:

Query Match 81.4% Score 258. DB 7: Length 546.
Best Local Similarity 90.8% Pred No 172e-172:
Matches 286: Conservative 0: Mismatches 29: Indels 0: Gaps 0:

Db 1 GAGCTCACCGAGTCTCCAGGCGCGCTTTGTTCTCCAGGCGGAAAGAGCCACCTCTCC 60
|||||
Qy 4 GAGCTCACCGAGTCTCCAGGCGCGCTTTGTTCTCCAGGCGGAAAGAGCCACCTCTCC 63
|||||

Db 61 TCGAGGGCGAGTCAAGAGTGTAGAGAGAGAGTACCTGAGTGTAGAGAGAGAGAGAGAGAG 120
|||||
Qy 64 TCGAGGGCGAGTCAAGAGTGTAGAGAGAGAGTACCTGAGTGTAGAGAGAGAGAGAGAG 123
|||||

Db 121 CAGGCTCCAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 180
|||||
Qy 124 CAGGCTCCAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATGATGATGATG 183
|||||

Db 181 TCCAGTGGCAGTGGGTGTGGGACAGAGTCTCTACCTATGATGATGATGATGATGATGATGAT 240
|||||
Qy 184 TCCAGTGGCAGTGGGTGTGGGACAGAGTCTCTACCTATGATGATGATGATGATGATGATGAT 243
|||||

Db 241 GATTGTGAGTGTACTACTGTGAGAGAGTATGATGATGATGATGATGATGATGATGATGATG 300
|||||
Qy 244 GATTGTGAGTGTACTACTGTGAGAGAGTATGATGATGATGATGATGATGATGATGATGATG 303
|||||

Db 301 AAGTGGGAACCAAA 315
|||||
Qy 304 AAGTGGGAACCAAA 318
|||||

RESULT 4
ID US-08-053-131-182 STANDARD: DNA; UNC: 900 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 182, Application US/08053131
CC Sequence 182, Application US/08053131
CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 200

CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent-In Release #1 0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 182:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 900 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 301e(116 163 351 650)
CC Sequence 900 BP: 229 A: 241 C: 201 G: 238 I: 0 Other:

Query Match 77.9% Score 247: DB 7: Length 900:
Best Local Similarity 96.2% Pred No 3.85e-154:
Matches 256: Conservative 0: Mismatches 10: Indels 0: Gaps 0:

Db 375 AGCGAGTCTCCAGGCGCGCTTTGTTCTCCAGGCGGAAAGAGCCACCTCTCCAGG 434
|||||
Qy 10 AGCGAGTCTCCAGGCGCGCTTTGTTCTCCAGGCGGAAAGAGCCACCTCTCCAGG 439
|||||

Db 435 GCAGTGTAGTGTGTAGAGAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATG 444
|||||
Qy 70 GCAGTGTAGTGTGTAGAGAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATG 449
|||||

Db 495 CCGAGGCTCCCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 554
|||||
Qy 130 CCGAGGCTCCCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 584
|||||

Db 555 GCAGTGTAGTGTGTAGAGAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATG 614
|||||
Qy 190 GCAGTGTAGTGTGTAGAGAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATG 649
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Db 615 GCAGTGTAGTGTGTAGAGAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATG 640
|||||
Qy 250 GCAGTGTAGTGTGTAGAGAGAGTCTCTACCTATGATGATGATGATGATGATGATGATGATG 675
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RESULT 5
ID PCT-US93-12501-1 STANDARD: DNA; UNC: 325 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9312501.
CC Sequence 1, Application PC/TUS9312501
CC GENERAL INFORMATION:

CC APPLICANT: Chang, Tse Wen
 CC TITLE OF INVENTION: ALLERGEN-SPECIFIC IgA MONOCLONAL ANTIBODIES AND
 CC TITLE OF INVENTION: RELATED PRODUCTS FOR ALLERGY TREATMENT
 CC NUMBER OF SEQUENCES: 10
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Tanox Biosystems, Inc
 CC STREET: 10101 Stella Link Rd.
 CC CITY: Houston
 CC STATE: Texas
 CC COUNTRY: USA
 CC ZIP: 77025
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5" Hi Density Diskette
 CC COMPUTER: IBM PS/2
 CC OPERATING SYSTEM: DOS, Version 3.30
 CC SOFTWARE: Wordperfect 5.1
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/12501
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER:
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Mirabel, Eric P
 CC REGISTRATION NUMBER: 31,211
 CC REFERENCE/DOCKET NUMBER: TXN92-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 713-664-2288
 CC TELEFAX: 713-664-8914
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 325 nucleotides
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double stranded
 CC TOPOLOGY: Linear
 CC Sequence 325 BP: 79 A; 93 C; 79 G; 74 T; 0 other;

Query Match 75.1%; Score 238; DB 11; Length 325;

Best Local Similarity 90.4%; Pred No. 2,57e-157;

Matches 282; Conservative 0; Mismatches 27; Indels 3; Gaps 3;

Db 13 AGCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAAGAGCCACCTCTCTCTCAGG 72

QY 10 AGCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAAGAGCCACCTCTCTCTCAGG 69

Db 73 GCCAGTCAGACTGTAGCAGCAACTACTTAGCTGGTACCAGCACAAACCTGGCCAGGT 132

QY 70 GCCAGTCAGACTGTAGCAGCAACTACTTAGCTGGTACCAGCACAAACCTGGCCAGGT 129

Db 133 CCCAGGCTCTCATCTATGCTACATCCATCCATCTGGCATCCCGACAGAGTTCACT 192

QY 130 CCCAGGCTCTCATCTATGCTACATCCATCCATCTGGCATCCCGACAGAGTTCACT 189

Db 193 GGCAGTGGGTCTGGACAGACTTCTACTCTACCATCAGCAGACTGGAGGCTGAAGATTTT 252

QY 190 GGCAGTGGGTCTGGACAGACTTCTACTCTACCATCAGCAGACTGGAGGCTGAAGATTTT 249

Db 253 GCAAGTATTACTGTTCAGCAGTTCGTAACCTCAGAGTGGAGTTCGGCCAGGACCAAG 312

QY 250 GCAAGTATTACTGTTCAGCAGTTCGTAACCTCAGAGTGGAGTTCGGCCAGGACCAAG 306

Db 313 GTTGAATCAAA 324

QY 307 GTTGAATCAAA 318

RESULT

ID US-08-053-131-178 STANDARD; DNA; UNC; 812 BP.

AC xxxxxx

DE 01-JAN-1900

Sequence 178, Application US/08053131

Sequence 178, Application US/08053131

CC Patent No. 5661016
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 197
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: One Market Plaza, Steuart Tower, Suite 200
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/053,131
 CC FILING DATE: 26-APR-1993
 CC CLASSIFICATION: 800
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/990,860
 CC FILING DATE: 16-DEC-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/810,279
 CC FILING DATE: 17-DEC-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/853,408
 CC FILING DATE: 18-MAR-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William W.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 178:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 812 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: join(199..246, 418..714)
 CC Sequence 812 BP: 201 A; 325 C; 187 G; 194 T; 0 other;

Query Match 67.8%; Score 215; DB 7; Length 812;

Best Local Similarity 93.9%; Pred No. 6.48e-140;

Matches 245; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

Db 442 AACAGAGTCTCCAGCAGCTCTCTTTTGTCTCCAGGGAAGAGCCACCTCTCTCTCAGG 501

QY 10 AACAGAGTCTCCAGCAGCTCTCTTTTGTCTCCAGGGAAGAGCCACCTCTCTCTCAGG 69

Db 502 GCCAGTCAGACTGTAGCAGTTCGTAACCTCAGAGTGGAGTTCGGCCAGGACCAAG 558

QY 70 GCCAGTCAGACTGTAGCAGTTCGTAACCTCAGAGTGGAGTTCGGCCAGGACCAAG 129

Db 559 CCCAGGCTCTCATCTATGCTACATCCATCCATCTGGCATCCCGACAGAGTTCACT 618

QY 130 CCCAGGCTCTCATCTATGCTACATCCATCCATCTGGCATCCCGACAGAGTTCACT 189

Db 619 GGCAGTGGGTCTGGACAGACTTCTACTCTACCATCAGCAGACTGGAGGCTGAAGATTT 678

QY 190 GGCAGTGGGTCTGGACAGACTTCTACTCTACCATCAGCAGACTGGAGGCTGAAGATTT 249

Db 679 GCAAGTATTACTGTTCAGCAGTTCGTAACCTCAGAGTGGAGTTCGGCCAGGACCAAG 699

QY 307 GTTGAATCAAA 318

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OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]

RP SEQUENCE.
 RA MILSTEIN C ; 2-301-304(1969)
 RL FEBS LETT. 2-301-304(1969)
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01891; K3H06
 DR HSP: P01607; IMCP
 KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA: 11635 MW: 4606868E CRC32:

Query Match 78.2%; Score 577; DB 5; Length 108;
 Best Local Similarity 76.2%; Pred. No. 5.68e-105;
 Matches 80; Conservative 14; Mismatches 9; Indels 2; Gaps 2;

Db 4 ltqspgtlslspgrraalscrasgslsngylawyyqkqgqaprllymgyssratgipdrf 63
 QY 3 LTQSPATLSLSPGERATLSGRASQSVN-KYLAWYQKQKQAPRLIYDASNATGIPAPF 61
 Db 64 sqsgsgdftltisrlpepfavvyqgyspftfggskleik 108
 QY 62 SGSGSGTDFLTISNLEPEFAVYCCQSDWV-TFGGKVEIK 105

RESULT 10

ID KV3C_HUMAN STANDARD: PRT: 109 AA.
 AC P04206;
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (GOL) (PHEUMATOID FACTOR)
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 86230578.
 RA NEWKIRK M., CHEN P. P., CARSON D. A., POSNETT D., CAPPA J. D.
 RL MOL. IMMUNOL. 23:239-244(1986)
 DR PIR: A01893; K3H06.
 DR HSP: P01607; 1DFB.
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11830 MW: 8930CC4A CRC32:

Query Match 77.5%; Score 572; DB 5; Length 109;
 Best Local Similarity 80.0%; Pred. No. 8.23e-104;
 Matches 84; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

Db 4 ltqspgtlslspgrraalscrasgslsngylawyyqkqgqaprllymgyssratgipdrf 63
 QY 3 LTQSPATLSLSPGERATLSGRASQSVN-KYLAWYQKQKQAPRLIYDASNATGIPAPF 61
 Db 64 sqsgsgdftltisrlpepfavvyqgyspftfggskleik 108
 QY 62 SGSGSGTDFLTISNLEPEFAVYCCQSDWV-TFGGKVEIK 105

RESULT 11

ID KV3C_HUMAN STANDARD: PRT: 100 AA.
 AC P01621;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (NG9) (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.

RN [1]
 PP SEQUENCE FROM N. A.
 RX MEDLINE: 84093600.
 RA BENTLEY D. L.;
 RL NATURE 307:77-80(1984).
 CC -1- THIS GENE WAS ISOLATED FROM THE NG9/a.1 HYBRIDOMA.
 DP PIR: A01894; K3H06.
 DR HSP: P01607; IAAG.
 KW IMMUNOGLOBULIN V REGION: SIGNAL: HYBRIDOMA.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NG9).
 FT DISULFID 27 93 BY SIMILARITY.
 FT NON_TER 100 100
 SQ SEQUENCE 100 AA: 10729 MW: 99A75233 CRC32:

Query Match 75.1%; Score 554; DB 5; Length 100;
 Best Local Similarity 88.6%; Pred. No. 1.23e-99;
 Matches 78; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Db 8 ltqspgtlslspgrraalscrasgslsngylawyyqkqgqaprllymgyssratgipdrf 67
 QY 3 LTQSPATLSLSPGERATLSGRASQSVN-KYLAWYQKQKQAPRLIYDASNATGIPAPF 61
 Db 68 sqsgsgdftltisrlpepfavvyqgyspftfggskleik 95
 QY 62 SGSGSGTDFLTISNLEPEFAVYCCQ 89

RESULT 12

ID KV3C_HUMAN STANDARD: PRT: 128 AA.
 AC P06311;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE: 86041852.
 RA KLOBECK H. G., MEINIG A., COMBIATO G., SOLOMON A., ZACHAU H. G.
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: 200021; G33179;
 DR PIR: A01899; K3H041.
 DR HSP: P01607; 3HPM.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 128 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA: 14070 MW: 318E08AF CRC32:

Query Match 75.1%; Score 554; DB 5; Length 128;
 Best Local Similarity 80.8%; Pred. No. 1.23e-99;
 Matches 84; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

Db 24 ltqspgtlslspgrraalscrasgslsngylawyyqkqgqaprllymgyssratgipdrf 83
 QY 3 LTQSPATLSLSPGERATLSGRASQSVN-KYLAWYQKQKQAPRLIYDASNATGIPAPF 62
 Db 84 sqsgsgdftltisrlpepfavvyqgyspftfggskleik 127
 QY 63 SGSGSGTDFLTISNLEPEFAVYCCQSDWV-TFGGKVEIK 105

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DR PIR: A01896; K3HUML.
DR HSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11746 MW; 7D9F5D75 CRC32;
BY SIMILARITY.

Query Match 81.3%; Score 600; DB 5; Length 109;
Best Local Similarity 84.8%; Pred. No. 2.53e-110;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 ltqspgtlslspgeratlscrasqsvsflwyqgkqgqaprllyvassratgiparf 63
Qy 3 ltqspatlslspgeratlscrasqsvnk-ylwyqgkqgqaprllyvassratgiparf 61
Db 64 sgsgsgtdftltisrlepedfavyqgqgsqstfgqgkveik 108
Qy 62 SGSGSGTDFTLTISNLEPEDFAVYQQRSDWV-TFGGKVEIK 105

RESULT 6
ID KV3D_HUMAN STANDARD: PPT: 109 AA
AC P01622:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (TI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE.
RX MEDLINE: 72188439.
RA SUTER L., BARNIKOL H.U., WATANABE S., HILSCHMANN N.;
PL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972)
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HUTI.
DR HSP: P01607; 2IMM.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DISULFID 23 89
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11788 MW; D0A70A81 CRC32.

Query Match 80.8%; Score 596; DB 5; Length 109;
Best Local Similarity 84.8%; Pred. No. 2.16e-109;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 ltqspgtlslspgeratlscrasqsvsflwyqgkqgqaprllyvassratgiparf 63
Qy 3 ltqspatlslspgeratlscrasqsv-NKYLAWYQKQPGQAPRLLYDASNPATGIPARF 61
Db 64 sgsgsgtdftltisrlepedfavyqgqgsqstfgqgkveik 108
Qy 62 SGSGSGTDFTLTISNLEPEDFAVYQQRSDWV-VTFGGKVEIK 105

RESULT 7
ID KV3H_HUMAN STANDARD: PPT: 129 AA
AC P04207;
DT 20-MAR-1987 (REL. 04, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (CLL) (RHEUMATOID FACTOR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 86177570.
RA JIRIK F.P., SORGE J., FONG S., HEITZMANN J.G., CURD J.G., CHEN P.P.,
RA GOLDFEIN P., CARSON D.A.;
PL PROC. NATL. ACAD. SCI. U.S.A. 83:2195-2199(1986)

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DR EMBL: M12740; G553436; -.
DR PIR: A01898; K3HOCCL.
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 59
FT DOMAIN 70 75
FT DOMAIN 77 108
FT DOMAIN 109 118
FT DOMAIN 119 129
FT DISULFID 43 108
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14275 MW; 2F344868 CRC32;
BY SIMILARITY.

Query Match 80.6%; Score 595; DB 5; Length 129;
Best Local Similarity 81.0%; Pred. No. 3.70e-109;
Matches 85; Conservative 11; Mismatches 7; Indels 2; Gaps 1;

Db 24 mtqspatlslspgeratlscrasqsvsnlawyqgkqgqpprlllygastratgiparf 83
Qy 3 ltqspatlslspgeratlscrasqsvnk-ylwyqgkqgqaprllyvassratgiparf 62
Db 84 sgsgsgtdftltisrlepedfavyqgqgsqstfgqgkveik 128
Qy 63 SGSGSGTDFTLTISNLEPEDFAVYQQRSDWV-TFGGKVEIK 105

RESULT 8
ID KV3E_HUMAN STANDARD: PPT: 109 AA.
AC P01624;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE.
RX MEDLINE: 1370:261-271(1976).
RA KLAPPER D.C., CAPRA J.D.;
PL ANN. INST. PASTEUR IMMUNOL. 1370:261-271(1976).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01897; K3HUPM
DR HSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11922 MW; A0C42C88 CRC32;
BY SIMILARITY.

Query Match 80.2%; Score 592; DB 5; Length 109;
Best Local Similarity 79.0%; Pred. No. 1.85e-108;
Matches 83; Conservative 12; Mismatches 8; Indels 2; Gaps 2;

Db 4 mtqspatlslspgeratlscrasqsvsflwyqgkqgqaprllygastratgiparf 63
Qy 3 ltqspatlslspgeratlscrasqsv-NKYLAWYQKQPGQAPRLLYDASNPATGIPARF 61
Db 64 sgsgsgtdftltisrlepedfavyqgqgsqstfgqgkveik 108
Qy 62 SGSGSGTDFTLTISNLEPEDFAVYQQRSDWV-TFGGKVEIK 105

RESULT 9
ID KV3A_HUMAN STANDARD: PPT: 108 AA.
AC P01619;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (B6)

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AC P18136;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA; TETRAPODA: MAMMALIA;
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLOC22; K3HUH1.
DR HSP: P01607; IDFB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC)
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 FRAMEWORK 3
FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 110 118 FRAMEWORK 3
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14070 MW: 10000366 CRC32.

Query Match 82.4%; Score 608; DB 5; Length 129;
Best Local Similarity 85.8%; Pred. No. 3.46e-112;
Matches 91; Conservative 3; Mismatches 8; Indels 4; Gaps 3;

Db 24 ltqspdtlslspgeratlsrsgsqvssylawyqkqpcqprlliygassratgipdrf 83
QY 3 LTQSPDTLSLSPGERATLSRSGSQVSSNK-YLAWYQKPCQAPRLLIYDASNPATGIPAPF 61
Db 84 sqsgsgtdftltisrlepddfavvyqgqygsspw-tfgggtkvek 128
QY 62 SGSGSGTDTLTISNLEPEDFAVYVCQPSDWV-IFGSGSTKVEIK 105

RESULT 3
ID KV3B_HUMAN STANDARD; PRT: 109 AA.
AC P01620;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA; TETRAPODA: MAMMALIA;
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUS1.
DR HSP: P01607; IDFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11775 MW: 10085050 CRC32.

Query Match 82.08%; Score 605; DB 5; Length 109;
Best Local Similarity 84.8%; Pred. No. 1.73e-111;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

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Db 4 ltqspdtlslspgeratlsrsgsqvssylawyqkqpcqprlliygassratgipdrf 63
QY 3 LTQSPDTLSLSPGERATLSRSGSQVSSNK-YLAWYQKPCQAPRLLIYDASNPATGIPAPF 61
Db 64 sqsgsgtdftltisrlepddfavvyqgqygsspw-tfgggtkvek 108
QY 62 SGSGSGTDTLTISNLEPEDFAVYVCQPSDWV-IFGSGSTKVEIK 105

RESULT 4
ID KV3L_HUMAN STANDARD; PRT: 129 AA.
AC P18135;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAI)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA; TETRAPODA: MAMMALIA;
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLOC22; K3HUH1.
DR HSP: P01607; IANG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAI)
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 FRAMEWORK 3
FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 110 118 FRAMEWORK 3
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14073 MW: 20448856 CRC32.

Query Match 81.8%; Score 604; DB 5; Length 129;
Best Local Similarity 85.7%; Pred. No. 2.96e-111;
Matches 90; Conservative 4; Mismatches 9; Indels 2; Gaps 2;

Db 24 ltqspdtlslspgeratlsrsgsqvssylawyqkqpcqprlliygassratgipdrf 83
QY 3 LTQSPDTLSLSPGERATLSRSGSQVSSNK-YLAWYQKPCQAPRLLIYDASNPATGIPAPF 61
Db 84 sqsgsgtdftltisrlepddfavvyqgqygsspw-tfgggtkvek 128
QY 62 SGSGSGTDTLTISNLEPEDFAVYVCQPSDWV-IFGSGSTKVEIK 105

RESULT 5
ID KV3E_HUMAN STANDARD; PRT: 109 AA.
AC P01623;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA; TETRAPODA: MAMMALIA;
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.

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[W][A][T][E][R][M][A][N]
[P][R][O][T][E][I][N]
[S][E][A][R][C][H]
[A][L][I][G][N][M][E][N][T]
[T][M]

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MPsearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:19:05 1998: MasPar time 4.86 Seconds
Tabular output not generated. 458.034 Million cell updates/sec

Title: >US-08-844-215-9
Description: (1-105) from US08844215.pep
Perfect Score: 738
Sequence: 1 AELTQSPATLSLSPGERATL.....YQQQSDNWTFGGTKVEIK 105

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 40.473; Variance 70.596; scale 0.573

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	626	84	8	KV3L_HUMAN	IG KAPPA CHAIN V-III	2 18e-116
2	608	82	4	KV3M_HUMAN	IG KAPPA CHAIN V-III	3 46e-112
3	605	82	0	KV3R_HUMAN	IG KAPPA CHAIN V-III	1 73e-111
4	604	81	8	KV3L_HUMAN	IG KAPPA CHAIN V-III	2 96e-111
5	600	81	3	KV3E_HUMAN	IG KAPPA CHAIN V-III	2 53e-110
6	596	80	8	KV3D_HUMAN	IG KAPPA CHAIN V-III	2 16e-109
7	595	80	6	KV3H_HUMAN	IG KAPPA CHAIN V-III	3 70e-109
8	592	80	2	KV3F_HUMAN	IG KAPPA CHAIN V-III	1 85e-108
9	577	78	2	KV3A_HUMAN	IG KAPPA CHAIN V-III	5 68e-105
10	572	77	5	KV3G_HUMAN	IG KAPPA CHAIN V-III	8 23e-104
11	554	75	1	KV3C_HUMAN	IG KAPPA CHAIN V-III	1 23e-99
12	554	75	1	KV3K_HUMAN	IG KAPPA CHAIN V-III	3 02e-99
13	548	74	3	KV3J_HUMAN	IG KAPPA CHAIN V-III	4 32e-97
14	543	73	6	KV3I_HUMAN	IG KAPPA CHAIN V-III	3 01e-96
15	525	71	1	KV3L_HUMAN	IG KAPPA CHAIN V-I RE	6 22e-93
16	522	70	7	KV3F_HUMAN	IG KAPPA CHAIN V-I RE	3 06e-92
17	520	70	5	KV3N_HUMAN	IG KAPPA CHAIN V-I RE	8 84e-92
18	516	69	9	KV3H_HUMAN	IG KAPPA CHAIN V-I RE	7 39e-91
19	514	69	6	KV3K_HUMAN	IG KAPPA CHAIN V-III	2 13e-90
20	514	69	6	KV3J_HUMAN	IG KAPPA CHAIN V-III	2 13e-90
21	509	69	0	KV3E_HUMAN	IG KAPPA CHAIN V-I RE	3 02e-89
22	507	68	7	KV3P_HUMAN	IG KAPPA CHAIN V-I RE	8 71e-89

ALIGNMENTS

RESULT	ID	KV31_HUMAN	STANDARD	PRT	115 AA
AC	P04433				
DT	13-AUG-1987	(REL. 05, CREATED)			
DT	13-AUG-1987	(REL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1990	(REL. 16, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN PRECURSOR V-III REGION (V9) (FRAGMENT).				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 85087932.				
RA	PECH M., ZACHAU H.G.;				
PL	NUCLEIC ACIDS RES. 12:922a-923a(1984).				
DR	EMBL; X01668; -- NOT ANNOTATED_CDS.				
DR	PIR; A01900; K3HUG.				
DR	HSSP; P01607; IAAG.				
KW	IMMUNOGLOBULIN V REGION; SIGNAL.				
FT	SIGNAL	1	20		
FT	CHAIN	21	>115		IG KAPPA CHAIN V-III REGION (VG).
FT	DOMAIN	21	43		FRAMEWORK 1
FT	DOMAIN	44	54		COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	55	69		FRAMEWORK 2
FT	DOMAIN	70	76		COMPLEMENTARITY-DETERMINING 2
FT	DOMAIN	77	108		FRAMEWORK 3
FT	DOMAIN	109	115		COMPLEMENTARITY-DETERMINING 3.
FT	DISULFID	43	108		BY SIMILARITY.
FT	NON_TER	115	115		
SQ	SEQUENCE	115 AA	12575 MW	375182PC CSC12	
Query Match 84.8%; Score 626; DB 5; Length 115;					
Best Local Similarity 95.6%; Pred. No. 2.18e-116;					
Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;					
Db	24 Itqspatlsppgeratlscrasgvsyylawvqgqpggprlllydasnratgiparls 83				
Qy	3 LIGSIATLSUSGGERATLSPPASVSVMKYLAWYQTAFAAPPLIYDASNRATGIPARIS 62				
Db	84 qsgsgtdftlltisslepedfavyvccqqrsw 114				
Qy	63 GSGGSDTDTLTISNIEPEDFAVYVCCQQRSDW 93				
RESULT	2				
ID	KV3M_HUMAN	STANDARD	PPT	129 AA	

DR WPI: 96-179601/18
 PI Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PI passive immunotherapy and detection of HIV infection.
 PS Example 3; Fig 19; 366pp; English.
 CC The sequences given in W01320-24 represent the light chain variable
 CC regions (VH) of a series of antibody fragments (Fab's) which are
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents
 CC the sequence of the clone, GL 41.19. These sequences represent light
 CC chains which bind to the heavy light chain clones given in W01315-19. A
 CC monoclonal antibody containing one of these Fab sequences may have the
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
 CC The Mab may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 109 AA;

Query Match 88.7%; Score 670; DB 19; Length 109;
 Best Local Similarity 90.7%; Pred. No. 1.41e-39;
 Matches 97; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgervivscrasvsnlyawyyqgqgagprlllygasmratgipd 61
 QY 1 AELTQSPGTLSLSPGERAILSGASVSFNSNYLAWYQYQAGPRLIYVSSSHATGIPD 60
 Db 62 rfsgsgsgdftltlslrlepedfavyycqgysg-tfqqgktkleik 107
 QY 61 RFGSGSGDFTLTISRLEPEDFAVYCYQYGSPPRTFGGKTLEIK 107

RESULT 12
 ID W01322 standard: Protein: 111 AA

AC W01322:
 DE 29-JAN-1997 (first entry)
 DE VL of Fab, GL 41.1, binds to HIV gp41.
 KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
 KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.

FN Key Location/Qualifiers

FT Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..97
 FT /label= CDR3
 FT Region 98..111
 FT /label= FR4

PN W09502273-A1.

PD 01-FEB-1996.

PP 11-JUL-1995; U08743.

PP 18-JUL-1994; US-275952.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

WPI: 96-179601/18

PI Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in

PI passive immunotherapy and detection of HIV infection.

PS Example 3; Fig 19; 366pp; English.

CC The sequences given in W01320-24 represent the light chain variable
 CC regions (VH) of a series of antibody fragments (Fab's) which are
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents
 CC the sequence of the clone, GL 41.1. These sequences represent light
 CC chains which bind to the heavy light chain clones given in W01315-19. A
 CC monoclonal antibody containing one of these Fab sequences may have the
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
 CC The Mab may be used for determining immunocompetence of a human anti-HIV

CC antibody and in the detection of HIV infection.
 SQ Sequence 111 AA;

Query Match 88.5%; Score 668; DB 19; Length 111;
 Best Local Similarity 87.9%; Pred. No. 1.98e-39;
 Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgervivscrasvsnlyawyyqgqgagprlllygasmratgipd 61
 QY 1 AELTQSPGTLSLSPGERAILSGASVSFNSNYLAWYQYQAGPRLIYVSSSHATGIPD 60
 Db 62 rfsgsgsgdftltlslrlepedfavyycqgysg-tfqqgktkleik 107
 QY 61 RFGSGSGDFTLTISRLEPEDFAVYCYQYGSPPRTFGGKTLEIK 107

RESULT 13
 ID R54277 standard: protein: 111 AA.

AC R54277:

DT 10-NOV-1994 (first entry)

DE Anti-HIV gp41 immunoglobulin light chain V region clone GL 41.1.

KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;

KW neutralisation; monoclonal antibody; light chain; variable region;

KW framework region; complementarity determining region.

OS Homo sapiens.

FN Key Location/Qualifiers

FT Region 1..23

FT /label= FR1

FT Region 24..35

FT /label= CDR1

FT Region 36..50

FT /label= FR2

FT Region 51..57

FT /label= CDR2

FT Region 58..89

FT /label= FR3

FT Region 90..97

FT /label= CDR3

FT Region 98..111

FT /label= FR4

PN W09407922-A.

PD 14-APR-1994.

PF 30-SEP-1993; U09328.

PR 30-SEP-1992; US-954148.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

WPI: 94-135516/16.

DR New human monoclonal antibodies neutralising HIV - react with

PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo

PT or in vitro diagnosis and for passive immuno-therapy

PS Claim 11; Page 217; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR

CC variable regions. The amplification products were inserted into a

CC dicistronic vector to produce a library of fragments. E.coli XL1.

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAB regions on their surface. Panning

CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VL region sequence R54277 neutralises HIV;

CC gp41.

CC Sequence 111 AA;

Query Match 88.5%; Score 668; DB 10; Length 111;

Best Local Similarity 87.9%; Pred. No. 1.98e-39;

Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgervivscrasvsnlyawyyqgqgagprlllygasmratgipd 61
 QY 1 AELTQSPGTLSLSPGERAILSGASVSFNSNYLAWYQYQAGPRLIYVSSSHATGIPD 60
 Db 62 rfsgsgsgdftltlslrlepedfavyycqgysg-tfqqgktkleik 107
 QY 61 RFGSGSGDFTLTISRLEPEDFAVYCYQYGSPPRTFGGKTLEIK 107

```

10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key
FT Region Location/Qualifiers
FT /label= FR1 1..21
FT /label= FR2 22..33
FT /label= CDR1 34 48
FT /label= FP2 49..55
FT /label= CDR2 56..87
FT /label= FR3 88..96
FT /label= CDR3 97..107
FT /label= FR4
PN WO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCR1 ) SCRIpps RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 180: 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence P54311 is from a gp120-
CC specific clone.
SQ Sequence 107 AA:

Query Match 88.7%; Score 670; DB 10; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.41e-39;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltsqspstlsppgeratlscrasqslsnnylawyqqkpgqaprllygsstrgtgipdr 60
QY 2 ELTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQQKPGQAPRLLYGVSSRAIGIPDP 61
Db 61 fsqgsgstftltisrlepedfavyvcghyansvytfgggtkleik 106
QY 62 FSGSGSGTFTLTISRLEPEDPAVYVQQYQSSPPTFGQGTGLEIK 107

RESULT 10
ID R54275 standard; protein; 109 AA.
AC R54275.
DE 10-NOV-1994 (first entry)
DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.
KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
KW neutralisation; monoclonal antibody; light chain; variable region;
KW framework region; complementarity determining region.
OS Homo sapiens.
FH Key
FT Region Location/Qualifiers
FT /label= FR1 1..23
FT /label= FR2 24..35
FT /label= CDR1 36..50
FT /label= FR2 51..57
FT /label= FR3
FT /label= FR4
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCR1 ) SCRIpps RES INST.
PI Barbas CF, Burton DR, Lerner RA;

10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key
FT Region Location/Qualifiers
FT /label= FR1 58..89
FT /label= FR2 90..97
FT /label= CDR3 98 109
FT /label= FR4
PN WO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCR1 ) SCRIpps RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Claim 11: Page 215-216; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence P54275 neutralises HIV1
CC gp41.
SQ Sequence 109 AA:

Query Match 88.7%; Score 670; DB 10; Length 109;
Best Local Similarity 90.7%; Pred. No. 1.41e-39;
Matches 97; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Db 2 aeltqspstlsppgeratlscrasqslsnnylawyqqkpgqaprllygsstrgtgipdr 61
QY 1 AELTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQQKPGQAPRLLYGVSSPATGIPD 60
Db 62 rfsqsgstftltisrlepedfavyvcghyansvytfgggtkveik 107
QY 61 FFSGSSTFTLTISRLEPEDPAVYVQQYQSSPPTFGQGTGLEIK 107

RESULT 11
ID W01320 standard; Protein; 109 AA.
AC W01320.
DE 29-JAN-1997 (first entry)
DE VL of Fab, DL 41 19, binds to HIV gp41.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key
FT Region Location/Qualifiers
FT /label= FR1 24..35
FT /label= CDR1 36..50
FT /label= FR2 51..57
FT /label= CDR2 58..89
FT /label= FR3 90..97
FT /label= CDR3 98..109
FT /label= FR4
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCR1 ) SCRIpps RES INST.
PI Barbas CF, Burton DR, Lerner RA;

```


PA (SCRI) SCRIPPS RES INST.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Barbas CF, Burton DR, Chanock RM, Crowe JE, Murphy RP;
 DP WPI: 94-118147/14
 PT Human neutralising monoclonal antibodies to respiratory syncytial
 PT virus - for treatment prophylaxis and diagnosis of RSV and other
 PT diseases of the respiratory tract
 PS Disclosure: Fig 4: 104pp; English.
 CC The sequences given in R50215-19 represent the heavy and light chain
 CC variable domains of various clones of a human monoclonal antibody
 CC which binds to an epitope on glycoprotein F of respiratory syncytial
 CC virus (RSV). These antibodies may be used as a reagent for the
 CC diagnosis of RSV disease and other viral mucosal diseases, eg
 CC influenza virus, rhinovirus and coronavirus. They are particularly
 CC useful in ameliorating RSV when delivered directly to the lungs, and
 CC may also be used for treating pneumonia and bronchiolitis.
 SQ Sequence 109 AA;
 Query Match 89.3%; Score 674; DB 9; Length 109;
 Best Local Similarity 88.8%; Pred. No. 7.15e-40;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 Db 2 aeltqspqtlslsgeratlsrscratssnnylawyqgqpgqaprllygasmratdipd 61
 Qy 1 AELTQSPQTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPD 60
 Db 62 rfsqsgsgtdftltisrlepedfavyycqygqsspxtfgqgtdveik 107
 Qy 61 PFGSGSGCTDFTLTISRLPEDFAVYCYCQYGGSPRTFGGKLEIK 107
 RESULT 7
 ID R38593 standard; peptide: 107 AA.
 AC R38593;
 DT 28-OCT-1993 (first entry)
 DE Human lambda light chain subgroup 3 (hL3).
 KW Antibody: variable domain: light; L; heavy: H; consensus:
 KW affinity: antigen: immunogenicity: humanisation: framework.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 96
 FT /note- residue conserved in less than 50% of the
 FT known sequences of hL3-
 FN W09311794-A.
 PD 24-JUN-1993.
 PF 14-DEC-1992; U10906.
 PR 13-DEC-1991; US-808464.
 PA (XOMA) XOMA CORP.
 PI Fishwild DM, Kohn FR, Little PG, Studnicka GM;
 DR WPI: 93-213827/25.
 PT Antibodies prepn. used for treatment of auto-immune diseases - by
 PT replacement of critical residues to reduce immunogenicity but
 PT retain binding affinity, etc.
 PS Claim 2: Page 93-94: 160pp; English.
 CC The consensus amino acid sequences for the subgroups of light
 CC chains (hL1 - R38590, hK3 - hK4 - R38591, hL2 -
 CC R48592, hL3 - R38593, hL6 - R48594, hK4 - R38595, hL4 - R38596,
 CC and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
 CC hH2 - R38600) of human variable domains may be used to prepare, for
 CC example, a modified mouse antibody variable domain that retains the
 CC affinity of the natural domain for antigen while exhibiting reduced
 CC immunogenicity in humans.
 CC Unlike other methods of humanisation, which advocate the
 CC replacement of entire antibody framework regions with those of human
 CC antibodies, this method involves only the introduction of human
 CC residues into those positions not critical for antigen binding.
 CC This ensures that the binding properties of the modified antibody
 CC are not diminished.
 SQ Sequence 107 AA;
 Query Match 88.9%; Score 671; DB 7; Length 107;
 Best Local Similarity 92.4%; Pred. No. 1.19e-39;
 Matches 97; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 4 ltspqtlslsgeratlsrscratssnnylawyqgqpgqaprllygasmratdipd 62
 Qy 3 LTQSPQTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDR 62
 Db 63 sqsgsgtdftltisrlepedfavyycqygqsspxtfgqgtdveik 107
 Qy 63 SGSGSGTDFLTLSRLPEDFAVYCYCQYGGSPRTFGGKLEIK 107
 RESULT 8
 ID W01269 standard; Protein: 107 AA.
 AC W01269;
 DT 28-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAb, clone B20.
 KW Heavy chain: light chain: variable region: VH: monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 98..107
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/14.
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example: Fig 11: 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of the
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, B20. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 107 AA;
 Query Match 88.7%; Score 670; DB 19; Length 107;
 Best Local Similarity 88.7%; Pred. No. 1.41e-39;
 Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltqspqtlslsgeratlsrscratssnnylawyqgqpgqaprllygasmratdipdr 60
 Qy 2 ELTQSPQTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDR 61
 Db 61 fsgsgsgtdftltisrlepedfavyycqygqsspxtfgqgtdveik 106
 Qy 62 FSGSGSGTDFLTLSRLPEDFAVYCYCQYGGSPRTFGGKLEIK 107

RESULT 9
 ID R54311 standard; protein: 107 AA.
 AC R54311;

AC R54316;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region b6.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN WO9407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993; U09328.
 PR 30-SEP-1992; US-954148.
 PA (SCRI) SCPIPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Example: Page 186; 248pp; English
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli Xcl
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAb regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54316 neutralises HIV1
 CC gp120.
 SQ Sequence 108 AA;

Query Match 90.7%; Score 685; DB 9; Length 108;
 Best Local Similarity 89.6%; Pred No. 111e-40; Indels 0; Gaps 0;
 Matches 95; Conservative 6; Mismatches 5;
 Db 1 eltsqsgtltslspgeratlscragssnylawyqgkpgqaprllyqasnratgipdr 60
 QY 2 ELTSPGTLTSLSPGERATLSGASQSVFNSNYLAWYQKPGQAPRLIYGVSSPATGIPDR 61
 Db 61 fsgsgsgtdftlslrlepedfavyycqyqtspytfgggtqldik 106
 QY 62 FSGSGSGTDTLTISRLEPEDFAVYICQYQYSSSPRTFGQGTKEIK 107

RESULT 5
 ID W01278 standard; Protein; 108 AA.
 AC W01278;
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b6.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV, human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1 21
 FT /label= FR1
 FT Region 22 33
 FT /label= CDR1
 FT Region 34..48

FT /label= FR2 49..55
 FT Region CDR2
 FT /label= FR3 56..87
 FT Region FR3
 FT /label= FR3 88 96
 FT Region CDR3
 FT /label= FR4 97..108
 FT Region FR4
 PN WO9602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U09743.
 PR 14-JUL-1994; US-276852.
 PA (SCRI) SCPIPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example: Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, b6. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 90.7%; Score 685; DB 19; Length 108;
 Best Local Similarity 89.6%; Pred No. 111e-40; Indels 0; Gaps 0;
 Matches 95; Conservative 6; Mismatches 5;
 Db 1 eltsqsgtltslspgeratlscragssnylawyqgkpgqaprllyqasnratgipdr 60
 QY 2 ELTSPGTLTSLSPGERATLSGASQSVFNSNYLAWYQKPGQAPRLIYGVSSPATGIPDR 61
 Db 61 fsgsgsgtdftlslrlepedfavyycqyqtspytfgggtqldik 106
 QY 62 FSGSGSGTDTLTISRLEPEDFAVYICQYQYSSSPRTFGQGTKEIK 107

RESULT 6
 ID R50217 standard; Protein; 109 AA.
 AC R50217;
 DT 31-OCT-1994 (first entry)
 DE HSV glycoprotein F binding MAB clone rsv6/11/21/22L VH/VL domain.
 KW Complementarity determination region; CDR1; human; bronchiolitis;
 KW monoclonal antibody; epitope; glycoprotein F; influenza virus;
 KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..98
 FT /label= CDR3
 FT Region 99..109
 FT /label= FR4
 PN WO9406448-A.
 PD 31-MAR-1994.
 PF 16-SEP-1993; U08786.
 PR 16-SEP-1992; US-945515.

Query Match	91.78;	Score 692;	DB 10;	Length 108;
Best Local Similarity	93.48;	pred. No. 3	38e-41.	

62 FSGSGTDFTLISRLEPEFAVYCCQQYGGSSPTFGGKLEIK 107

RESULT 4
ID R54316 standard; protein; 108 AA.

WIRE (TM)

Release 2 ID John F. Collins, Biocomputing Research Unit
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Mbsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:22:10 1998; MasPar time 6.74 Seconds
Tabular output not generated. 220.599 Million cell updates/sec

Title: >US-08-844-215-10
Description: (1-107) from US08844.215.pep
Perfect Score: 755
Sequence: 1 AELTQSPGTLSPGERATL CQQYGSPPRTFGQGTGLEIK 107

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13889129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 29.661; Variance 168.850; scale 0.176
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No	Score	Query Match Length	ID	Description
1	696	92.2	129 7 R38672	vk325-Jk2.
2	692	91.7	108 10 R54307	Anti-HIV gp120 immuno
3	692	91.7	108 19 W01265	VL region of HIV neut
4	685	90.7	108 9 R54316	Anti-HIV gp120 immuno
5	685	90.7	108 19 W01278	VL region of HIV neut
6	674	89.3	109 9 P50217	HSV glycoprotein F bi
7	671	88.9	107 7 R38593	Human lambda light ch
8	670	88.7	107 14 W01264	VL region of HIV neut
9	670	88.7	107 10 R54311	Anti-HIV gp120 immuno
10	670	88.7	109 10 R54275	Anti-HIV gp120 immuno
11	670	88.7	109 19 W01320	VL of Fab, DL 41 19.
12	668	88.5	111 19 W01322	VL of Fab, GL 41 1, b
13	668	88.5	111 10 R54277	Anti-HIV gp41 immuno
14	661	87.5	129 7 R41296	F105 rearranged varia
15	658	87.2	129 7 P39672	F105VK-F105JK.
16	657	87.0	104 9 R54317	Anti-HIV gp120 immuno
17	657	87.0	104 19 W01279	VL region of HIV neut
18	657	87.0	134 20 W11155	Anti-lung tumour anti
19	653	86.5	108 19 W01289	VL region of HIV neut
20	650	86.1	107 19 W01266	VL region of HIV neut

21	650	86.1	107 10 R54308	Anti-HIV gp120 immuno
22	650	86.1	108 10 R54355	Anti-HIV gp120 immuno
23	650	86.1	108 19 W01275	VL region of HIV neut
24	650	86.1	109 9 P50218	HSV glycoprotein F bi
25	649	86.0	109 10 R56286	Light chain of Amb al
26	646	85.4	109 10 R54363	Anti-HIV gp120 immuno
27	638	84.5	124 22 W24339	Immunoglobulin F101-2
28	637	84.4	108 19 W01267	VL region of HIV neut
29	636	84.2	214 19 W07615	Ulcerative colitis-as
30	633	83.8	215 19 W07616	Ulcerative colitis-as
31	628	83.2	112 10 R54379	Anti-HIV gp41 immuno
32	628	83.2	112 19 W01324	VL of Fab, SS 41 8, E
33	626	82.9	115 11 R62930	Human V-kappa vk55.8
34	626	82.9	116 22 W03449	DNA fragment vk65.9
35	625	82.9	116 7 P38450	Human V-kappa fragment
36	624	82.6	108 10 R54309	Anti-HIV gp120 immuno
37	619	82.0	100 5 P25324	VL region of human rh
38	615	81.5	107 9 P54328	Anti-HIV gp120 immuno
39	615	81.5	107 19 W01399	VL region of HIV neut
40	614	81.3	105 9 R54314	Anti-HIV gp120 immuno
41	614	81.3	105 19 W01272	VL region of HIV neut
42	614	81.3	107 9 P54327	Anti-HIV gp120 immuno
43	614	81.3	107 19 W01398	VL region of HIV neut
44	611	80.9	104 9 R54315	Anti-HIV gp120 immuno
45	611	80.9	104 19 W01373	VL region of HIV neut

ALIGNMENTS

RESULT 1
ID R38672 standard; Protein: 129 AA.
AC R38672:
DI 01-NOV-1993 (first entry)
DE vk325-Jk2.
KW Monoclonal antibody; MAB; envelope: glycoprotein; gp120; HIV; AIDS;
CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide 21..129
FT Protein 1..116
FT /label= mat_protein 117..129
FT Region 110, 117
FT /label= vk325 44..55
FT /label= Jk2 71..77
FT /label= CDR1 110, 117
FT /label= CDR2
FT /label= CDR3
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FT /note= "Met encoded by ATC (sic)"
FT Misc_difference 35
FT /note= "Pro encoded by GCA (sic)"
FT Misc_difference 99
FT /note= "Leu encoded by GTG (sic)"
FT Misc_difference 113
FT /note= "Gly encoded by GAR (sic)"
FT Misc_difference 114
FT /note= "Ser encoded by AAC (sic)"
FT /note= "Pro encoded by GTT (sic)"
FN W0391233-A.
PD 24-JUN-1993
PF 10-DEC-1992; U10928.
PP 10-DEC-1991; US-804652.
PA (DAND) DANA FABER CANCER INST INC.
(NEMO-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JC;
DR WP1: 93-214174/26.

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Db 4 ltqspdtlspqeratlsqrasqssvslawyqkqgqaprllyqasratgipdrf 63
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QY 3 LTQSPGTLSPGEATLSGASQSVPSNYLAWYQKQKQCAPRLIYGVSSPATGIPDPF 62
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Db 64 sgsasatdftltisrlepedfavyvqgqgssppafgqgatkveik 108
|||||
QY 63 SGSGSGTDFLTISPLEPEDFAVYVQYQYSSPPTFGWTKLEIK 107
|||||

RESULT 10
ENTRY K3HUHI *type complete
TITLE Ig kappa chain precursor V-III region (Hic) - human
ORGANISM *formal_name Homo sapiens *common_name man
DATE 30-Jun-1990 *sequence_revision 30-Jun-1990 *text_change
30-May-1997
ACCESSIONS PLO021
REFERENCE PLO021
#authors Kipps, T.J.; Tomhave, E.; Chen, P P ; Carson, D A
#journal J. Exp. Med. (1988) 167:840-852
#title Autoantibody-associated kappa light chain variable region
gene expressed in chronic lymphocytic leukemia with little
or no somatic mutation. Implications for etiology and
immunotherapy.
#cross-references MUID:88171307
#accession PLO021
#molecule_type mRNA
#residues 1-129 **label KIP
COMMENT The protein is one of the surface immunoglobulin M autoantibodies
expressed in patients with chronic lymphocytic leukemia.
GENETICS
#gene GDB:IGKV3
#cross-references GDB:136266
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION *superfamily immunoglobulin V region: immunoglobulin homology
autoantibody: chronic lymphocytic leukemia; heterotetramer;
immunoglobulin
FEATURE
1-20
21-129
*domain signal sequence #status predicted #label sIgN
*product Ig kappa chain V-III region (Hic) #status
predicted #label KAP
*region V segment\
*region complementarity-determining 1\
*region complementarity-determining 2\
*region complementarity-determining 3\
*region J segment (JK1)\
*disulfide_bonds #status predicted
*length 129 #molecular_weight 14070 #checksum 8174
SUMMARY
Query Match 91.78; Score 692; DB 2; Length 129;
Best Local Similarity 91.78; Pred. No. 8,576;66;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 24 ltqspdtlspqeratlsqrasqssvslawyqkqgqaprllyqasratgipdrf 83
|||||
QY 3 LTQSPGTLSPGEATLSGASQSVPSNYLAWYQKQKQCAPRLIYGVSSPATGIPDPF 62
|||||

Db 84 sgsasatdftltisrlepedfavyvqgqgssppafgqgatkveik 128
|||||
QY 63 SGSGSGTDFLTISPLEPEDFAVYVQYQYSSPPTFGWTKLEIK 107
|||||

RESULT 11
ENTRY R30601 *type fragment
TITLE Ig kappa chain V-III region (Glo) - human (fragment)
ORGANISM *formal_name Homo sapiens *common_name man
DATE 29-Jun-1989 *sequence_revision 29-Jun-1989 *text_change
16-Aug-1996

```

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ACCESSIONS B30601
REFERENCE A30601
#authors Goni, F R ; Chen, P P ; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession B30601
#status preliminary
#molecule_type protein
#residues 1-109 **label GON
CLASSIFICATION *superfamily immunoglobulin V region: immunoglobulin homology
heterotetramer; immunoglobulin
KEYWORDS #length 109 #checksum 5911
SUMMARY
Query Match 91.5%; Score 691; DB 7; Length 109;
Best Local Similarity 94.3%; Pred. No. 1,136-65;
Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltqspdtlspqeratlsqrasqssvslawyqkqgqaprllyqasratgipdrf 63
|||||
QY 3 LTQSPGTLSPGEATLSGASQSVPSNYLAWYQKQKQCAPRLIYGVSSPATGIPDPF 62
|||||

Db 64 sgsasatdftltisrlepedfavyvqgqgsspltfqgqatkveik 108
|||||
QY 63 SGSGSGTDFLTISPLEPEDFAVYVQYQYSSPPTFGWTKLEIK 107
|||||

RESULT 12
ENTRY S47181 *type complete
TITLE Ig kappa chain - human
ORGANISM *formal_name Homo sapiens *common_name man
DATE 09-Jan-1995 *sequence_revision 06-Jan-1995 *text_change
16-Aug-1996
ACCESSIONS S47181
REFERENCE S47181
#authors McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weeman, A.P.
#submission submitted to the EMBL Data Library, June 1994
#description Cloning and analysis of IgM anti-thyroglobulin autoantibodies
from patients with Hashimoto's thyroiditis.
#accession S47181
#status preliminary
#molecule_type mRNA
#residues 1-109 **label MCI
#cross-references EMBL:X79784
CLASSIFICATION *superfamily immunoglobulin V region: immunoglobulin homology
heterotetramer; immunoglobulin
KEYWORDS #length 109 #molecular_weight 11982 #checksum 4729
SUMMARY
Query Match 91.5%; Score 691; DB 7; Length 109;
Best Local Similarity 91.5%; Pred. No. 1,136-65;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 3 eltcspdtlspqeratlsqrasqssvslawyqkqgqaprllyqasratgipdrf 62
|||||
QY 2 ELTQSPGTLSPGEATLSGASQSVPSNYLAWYQKQKQCAPRLIYGVSSPATGIPDR 61
|||||

Db 63 fgsqsgtdftltisrlepedfavyvqgqgsspltfqgqatkveik 108
|||||
QY 62 FSGSGTDFLTISPLEPEDFAVYVQYQYSSPPTFGWTKLEIK 107
|||||

RESULT 13
ENTRY F30607 *type fragment
TITLE Ig kappa chain V-III region (Bor) - human (fragment)
ORGANISM *formal_name Homo sapiens *common_name man
DATE 29-Jun-1989 *sequence_revision 29-Jun-1989 *text_change
16-Aug-1996
ACCESSIONS F30607
REFERENCE A30601
#authors Goni, F R ; Chen, P P ; McGinnis, D.; Arjonilla, M.L.;

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SUMMARY      #length 109 #checksum 5951
Query Match  92.2%; Score 696; DB 7; Length 109;
Best Local Similarity 95.2%; Pred. No. 2,85e-66;
Matches 100; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltqspgtlslsperatlscrasqsvssylawyyqkpgqaprllygassratgipdrf 63
|||||
QY 3 LTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDRF 62
|||||

Db 64 sqsgsgtdftltisrlepedfavyycqygsspytfgqgkkleik 108
|||||
QY 63 SSGSGGTDFTLTISRLPEDFAVYVCQYQYGSPPRTFGGQGTKEIK 107
|||||

RESULT 6
ENTRY S20636 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
16-Aug-1996
ACCESSIONS S20636
REFERENCE S20631
#authors Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
#submission Submitted to the EMBL Data Library, April 1992
#accession S20636
#status preliminary
#molecule_type mRNA
#residues 1-128 #label LEE
#cross-references EMBL:211894
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 128 #molecular_weight 13915 #checksum 4511

Query Match 91.9%; Score 694; DB 7; Length 128;
Best Local Similarity 93.3%; Pred. No. 4.94e-66;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 24 ltqspgtlslsperatlscrasqsvssylawyyqkpgqaprllygassratgipdrf 83
|||||
QY 3 LTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDRF 62
|||||

Db 84 sqsgsgtdftltisrlepedfavyycqygdsprtfqggtkveik 128
|||||
QY 63 SSGSGGTDFTLTISRLPEDFAVYVCQYQYGSPPRTFGGQGTKEIK 107
|||||

RESULT 7
ENTRY S49532 #type complete
TITLE anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Feb-1995 #sequence_revision 12-May-1995 #text_change
02-Jun-1995
ACCESSIONS S49532
REFERENCE S48797
#authors Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
#submission Submitted to the EMBL Data Library, October 1994
#description Molecular characterization of natural human anti-Sm
autoantibodies.
#accession S49532
#status preliminary
#molecule_type mRNA
#residues 1-129 #label MAH
#cross-references EMBL:246345
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 129 #molecular_weight 14093 #checksum 5407

Query Match 91.9%; Score 694; DB 7; Length 129;
Best Local Similarity 94.3%; Pred. No. 4.94e-66;
Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 24 ltqspgtlslsperatlscrasqsvssylawyyqkpgqaprllygassratgipdrf 83
|||||

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QY 3 LTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDRF 62
|||||
Db 84 sqsgsgtdftltisrlepedfavyycqygsspytfgqgkkleik 128
|||||
QY 63 SSGSGGTDFTLTISRLPEDFAVYVCQYQYGSPPRTFGGQGTKEIK 107
|||||

RESULT 8
ENTRY F44151 #type fragment
TITLE Ig kappa chain V region (JM-01) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS F44151
REFERENCE A44151
#authors Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.;
Graff, P.; DeGraw, J.; Pyaril, J.; Lapolla, P.; Burton,
D.R.; Lerner, R.A.; Thornton, G.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
#title Human combinatorial antibody libraries to hepatitis B surface
antigen.
#accession F44151
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-109 #label ZEB
#note nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5518

Query Match 91.8%; Score 693; DB 7; Length 109;
Best Local Similarity 92.5%; Pred. No. 6.51e-66;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 1 aeltqspgtlslsperatlscrasqsvsfnylawyqkpgqaprllygassratgipdrf 60
|||||
QY 1 AELTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDRF 60
|||||

Db 61 rfsqsgsgtdftltisrlepedfavyycqygsspytfgqgkveik 107
|||||
QY 61 RFSQSGSGTDFTLTISRLPEDFAVYVCQYQYGSPPRTFGGQGTKEIK 107
|||||

RESULT 9
ENTRY PH0963 #type fragment
TITLE Ig kappa chain V region (G6+ CLL-SM1) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0963
REFERENCE PH0952
#authors Martin, T.; Buffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MIMD-922028R0
#accession PH0963
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-109 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-50 #region framework 2\
51-56 #region complementarity-determining 2\
57-89 #region framework 3\
90-97 #region complementarity-determining 3\
SUMMARY #length 109 #checksum 5292

Query Match 91.7%; Score 692; DB 7; Length 109;
Best Local Similarity 93.3%; Pred. No. 8.57e-66;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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#authors      Goni, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
               Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
#journal      J. Immunol. (1989) 142:3158-3163
#title       Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession   C30608
#status      preliminary
#molecule_type protein
#residues    1-108 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
SUMMARY       #length 108 #checksum 1607

Query Match 93.4%; Score 705; DB 7; Length 108;
Best Local Similarity 95.2%; Pred. No. 2,39e-67;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltqspatlsppgeratlsrscasvssvslawyqgkpgqaprllygassratgipdrf 63
    |||||
Qy 3 LTQSPGTLSPGERATLSRLEPEDFAVYQYGGSSPRTFGGKLEIK 107
    |||||

Db 64 sgsgsgtdftltisrlepdefavvyqgyqasspwtfggktleik 108
    |||||
Qy 63 SGSGSGTDFLTISRLEPEDFAVYQYGGSSPRTFGGKLEIK 107
    |||||

RESULT 3
ENTRY D30601 #type fragment
TITLE Ig kappa chain V-III region (Cur) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS D30601
REFERENCE Goni, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
#authors Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities
#cross-references MUID:89215279
#accession D30601
#status preliminary
#molecule_type protein
#residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6151

Query Match 93.4%; Score 705; DB 7; Length 109;
Best Local Similarity 95.2%; Pred. No. 2,39e-67;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltqspatlsppgeratlsrscasvssvslawyqgkpgqaprllygassratgipdrf 63
    |||||
Qy 3 LTQSPGTLSPGERATLSRLEPEDFAVYQYGGSSPRTFGGKLEIK 107
    |||||

Db 64 sgsgsgtdftltisrlepdefavvyqgyqasspwtfggktleik 108
    |||||
Qy 63 SGSGSGTDFLTISRLEPEDFAVYQYGGSSPRTFGGKLEIK 107
    |||||

RESULT 4
ENTRY K3HURA #type complete
TITLE Ig kappa chain precursor V-III region (Hah) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
30-May-1997
ACCESSIONS PL0022
REFERENCE Kippes, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
#authors

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#journal J. Exp. Med. (1988) 167:840-852
#title Autoantibody-associated kappa light chain variable region
               gene expressed in chronic lymphocytic leukemia with little
               or no somatic mutation. Implications for etiology and
               immunotherapy.
#cross-references MUID:88171307
#accession FJ0022
#molecule_type mRNA
#residues 1-129 ##label KIP
COMMENT The protein is one of the surface immunoglobulin M autoantibodies
               expressed in patients with chronic lymphocytic leukemia.
GENETICS
#gene GDB:IGKV3
#cross-references GDB:136266
               An immunoglobulin heterotetramer subunit consists of two
               identical light (kappa or lambda) and two identical heavy
               (alpha, delta, epsilon, gamma, or mu) chains usually
               stabilized by interchain disulfide bonds. In some cases,
               such as IgA and IgM, the subunits associate into larger
               oligomers.
               #superfamily immunoglobulin V region: immunoglobulin homology
               autoantibody; chronic lymphocytic leukemia; heterotetramer;
               immunoglobulin
CLASSIFICATION
KEYWORDS #domain signal sequence #status predicted #label SIGN
               #product Ig kappa chain V-III region (Hah) #status
               predicted #label MATN
               #region V segment
               #region complementarity-determining 1N
               #region complementarity-determining 2N
               #region complementarity-determining 3N
               #region J segment (JK1)
               #disulfide_bonds #status predicted
               #length 129 #molecular_weight 14073 #checksum 7361
SUMMARY

Query Match 93.1%; Score 703; DB 2; Length 129;
Best Local Similarity 94.3%; Pred. No. 4,13e-67;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratlsrscasvssvslawyqgkpgqaprllygassratgipdrf 83
    |||||
Qy 3 LTQSPGTLSPGERATLSRLEPEDFAVYQYGGSSPRTFGGKLEIK 107
    |||||

Db 84 sgsgsgtdftltisrlepdefavvyqgyqasspwtfggktleik 128
    |||||
Qy 63 SGSGSGTDFLTISRLEPEDFAVYQYGGSSPRTFGGKLEIK 107
    |||||

RESULT 5
ENTRY H30601 #type fragment
TITLE Ig kappa chain V-III region (Gar and Flo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS H30601; E30601
REFERENCE Goni, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
#authors Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession H30601
#status preliminary
#molecule_type protein
#residues 1-109 ##label GON1
#accession E30601
#status preliminary
#molecule_type protein
#residues 1-109 ##label GON2
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin

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WIREA

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07:23:29 1998. MasPar time 7.55 Seconds
Tabular output not generated.
431.742 Million cell updates/sec

Title: >US-08-844-215-10
Description: (1-107) from US08A44215 pep
Perfect Score: 755
Sequence: 1 AELTQSPGTLSLSPGERATL.....CQYGSPPRTFGQTKLEIK 107

Scoring table: PAM 150
Gap 11
Searched: 95051 seqs, 30465580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r53
1:unnn1 2:unnn2 3:unnn3 4:unnn4 5:unnn5 6:unnn6 7:unnn7 8:unnn8
8:unnn4 9:unnn5 10:unnn6 11:unnn7 12:unnn8
13:unnn9 14:unnn10 15:unnn11 16:unnn12 17:unnn13
18:unnn14

Statistics: Mean 40.248; Variance 138.316; scale 0.291
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	722	95.6	109	7	Ig kappa chain V-III	2.18e-69	
2	705	93.4	109	7	Ig kappa chain V-III	2.38e-67	
3	705	93.4	109	7	Ig kappa chain V-III	2.38e-67	
4	703	93.1	129	7	Ig kappa chain V-III	4.13e-67	
5	696	92.2	109	7	Ig kappa chain V-III	2.85e-66	
6	694	91.9	128	7	Ig kappa chain V-III	4.94e-66	
7	694	91.9	128	7	Ig kappa chain V-III	4.94e-66	
8	694	91.9	128	7	Ig kappa chain V-III	4.94e-66	
9	692	91.7	109	7	Ig kappa chain V-III	8.57e-66	
10	692	91.7	109	7	Ig kappa chain V-III	8.57e-66	
11	691	91.5	109	7	Ig kappa chain V-III	1.13e-65	
12	691	91.5	109	7	Ig kappa chain V-III	1.13e-65	
13	690	91.4	109	7	Ig kappa chain V-III	1.49e-65	
14	690	91.4	109	7	Ig kappa chain V-III	1.49e-65	
15	690	91.4	109	7	Ig kappa chain V-III	1.49e-65	
16	689	91.3	114	7	Ig kappa chain V-III	1.96e-65	
17	689	91.3	129	7	Ig kappa chain V-III	1.96e-65	
18	689	91.3	134	7	Ig kappa chain V-III	1.96e-65	
19	688	91.1	109	7	Ig kappa chain V-III	2.58e-65	
20	687	91.0	110	7	Ig kappa chain V-III	3.40e-65	

21	695	90.7	108	2	K3HUB6	Ig kappa chain V-III	5.90e-65
22	692	90.3	109	2	K3HUB6	Ig kappa chain V-III	1.35e-64
23	682	90.3	130	7	S20637	Ig kappa chain V-reg	1.35e-64
24	680	90.1	107	7	P09665	Ig kappa chain V-reg	2.34e-64
25	680	90.1	108	7	H44151	Ig kappa chain V-reg	2.34e-64
26	680	90.1	110	7	E30607	Ig kappa chain V-III	2.34e-64
27	676	89.5	109	7	A30608	Ig kappa chain V-III	7.03e-64
28	672	89.4	109	2	K3HUB6	Ig kappa chain V-III	2.78e-63
29	671	88.9	109	7	G30607	Ig kappa chain V-III	2.78e-63
30	669	88.6	108	7	B30608	Ig kappa chain V-III	4.82e-63
31	664	87.9	121	7	S40327	Ig kappa chain - hum	1.91e-62
32	663	87.8	129	7	A32274	Ig kappa chain - hum	2.51e-62
33	661	87.5	109	2	K3HUB6	Ig kappa chain V-III	4.35e-62
34	659	87.3	108	7	E30609	Ig kappa chain V-III	7.54e-62
35	659	87.3	124	7	S20633	Ig kappa chain - hum	7.54e-62
36	653	86.5	110	7	S44120	Ig kappa chain V-J r	3.92e-61
37	647	85.7	129	7	S40325	Ig kappa chain - hum	2.04e-60
38	646	85.6	215	15	A23746	Ig kappa chain V-III	2.88e-60
39	644	85.3	108	7	S33988	Ig kappa chain V-reg	4.64e-60
40	642	85.3	145	7	S20631	Ig kappa chain - hum	8.70e-60
41	635	84.1	104	7	PH0964	Ig kappa chain V-reg	5.48e-59
42	628	83.2	127	7	S40380	Ig kappa light chain	3.73e-58
43	626	82.9	96	7	A30601	Ig kappa chain V-III	6.46e-58
44	626	82.9	116	7	R27594	Ig kappa chain - hum	6.46e-58
45	626	82.9	130	7	S40360	Ig kappa chain - hum	6.46e-58

ALIGNMENTS

RESULT 1
ENTRY G30601 #type fragment
TITLE Ig kappa chain V-III region (Got) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
ACCESSIONS G30601
REFERENCE A30601
#authors Geni, F.P.; Chen, F.P.; McGinnis, B.; Aricoili, M.L.; Fernandez, J.; Carlson, D.; Solomon, A.; Mende, F.; Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession G30601
#status Preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin heterotetramer: immunoglobulin
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 5641

Query Match 95.6%; Score 722; DB 7; Length 109;
Best Local Similarity 97.1%, Fred. No. 2.18e-69;
Matches 102, Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 4 1rsgpdtlsprvratlsrsgsvrsvybwvqgpggprlllygassratqndrf 63
|||||
QY 3 LTQSPGTLSPGERATLSGASQSVPSNYLANVQOKPGGAPRLIYGVSSPATGIRPP 62
|||||
Db 64 srsqsgtdftlsisledpavvyvqgysprrfaggtkleik 108
|||||
QY 63 SAGSGGTRPTLTISRPDRFAVYVQCGVSSPRTFGQTKLEIK 107
|||||
RESULT 2
ENTRY G30608 #type fragment
TITLE Ig kappa chain V-III region (Pie) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
ACCESSIONS G30608
REFERENCE A30601


```

Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
J. Immunol. (1989) 142:3158-3163
#journal
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MIMD:89215279
#accession F30607
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6514

Query Match 91.4%; Score 690; DB 7; Length 109;
Best Local Similarity 92.4%; Pred. No. 1.49e-65;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 Ltqspgtlslsperatlsctasqsvssylawyqkqgqprlllyqasratgipdrf 63
QY 3 LTQSPGTLSLSPGPATLSCTASQSVSNLYAWYQKQGPAPPLLIYGVSSPATGIPDRF 62

Db 54 sqsqsatdflltislrepedfavyvqgqygnspqtfgggkveik 108
QY 63 SGSSGSDTFLIISLPEDEFAVYVQGVSSSPRTFGSGTKLEIK 107

RESULT 14
ENTRY K3HUSI #type complete
TITLE Ig kappa chain V-II region (Sie) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jul-1982 #sequence_revision 06-Jul-1982 #ext_change
06-Sep-1995
ACCESSION A01892
REFERENCE A90450
#journal Andrews, D. W.; Capra, J. D.
#title Biochemistry (1981) 20:5816-5822
#cross-references MIMD:82046598
#accession A01892
##molecule_type protein
##residues 1-109 ##label AND
COMMENT This chain was isolated from an IgM with anti-gamma globulin
activity.
GENETICS
#gene GDB:IGKV3
#cross-references GDB:I36266
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer
FEATURE
15-91
23-89
SUMMARY #domain immunoglobulin homology #label IMM
#disulfide_bonds #status predicted
#length 109 #molecular_weight 11775 #checksum 5885

Query Match 91.4%; Score 690; DB 2; Length 109;
Best Local Similarity 91.4%; Pred. No. 1.49e-65;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 4 Ltqspgtlslsperatlsctasqsvssylawyqkqgqprlllyqasratgipdrf 63
QY 3 LTQSPGTLSLSPGPATLSCTASQSVSNLYAWYQKQGPAPPLLIYGVSSPATGIPDRF 62

Db 54 sqsqsatdflltislrepedfavyvqgqygnspqtfgggkveik 108
QY 63 SGSSGSDTFLIISLPEDEFAVYVQGVSSSPRTFGSGTKLEIK 107

```

RESULT 15

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ENTRY F30601 #type fragment
TITLE Ig kappa chain V-II region (Neu) - human (truncated)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 26-Jun-1989 #sequence_revision 26-Jun-1989 #ext_change
16-Aug-1995
ACCESSION F30601
REFERENCE A30601
#journal Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MIMD:89215279
#accession F30601
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 4627

Query Match 91.4%; Score 690; DB 7; Length 109;
Best Local Similarity 92.4%; Pred. No. 1.49e-65;
Matches 97; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 4 Ltqspgtlslsperatlsctasqsvssylawyqkqgqprlllyqasratgipdrf 63
QY 3 LTQSPGTLSLSPGPATLSCTASQSVSNLYAWYQKQGPAPPLLIYGVSSPATGIPDRF 62

Db 64 tsgsgtdftltislrepedfavyvqgqygnspqtfgggkveik 108
QY 63 SGSSGSDTFLIISLPEDEFAVYVQGVSSSPRTFGSGTKLEIK 107

Search completed: Tue Feb 24 07:21:53 1998
Job time : 24 secs.

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CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SC1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA: 11956 MW: 63169 GN:

Query Match 88.58; Score 668; DB 7; Length 111;
Best Local Similarity 87.98; Pred. No. 4,06e-44;
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 2 AELTQSGTILSLSPGERATLSFGASVSNGYLAWYQKPGAPPLLIYGASTPATIDIPD 61
QY 1 AELTQSGTILSLSPGERATLSFGASVSNGYLAWYQKPGAPPLLIYGASTPATIDIPD 60

Db 62 RFGSGSGADFTLAISLEPEDEFAVYCCQYAGS-HTFGGKLEIK 107
QY 61 RFGSGSGIDFTLTISLEPEDEFAVYCCQYAGSPTFGGKLEIK 107

Search completed: Tue Feb 24 07:48:37 1998
Job time : 12 secs.

CC INFORMATION FOR SEQ ID NO: 90:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11705 MW: 52938 CN:

Query Match 88.7% Score 670; DB 13; Length 107;
Best Local Similarity 88.7% Pred No 2 80e-44;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGCAPPLLYGSSTRGTGIPDR 60
QY 2 ELTQSPGTLSPGEPATLSCPASQSVPSNYLAWYQKPGCAPPLLYGVSSPATGIPDR 61

Db 61 FSGSGSGTDFLTISRLEPEDFAVYCOYHNSVYTFGGTKLEIK 106
QY 62 FSGSGSGTDFLTISRLEPEDFAVYCOYHNSVYTFGGTKLEIK 107

RESULT 11
ID US-08-276-852-90 STANDARD: PRT: 107 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 90, Application US/08276852.

XX Sequence 90, Application US/08276852

CC Patent No. 5652138

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R

CC APPLICANT: Barbas, Carlos F

CC APPLICANT: Lerner, Richard A

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute, Office of

CC ADDRESSEE: Patent Counsel

CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276.852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCPI452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 90.

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 107 amino acids

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11705 MW: 52938 CN:

Query Match 88.7% Score 670; DB 7; Length 107;
Best Local Similarity 88.7% Pred No 2 80e-44;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGCAPPLLYGSSTRGTGIPDR 60
QY 2 ELTQSPGTLSPGEPATLSCPASQSVPSNYLAWYQKPGCAPPLLYGVSSPATGIPDR 61

Db 61 FSGSGSGTDFLTISRLEPEDFAVYCOYHNSVYTFGGTKLEIK 106
QY 62 FSGSGSGTDFLTISRLEPEDFAVYCOYHNSVYTFGGTKLEIK 107

RESULT 12
ID US-08-276-852-147 STANDARD: PRT: 109 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 147, Application US/08276852.

XX Sequence 147, Application US/08276852

CC Patent No. 5652138

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R

CC APPLICANT: Barbas, Carlos F

CC APPLICANT: Lerner, Richard A

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute, Office of

CC ADDRESSEE: Patent Counsel

CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276.852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCPI452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 147:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 109 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/487,200
 CC FILING DATE: 7-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002610
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 86:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: rsv 9L; 11L; 21L; anad 22L
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..109
 CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match 90.3%; Score 682; DB 7; Length 108;
 Best Local Similarity 92.4%; Pred. No. 3,04e-45;
 Matches 97; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

D6 4 LTQSPGTLSPGERATLSRATLSGASQSVSSVYLGWYQKPGQCAPPLLIYGRASSRATGIPDPF 63
 QY 3 LTQSPGTLSPGERATLSGASQSVSSVYLGWYQKPGQCAPPLLIYGVSSRATGIPDPF 62

D6 64 SGSGSGDTFTLTISRLEPEDFAVYQYQYGLRTEFGQGTKEIK 108
 QY 63 SGSGSGDTFTLTISRLEPEDFAVYQYQYGLRTEFGQGTKEIK 107

RESULT 9
 ID PCT-US93-08786-23 STANDARD: PRT: 109 AA.
 XX xxxxxx
 AC
 XX 01-JAN-1900
 DT
 DE Sequence 23, Application PC/TUS9308786.
 XX
 CC Sequence 23, Application PC/TUS9308786
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis F
 CC APPLICANT: Barbas, III, Carlos F.
 CC APPLICANT: Chanock, Robert M.
 CC APPLICANT: Murphy, Brian R.
 CC APPLICANT: Crowe, Jr., James E.
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC NUMBER OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn, Juba & Lubitz
 CC STREET: 1890 Century Park East, Suite 500

CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08786
 CC FILING DATE: 16-SEP-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Wetherell, Jr., Ph.D., John R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD-2791
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-3100
 CC TELEFAX: (619) 455-3110
 CC INFORMATION FOR SEQ ID NO: 23:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 109 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: rsv 5L; 11L; 21L; anad 22L
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..109
 CC SEQUENCE 109 AA; 12099 MW; 62556 CN;

Query Match 89.3%; Score 674; DB 11; Length 109;
 Best Local Similarity 88.8%; Pred. No. 1.34e-44;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

D6 2 AELTSPGTLSPGERATLSRATLSGASQSVSSVYLGWYQKPGQCAPPLLIYGRASSRATGIPDP 61
 QY 1 AELTSPGTLSPGERATLSGASQSVSSVYLGWYQKPGQCAPPLLIYGVSSRATGIPDP 60

D6 62 PFSSGSGDTFTLTISRLEPEDFAVYQYQYGLRTEFGQGTKEIK 108
 QY 61 PFSSGSGDTFTLTISRLEPEDFAVYQYQYGLRTEFGQGTKEIK 107

RESULT 10
 ID PCT-US95-08743-90 STANDARD: PRT: 107 AA.
 XX xxxxxx
 AC
 XX 01-JAN-1900
 DT
 DE Sequence 90, Application PC/TUS9508743.
 XX
 CC Sequence 90, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC NUMBER OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/COCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 90.3% Score 682; DB 6; Length 108;
Best Local Similarity 92.4% Pred No 3 04e-45;
Matches 97; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 4 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQAPRLIYGASSPATGIPDPF 63
QY 3 LTSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLIYGVSRRATGIPDPF 62
Db 64 SGSGSGTDFTLTISRLEPEDEFAVYVYQYQYGLGRTFGGQTKVEIK 108
QY 63 SGSGSGTDFTLTISRLEPEDEFAVYVYQYQYQYGLGRTFGGQTKLEIK 107

RESULT 7
ID US-08-474-040-86 STANDARD: PRT: 108 AA.

XX XXXXXX
XX 01-JAN-1900
XX Sequence 86, Application US/08474040.
XX Sequence 86, Application US/08474040
CC Patent No. 5693761
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELLINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khorrie and Crew
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,040
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/COCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN;

Query Match 90.3% Score 682; DB 7; Length 108;
Best Local Similarity 92.4% Pred No 3 04e-45;
Matches 97; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 4 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQAPRLIYGASSPATGIPDPF 63
QY 3 LTSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLIYGVSRRATGIPDPF 62
Db 64 SGSGSGTDFTLTISRLEPEDEFAVYVYQYQYGLGRTFGGQTKVEIK 108
QY 63 SGSGSGTDFTLTISRLEPEDEFAVYVYQYQYQYGLGRTFGGQTKLEIK 107

RESULT 8
ID US-08-487-200-86 STANDARD: PRT: 108 AA.

XX XXXXXX
XX 01-JAN-1900
XX Sequence 86, Application US/08487200
XX Sequence 86, Application US/08487200
CC Patent No. 5693762
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELLINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC Street: 379 Lytton Avenue
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US

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RESULT 2
ID US-08-276-852-86 STANDARD: PRT: 108 AA.
XX
AC xxxxxx
XX
DE 01-JAN-1900
XX
DE Sequence 86, Application US/08276852.
XX
CC Sequence 86, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276.852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11769 MW: 65957 CN:
Query Match 91.7% Score 692; DB 7; Length 108;
Best Local Similarity 93.4% Pred No. 4 78e-46.
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGERATLSCPAQSVISNYLAWYQKPGCAPRLIYGVSNPATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSCGASQSVISNYLAWYQKPGCAPRLIYGVSSRATGIPDR 61
Db 61 FSGSGSGTDFLTISRLEPEDFAVYCCYVGIHWTFEGGKLEIK 106
QY 62 FSGSGSGTDFLTISRLEPEDFAVYCCYVGIHWTFEGGKLEIK 107
RESULT 3
ID US-08-276-852-99 STANDARD: PRT: 108 AA.

XX
AC xxxxxx
XX
DE 01-JAN-1900
XX
DE Sequence 99, Application US/08276852.
XX
CC Sequence 99, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276.852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN:
Query Match 90.7% Score 685; DB 7; Length 109;
Best Local Similarity 89.6% Pred. No. 1.75e-45;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGERATLSCPAQSVISNYLAWYQKPGCAPRLIYGVSNPATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSCGASQSVISNYLAWYQKPGCAPRLIYGVSSRATGIPDR 61
Db 61 FSGSGSGTDFLTISRLEPEDFAVYCCYVGIHWTFEGGKLEIK 106
QY 62 FSGSGSGTDFLTISRLEPEDFAVYCCYVGIHWTFEGGKLEIK 107
RESULT 4
ID PCT-US95-08743-99 STANDARD: PRT: 108 AA.
XX
AC xxxxxx
XX

Result No.	Score	Query %		Length	DB	ID	Description	Pred. No.	
		Match	Recall						
SUMMARIES									
1	692	91.7	108	13	PCT-US95-0	Sequence 86,	Applicati	4,78e-46	
2	532	91.7	108	7	US-08-276-	Sequence 86,	Applicati	4,78e-46	
3	695	90.7	108	7	US-08-276-	Sequence 99,	Applicati	1,75e-45	
4	695	90.7	108	13	PCT-US95-0	Sequence 99,	Applicati	1,75e-45	
5	692	90.3	108	6	US-08-477-	Sequence 86,	Applicati	3,04e-45	
6	692	90.3	108	6	US-07-634-	Sequence 86,	Applicati	3,04e-45	
7	692	90.3	108	7	US-08-474-	Sequence 86,	Applicati	3,04e-45	
8	692	90.3	108	7	US-08-487-	Sequence 86,	Applicati	3,04e-45	
9	574	89.3	107	13	PCT-US93-0	Sequence 23,	Applicati	1,34e-44	
10	670	88.7	107	13	PCT-US95-0	Sequence 90,	Applicati	2,80e-44	
11	570	88.7	107	7	US-08-276-	Sequence 99,	Applicati	2,80e-44	
12	670	88.7	109	7	US-08-276-	Sequence 147,	Applicat	2,80e-44	
13	670	88.7	109	13	PCT-US95-0	Sequence 147,	Applicat	2,80e-44	
14	698	88.5	111	13	PCT-US95-0	Sequence 149,	Applicat	4,06e-44	
15	698	88.5	111	7	US-08-276-	Sequence 149,	Applicat	4,06e-44	
16	657	87.0	104	13	PCT-US95-0	Sequence 100,	Applicat	3,10e-43	
17	657	87.0	104	7	US-08-276-	Sequence 100,	Applicat	3,10e-43	
18	653	86.5	108	7	US-08-276-	Sequence 110,	Applicat	6,50e-43	
19	653	86.5	108	13	PCT-US95-0	Sequence 110,	Applicat	6,50e-43	
20	550	86.1	107	7	US-08-276-	Sequence 87,	Applicat	1,13e-42	
21	650	86.1	107	13	PCT-US95-0	Sequence 87,	Applicat	1,13e-42	
22	550	86.1	108	7	US-08-276-	Sequence 96,	Applicati	1,13e-42	



US-08-844-215-10.rsp

Thu, Feb 26 07:03:43 1998

RESULT 13
ID KVM_HUMAN STANDARD; PRT: 108 AA.
AC PO1605;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 77038198
RA CAPRA J.D., KLAPPER D.G.;
RL SCAND. J. IMMUNOL. 5:677-684(1976).
CC -!- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
CC PIR: A01871; KIHULY.
DR HSP: PO1607; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 22228B0C CPC32;

Query Match 72.5%; Score 547; DB 5; Length 108;
Best Local Similarity 67.0%; Pred. No. 3.28e-99;
Matches 71; Conservative 20; Mismatches 14; Indels 1; Gaps 1;
Db 3 qmtgssslsvsgdrvtitcgaqynva-ylwlygkqkqqlapkllygastragvpsr 61
QY 2 ELTQSPGTLISLSPGERATLSGASQSVRSNYLAWYQKQAPRLLIYGVSSRATGIPDR 61
Db 62 fsgsgsgtdfttisslpediatyccqynwptfagqtkvevk 107
QY 62 FSGSGSGTDFTLTISRLEPEDFAVYICQYGGSSPRTFGQTKLEIK 107

RESULT 14
ID KVM_HUMAN STANDARD; PRT: 116 AA.
AC PO4434; 1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECIPFOR V-III REGION (VH) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85087932.
RA PECH M., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:9229-9236(1984).
CC EMBL; X07225; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HUVH.
DR HSP: PO1607; 1MCP.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH).
FT DOMAIN 21 43
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 71 77

Query Match 71.0%; Score 536; DB 5; Length 108;
Best Local Similarity 64.2%; Pred. No. 1.22e-96;
Matches 68; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
Db 3 qmtgssslsvsgdrvtitcgaqynva-ylwlygkqkqqlapkllygastragvpsr 61
QY 2 ELTQSPGTLISLSPGERATLSGASQSVRSNYLAWYQKQAPRLLIYGVSSRATGIPDR 61
Db 62 fsgsgsgtdfttisslpediatyccqynwptfagqtkvevk 107
QY 62 FSGSGSGTDFTLTISRLEPEDFAVYICQYGGSSPRTFGQTKLEIK 107

Search completed: Tue Feb 24 07:21:11 1998
Job time : 15 secs.

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DR HSSP: P01607: 1AAG
KW IMMUNOGLOBULIN V REGION: SIGNAL
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (CLL).
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14275 MW: 2F344868 CRC32.

Query Match 81.1% Score 612, DB 5, Length 129.
Best Local Similarity 81.1% Pred. No. 174e-114;
Matches 85; Conservative 13; Mismatches 5; Indels 2; Gaps 2;

Db 24 mtqspatlsvpggeratlsrsgsv:snrlawyqgkpgqpprlliygastratgiparf 82
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGQAPRLLIYGVSSPATGIPDPF 62
Db 83 sgsqsgtftltisrlsgedfavyycqgynnwppwtfgqtrveik 128
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQYGS-SPRTGQGTKEIK 107

RESULT 10
ID KV3C_HUMAN STANDARD: PRT: 100 AA.
AC P01621;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (NG9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N A.
RX MEDLINE: 84093600.
RA BENTLEY D.L.;
PT NATURE 307:77-80(1984)
CC -!- THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIP: A01944: K3HUNG
DR HSSP: P01607: 1AAG
KW IMMUNOGLOBULIN V REGION: SIGNAL: HYBRIDOMA
FT SIGNAL 1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NG9).
FT DISULFID 27 93 BY SIMILARITY
FT NON_TER 100 100
SQ SEQUENCE 100 AA: 10729 MW: 99A75223 CRC32.

Query Match 80.4% Score 607, DB 5, Length 100.
Best Local Similarity 92.4% Pred. No. 2.63e-113;
Matches 85; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 8 ltqspatlsvpggeratlsrsgsv:snrlawyqgkpgqpprlliygastratgipdrf 67
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGQAPRLLIYGVSSPATGIPDPF 62
Db 68 sgsasatdftltisrlsgedfavyycqgyns 94
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQYGS 94

RESULT 11
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01624;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RA KLAPPER D.G., CAPPA J.D.;
RL ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976).
CC -!- THIS CHAIN WAS ISOLATED FROM AN ICM WITH ANTI-GAMMA GLOBULIN
ACTIVITY.
DR PIP: A01897: K3HUPM
DR HSSP: P01607: 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11922 MW: A0C42C88 CRC32.

Query Match 79.7% Score 602, DB 5, Length 109.
Best Local Similarity 77.1% Pred. No. 3.96e-112;
Matches 81; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

Db 4 mtqspatlsvpggeratlsrsgsv:snrlawyqgkpgqpprlliygastratgiparf 63
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGQAPRLLIYGVSSPATGIPDPF 62
Db 64 sgsqsgtftltisrlsgedfavyycqgynnwppwtfgqtrveik 108
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQYGS-SPRTGQGTKEIK 107

RESULT 12
ID KV3I_HUMAN STANDARD: PRT: 115 AA.
AC P04433;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N A.
RX MEDLINE: 85087932.
RA PECH M., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:4239-4234(1984)
DR EMBL: X01668: -; NOT_ANNOTATED_CDS.
DR PIP: A01900: K3HUVG.
DR HSSP: P01607: 1AAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA: 12575 MW: 37E182FC CRC32.

Query Match 72.7% Score 549, DB 5, Length 115.
Best Local Similarity 89.8% Pred. No. 1.12e-99;
Matches 79; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Db 24 ltqspatlsvpggeratlsrsgsv:snrlawyqgkpgqpprlliygastratgiparf 82
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGQAPRLLIYGVSSPATGIPDPF 62
Db 83 sgsqsgtftltisrlsgedfavyycqgyns 110
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQYGS 90

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Matches 97: Conservative 2: Mismatches 6: Indels 0: Gaps 0:

Db 4 ltspgtlslspgeratlscrasqvsnylawyqkqgqaprllygassratgipdrf 63
 |||||
 QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKQGPAPPLIYGVSSPATGIPDRF 62
 |||||
 Db 64 ssgsgtdftltisrlepedfavyycqygsgrtfgagtkveik 108
 |||||
 QY 63 SSGSGTDFLTLSRLEPEDFAVYCYQYGSPPRTFGGKLEIK 107
 |||||

RESULT 6 STANDARD: PRT: 109 AA.

ID KV3D_HUMAN
 AC P01522
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (TI)
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA: METAZOA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE
 RX MEDLINE: 72188439
 RA SUTER L, RABINIKOL H U, WATANABE S, HILSCHMANN N.;
 RL HOPPE-SEYLER'S 2. PHYSIC. CHEM. 353:183-238(1972)
 CC -/- THE C REGION OF THIS CHAIN HAS THE INV (3) MAPKER.
 CC -/- THIS IS A BENCE-JONES PROTEIN
 DR PIR: A01895; K3HUT1.
 DR HSSP: P01607; 2IMM.
 KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN
 FT DISULFID 23 89 BY SIMILARITY
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11788 MW; D03795R1 CPC32:

Query Match 89.5%; Score 672; DB 5; Length 109;

Best Local Similarity 90.5%; Pred. No. 1,10e-129;
 Matches 95: Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 4 ltspgtlslspgeratlscrasqvsnylawyqkqgqaprllygassratgipdrf 63
 |||||
 QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKQGPAPPLIYGVSSPATGIPDRF 62
 |||||
 Db 64 ssgsgtdftltisrlepedfavyycqygsgrtfgagtkveik 108
 |||||
 QY 63 SSGSGTDFLTLSRLEPEDFAVYCYQYGSPPRTFGGKLEIK 107
 |||||

RESULT 7 STANDARD: PRT: 109 AA.

ID KV3G_HUMAN
 AC P04206
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (GOL) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN)
 CC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE
 RX MEDLINE: 86230578.
 RA NEWKIRK M., CHEN P.P., CARSON D.A., POSNETT D., CAPPA J.D.;
 RL MOL IMMUNOL 23:239-244(1986).
 DR PIR: A01893; K3HUGO
 DR HSSP: P01607; 1DPR
 KW IMMUNOGLOBULIN V REGION
 FT DISULFID 23 89 BY SIMILARITY
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11840 MW; 893DC04A CPC32:

Query Match 87.5%; Score 661; DB 5; Length 109;

Best Local Similarity 88.6%; Pred. No. 4.48e-126;
 Matches 93: Conservative 4; Mismatches 8; Indels 0; Gaps 0.

RESULT 8

ID KV3K_HUMAN STANDARD: PPT: 128 AA.
 AC P06311
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECIP SOP V-III REGION (IAPC/BL41).
 OS HOMO SAPIENS (HUMAN)
 CC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA KLOECK H.G., MEINEL A., COMBRIATO G., SOLOWEN A., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: Z00021, G33173.
 DR PIR: A01899; K3H041
 DR HSSP: P01607; 3HEM.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IAPC/BL41).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 128 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA: 14070 MW; 318E08AF CPC32:

Query Match 81.1%; Score 612; DB 5; Length 128;

Best Local Similarity 86.7%; Pred. No. 1.74e-114;
 Matches 91: Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Db 24 ltspgtlslspgeratlscrasqvsnylawyqkqgqaprllygassratgipdrf 82
 |||||
 QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKQGPAPPLIYGVSSPATGIPDRF 62
 |||||
 Db 83 ssgsgtdftltisrlepedfavyycqygsgrtfgagtkveik 107
 |||||
 QY 63 SSGSGTDFLTLSRLEPEDFAVYCYQYGSPPRTFGGKLEIK 107
 |||||

RESULT 9

ID KV3H_HUMAN STANDARD: PPT: 129 AA.
 AC P04207
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECIP SOP V-III REGION (CII) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN)
 CC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86177570.
 RA JIPIK F.P., SORGE J., PONG S., HEITZMANN I.G., CHUP T.G., CHEN P.P.,
 RA GOLDFIEN R., CARSON D.A.;
 RL PROG. NATL. ACAD. SCI. U.S.A. 84:2195-2199(1986).
 DR EMBL: M12740; G553486;
 DR PIR: A01898; K3HUC1.

Query Match 81.1%; Score 612; DB 5; Length 129;

Best Local Similarity 86.7%; Pred. No. 1.74e-114;
 Matches 91: Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Db 24 ltspgtlslspgeratlscrasqvsnylawyqkqgqaprllygassratgipdrf 82
 |||||
 QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKQGPAPPLIYGVSSPATGIPDRF 62
 |||||
 Db 83 ssgsgtdftltisrlepedfavyycqygsgrtfgagtkveik 107
 |||||
 QY 63 SSGSGTDFLTLSRLEPEDFAVYCYQYGSPPRTFGGKLEIK 107
 |||||

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RESULT 2
ID KV3M_HUMAN STANDARD: PRT: 129 AA.
AC P18136;
DT 01-NOV-1990 (REL 16, CREATED)
DT 01-NOV-1990 (REL 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.:
PL 1 EXP MED 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P10021; K3HUB1.
DR HSP: P01607; IDPB.
KW IMMUNOGLOBULIN V REGION: SIGNAL
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC)
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 109 BY SIMILARITY
FT NON_TER 129 129
SQ SEQUENCE 129 AA: DD00C369 CRC32;

Query Match 91.7% Score 592; DB 5; Length 129;
Best Local Similarity 91.7% Pred. No. 196e-133;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 24 ltspgtlslspgeratlscrasqsvssylawygkpgqaprllygssratgipdrf 83
|||||
QY 3 LTQSPGTLSPGERATLSGASQSVSPNYLAWYQKPGQAPRLLYGVSSPATGIPDRF 62
|||||

Db 84 sgsasqtdftltisrlpddfavyyccqygssptfgqskveik 128
|||||
QY 63 SGSSGTDFTLTISRLPEDFAVYCCQYGVSSPRTFGQTKLEIK 107
|||||

RESULT 3
ID KV3B_HUMAN STANDARD: PRT: 109 AA.
AC P01620;
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598
RA ANDREWS D.W., CAPPA J.D.:
RL BIOCHEMISTRY 20:5816-5822(1981)
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUS1
DR HSP: P01607; IDPB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 00B5DD5D CRC32;

Query Match 91.4% Score 690; DB 5; Length 109;
Best Local Similarity 91.4% Pred. No. 4.65e-131;

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Best Local Similarity 91.4%; Pred. No. 5.84e-133;
Matches 96; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltspgtlslspgeratlscrasqsvssylawygkpgqaprllygssratgipdrf 63
|||||
QY 3 LTQSPGTLSPGERATLSGASQSVSPNYLAWYQKPGQAPRLLYGVSSPATGIPDRF 62
|||||

Db 64 sgsasqtdftltisrlpddfavyyccqygssptfgqskveik 108
|||||
QY 63 SGSSGTDFTLTISRLPEDFAVYCCQYGVSSPRTFGQTKLEIK 107
|||||

RESULT 4
ID KV3A_HUMAN STANDARD: PRT: 108 AA.
AC P01619;
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (B6)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 2-301-304(1959).
RA MILSTEIN C.:
PL FEBS LETT 2-301-304(1959).
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01891; K3HUB6.
DR HSP: P01607; IMCP.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN
FT DISULFID 23 89 BY SIMILARITY
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 46D6B68E CRC32;

Query Match 90.7% Score 685; DB 5; Length 108;
Best Local Similarity 88.8% Pred. No. 9.01e-132;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltspgtlslspgeratlscrasqsvssylawygkpgqaprllygssratgipdrf 63
|||||
QY 3 LTQSPGTLSPGERATLSGASQSVSPNYLAWYQKPGQAPRLLYGVSSPATGIPDRF 62
|||||

Db 64 sgsasqtdftltisrlpddfavyyccqygssptfgqskveik 108
|||||
QY 63 SGSSGTDFTLTISRLPEDFAVYCCQYGVSSPRTFGQTKLEIK 107
|||||

RESULT 5
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01623;
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598
RA ANDREWS D.W., CAPPA J.D.:
RL BIOCHEMISTRY 20:5816-5822(1981)
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01896; K3HUBL.
DR HSP: P01607; IDPB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11746 MW: 7D8F5D75 CRC32;

Query Match 90.3% Score 682; DB 5; Length 109;
Best Local Similarity 92.4% Pred. No. 4.65e-131;

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[W][O][R][D]

(TM)

Release 2.1d John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:20:56 1998; Mapar time 5.03 Seconds
Tabular output not generated. 451 310 Million cell updates/sec

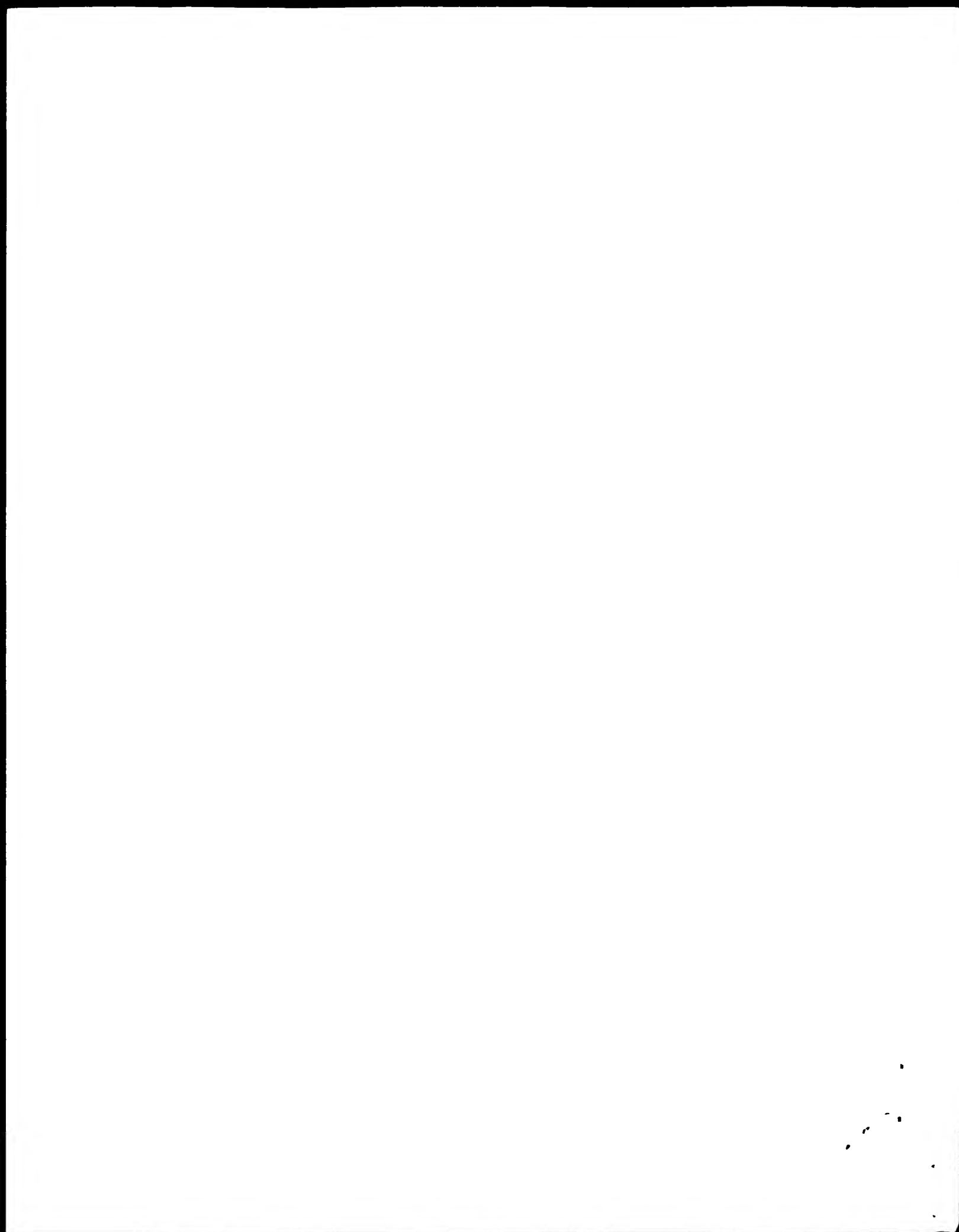
Title: >US-08-844-215-10
Description: (1-107) from US08844215.pep
Perfect score: 755
Sequence: 1 AELTQSPGTLUSLSPGPRATL CQYGGSSPTFGQTKLEIK 107
Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 40 349; Variance 69.606; scale 0.580

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		Match		Length		DR		ID		Description		Pred No.	
No	Score	No	Score	No	Score	No	Score	No	Score	No	Score	No	Score	No	Score
1	703	93	1	129	5	KV1L_HUMAN	IG KAPPA CHAIN PRECUR	4	73e-136						
2	692	91	7	129	5	KV3M_HUMAN	IG KAPPA CHAIN PRECUR	1	96e-133						
3	690	91	4	109	5	KV3E_HUMAN	IG KAPPA CHAIN V-III	5	84e-133						
4	685	90	7	109	5	KV3A_HUMAN	IG KAPPA CHAIN V-III	9	01e-132						
5	682	90	3	109	5	KV3E_HUMAN	IG KAPPA CHAIN V-III	4	65e-131						
6	672	89	0	109	5	KV3D_HUMAN	IG KAPPA CHAIN V-III	1	10e-128						
7	661	87	5	109	5	KV3C_HUMAN	IG KAPPA CHAIN V-III	4	48e-126						
8	612	81	1	129	5	KV3I_HUMAN	IG KAPPA CHAIN PRECUR	1	74e-114						
9	612	81	1	129	5	KV3H_HUMAN	IG KAPPA CHAIN PRECUR	1	74e-114						
10	607	80	4	100	5	KV3C_HUMAN	IG KAPPA CHAIN PRECUR	2	63e-113						
11	602	79	7	109	5	KV3F_HUMAN	IG KAPPA CHAIN V-III	3	96e-112						
12	549	72	7	115	5	KV3I_HUMAN	IG KAPPA CHAIN PRECUR	1	12e-99						
13	547	72	5	108	5	KV1M_HUMAN	IG KAPPA CHAIN V-I RE	3	28e-99						
14	545	72	2	116	5	KV3I_HUMAN	IG KAPPA CHAIN PRECUR	9	63e-99						
15	536	71	0	108	5	KV1K_HUMAN	IG KAPPA CHAIN V-I RE	1	22e-96						
16	524	64	4	108	5	KV1N_HUMAN	IG KAPPA CHAIN V-I RE	7	76e-94						
17	523	64	3	108	5	KV1F_HUMAN	IG KAPPA CHAIN V-I RE	1	43e-93						
18	518	68	6	108	5	KV1F_HUMAN	IG KAPPA CHAIN V-I RE	1	94e-92						
19	516	68	3	108	5	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE	5	68e-92						
20	515	68	2	108	5	KV1H_HUMAN	IG KAPPA CHAIN V-I RE	9	72e-92						
21	513	67	0	109	5	KV1E_HUMAN	IG KAPPA CHAIN V-I RE	2	84e-91						
22	510	67	5	114	5	KV4A_HUMAN	IG KAPPA CHAIN V-IV R	1	42e-90						

ALIGNMENTS

RESULT	1	STANDARD	PFT	129 AA
ID	KV1L_HUMAN	IG KAPPA CHAIN PRECUR		
AC	P18135			
DT	01-NOV-1990 (REL. 16, CREATED)			
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)			
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN PRECURSOR V-III REGION (HAH)			
OS	HOMO SAPIENS (HUMAN)			
OC	EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES;			
RN	[1]			
RP	SEQUENCE FROM N A			
RX	MEDLINE: 88171307			
RA	KIPPS T J, TOMHAVE F, CHEN P P, CARSON D A ;			
RL	J. EXP. MED. 167:840-852(1988).			
CC	-I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M			
CC	AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC			
CC	LEUKEMIA			
DR	PIR: P18022; K3HUHA.			
DR	HSP; P01607; IAAG.			
KW	IMMUNOGLOBULIN V REGION; SIGNAL			
FT	SIGNAL	1 20		
FT	CHAIN	21 129		
FT	DOMAIN	21 43		
FT	DOMAIN	44 55		
FT	DOMAIN	56 70		
FT	DOMAIN	71 77		
FT	DOMAIN	78 109		
FT	DOMAIN	110 118		
FT	DOMAIN	119 129		
FT	DISULFID	43 109		
FT	NON_TER	129 129		
SQ	SEQUENCE	129 AA; 14077 MW; 2044085E CMC32;		
Query Match 93 19; Score 703; DP 5; Length 129;				
Best Local Similarity 94 38; Pred. No. 4.74e-136;				
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;				
Rh	24	ltgpgtstlsppgrtlscraesvssylwyqkpgtaptllygassratqtdprf	83	
Qy	3	ltgpgtstlsppgrtlscraesvssylwyqkpgtaptllygassratqtdprf	83	
Rh	84	sgsgsgtftltstlspodfayvvygagysptfsggkqvsk 128		
Qy	63	sgsgsgtftltstlspodfayvvygagysptfsggkqvsk 128		



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PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-163947/22.
DR N-PSDB: Q11879
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 4; Fig 16; 104pp; English.
CC This sequence is derived from the nucleotide sequence encoding the
CC light chain variable region. The "x" residues represent nonsense
CC codons. The coding sequence has been translated in all 3 reading
CC frames (see also P12130 and P12131). The L'V region is duplicated
CC in so-called "aberrant" light chains (see Q11878), conferring
CC increased avidity on antibodies comprising such aberrant chains.
CC See also Q11880.
SQ Sequence 401 AA:

Query Match 79.0%; Score 589; DB 2; Length 401;
Best Local Similarity 79.2%; Pred. No. 2.27e-32;
Matches 84; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Db 230 ltqspatlsfgxratlsctasgsqsy:lawyggkpgqgprpliydasratgiparfs 289
QY 3 LTQSPATLSVSPGERASLSCPASQSVGNLAWYQKPKQAPPLIYGGNTPATGIPDPFS 62
Db 290 gsgsgtdftltisslepedfavyycqhrdnwppgatfgggtkveik 335
QY 63 GSGSGTEFTLTISLSQSEDFAVYFCQHYSTWP--LTFGGGTKVEFK 106

RESULT 15
ID R13111 standard; Protein: 414 AA.
AC R13111:
DT 10-MAR-1993 (revised)
DE 01-AUG-1991 (first entry)
DE 1B1 IgG aberrant light chain with duplicated variable region.
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= leader peptide
FT Region 18..130
FT /label= variable region
FT /note= "L'V 1"
FT Region 131..243
FT /label= variable region
FT /note= "L'V 2"
FT Region 244..345
FT /label= constant region
PN W09106305-A
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-163947/22.
DR N-PSDB: Q11878.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 5; Fig 16; 104pp; English.
CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
CC the amino acid sequence beyond the first stop codon ("x" in the
CC sequence represents a nonsense codon). The clone is incomplete,
CC starting from the G of the ATG initiator codon, but the initial Met
CC is given. Antibody molecules of the invention can include one or two
CC aberrant light chains containing a duplicated variable region. To
CC produce heavier antibodies, these heavier antibodies were found to
CC have higher avidity than antibodies with just a single copy of the
CC L'V region. The antibodies can be used to treat disease, e.g.
CC infection by Streptococcus agalactiae. They are able to pass across

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CC the placenta.
CC See also Q11879 and Q11880.
SQ Sequence 414 AA:

Query Match 79.0%; Score 590; DB 2; Length 414;
Best Local Similarity 79.2%; Pred. No. 2.27e-32;
Matches 84; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Db 24 ltqspatlsfgxratlsctasgsqsy:lawyggkpgqgprpliydasratgiparfs 83
QY 3 LTQSPATLSVSPGERASLSCPASQSVGNLAWYQKPKQAPPLIYGGNTPATGIPDPFS 52
Db 84 gsgsgtdftltisslepedfavyycqhrdnwppgatfgggtkveik 129
QY 63 GSGSGTEFTLTISLSQSEDFAVYFCQHYSTWP--LTFGGGTKVEFK 106

Search completed: Tue Feb 24 07:24:52 1998
Job time : 38 secs.

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ID	R12128	standard: Protein: 349 AA.
AC	R12128;	
DT	01-AUG-1991	(first entry)
DE	1B1 IGC aberrant light chain with duplicated variable region.	
DE	immunoglobulin G; light chain; variable region; duplication;	
DE	passive immunity; group B streptococci.	
OS	Homo sapiens	
FFH	Key	Location/Qualifiers
FT	Peptide	1..17
FT	/label= leader peptide	
FT	/Region	18..130
FT	/label= variable region	
FT	/note= "L'V 1"	
FT	/Region	131..243
FT	/label= variable region	
FT	/note= "L'V 2"	
FT	/Region	244..345
FT	/label= constant region	
FT	/W09106305-A.	
PN	16-MAY-1991.	
PU	06-NOV-1990; U06426.	
PF	07-NOV-1989; US-432700.	
PR	(Br1M) BRISTOL-MYERS SQUIB.	
PPA	Shutord NW, Harris LJ, Roff HV;	
PT	WPI: 91-163947/22.	
DR	N-PSDB: Q11878.	
DR	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -	
PT	formed by duplicating esp. variable region of light chain of IgG	
PT	class	
PT	Example 5: Fig 16; 104pp; English.	
CCC	This sequence is deduced from the cDNA clone 4B9-Vk15 and includes	
CCC	the amino acid sequence beyond the first stop codon. The clone is	
CCC	incomplete, starting from the G of the ATG initiator codon, but the	
CCC	initial Met is given. Antibody molecules of the invention can	
CCC	include one or two aberrant light chains containing a duplicated	
CCC	variable region, to produce heavier antibodies. These heavier	
CCC	antibodies were found to have higher avidity than antibodies with	
CCC	just a single copy of the L'V region. The antibodies can be used to	
CCC	treat disease, e.g. infection by Streptococcus agalactiae. They are	
CCC	able to pass across the placenta.	
CCC	See also Q11879 and Q11880.	
SO	Sequence 349 AA;	

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Query Match      79.04: Score 589: DB 2: Length 349:
Best Local Similarity 79.24: Fred. No. 2.27e-32:
Matches      84: Conservative 10: Mismatches 10: Indels 2: Gaps
Ddb      24  ltqspatlispggeratlsrassgsqsyllawvqqqkpgqcaprllydasnratatcarfs 83
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3  ltqspatllsvsppgeralslscascsvnnlawaytqkpgvapeelllygsnlpaaigstprfs 62
Ddb      84  gsgsgtdftllslalepdfavvyqchrdnawppgatfggqtkvek 129
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      63  ssgsgtpefltlsslqsedfavvfcuhystwtp--lffggsgikvek 106
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT      14
ID R12129 standard: Protein: 401 AA.

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KI2129:		
AC	(first entry)	
DT	01-AUG-1991	
DE	QF 1 of IgG light chain variable region clone.	
KE	immunoglobulin G; light chain; variable region; duplication.	
DW	passive immunity; group B streptococi.	
KK	Homo sapiens.	
OS	Key	Location/Qualifiers
FH	Peptide	224..336
FT	/label= L'V region	
FT	/note= "last 3 amino acids of leader and variable region"	
PN	WC9106305-A.	
PD	16-MAY-1991.	
PF	06-NOV-1990: U05426.	

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FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
PN W09602273-A1
PD 01-FEB-1995; 008743.
PF 11-JUL-1995; US-276852.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection
PS Example, Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein: gp120 and are capable of the
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, b6. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The Mab
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;

Query Match 79.2%; Score 591; DB 19; Length 108;
Best Local Similarity 74.5%; Pred. No. 1.64e-32;
Matches 79; Conservative 19; Mismatches 7; Indels 1; Gaps 1;

Dd 1 elctqpgtislsgperatiscragqsisnylawyqgkpgqaprllygasnratgipdr 60
Qy 2 ELTQSPATLSVSPSPSPASUSQASQSVNN-LAWYQKPGQAPRLLYGSGNTRATGTPDR 60
Dd 61 fsgsgsgtdftlslsrlpepfavvyccgqgtspytfgggtgldik 106
Qy 61 FSGSGSGTEFTLTLSLSLQSEDFAVYFCQHYSTWPLTFGGSGTKVEFK 106

RESULT 11
ID W01266 standard; protein: 107 AA.
AC W01266;
DE 28-JAN-1997 (first entry)
DE VL region of HIV neutralising Mab, clone B30.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107
FT /label= FR4
PN W09602273-A1
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 used in
PT passive immunotherapy and detection of HIV infection.
PS Example, Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, B30. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The Mab
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

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QY 2 ELTGSPATLSVSGERASLSRASQSVNN-LAWYTKPSQAPPLLIYGSNTRATSIPIR 60
 Db 61 fsgsgsttdltlslrlepedfayvscqyqgysvtfqggtkveik 106
 QY 61 FSGSGSGTETLTLSLSQSEDFAYVFCQHYSTWPLTFGGGKVEPK 106

RESULT 7
 ID R54307 standard; protein: 108 AA.
 AC R54307;
 DI 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain: variable region: b24.
 KW Human immunodeficiency virus: HIV1: glycoprotein gp120; epitope:
 KW neutralisation: monoclonal antibody: kappa light chain;
 KW variable region: framework: complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; 008743.
 PR 18-JUL-1994; US-276852.
 PA (SCPI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Example: Page 177-178; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAb regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54307 is from a gp120-
 CC specific clone
 SQ Sequence 108 AA;

Query Match 79.58; Score 593; DB 10; Length 108;
 Best Local Similarity 80.28; Pred. No. 1,18e-32;
 Matches 85; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

Db 1 eltgspatlsvsgeratlsrasqsvsnlylawyqkqgqaprllyqvsnratgipdr 60
 QY 2 ELTGSPATLSVSGERASLSRASQSVNN-LAWYTKPSQAPPLLIYGSNTRATSIPIR 60
 Db 61 fsgsgsttdltlslrlepedfayvscqyqgysvtfqggtkveik 106
 QY 61 FSGSGSGTETLTLSLSQSEDFAYVFCQHYSTWPLTFGGGKVEPK 106

RESULT 8
 ID W01265 standard; protein: 108 AA.
 AC W01265;
 DI 28-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAb, clone b24.
 KW Heavy chain; light chain; variable region; VH: monoclonal antibody;

KW MAB, HIV, human immunodeficiency virus, glycoprotein, gp120, clone:
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; 008743.
 PR 18-JUL-1994; US-276852.
 PA (SCPI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example: Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the VL
 CC gene clone, b24. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 79.58; Score 593; DB 10; Length 108;
 Best Local Similarity 80.28; Pred. No. 1,18e-32;
 Matches 85; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

Db 1 eltgspatlsvsgeratlsrasqsvsnlylawyqkqgqaprllyqvsnratgipdr 60
 QY 2 ELTGSPATLSVSGERASLSRASQSVNN-LAWYTKPSQAPPLLIYGSNTRATSIPIR 60
 Db 61 fsgsgsttdltlslrlepedfayvscqyqgysvtfqggtkveik 106
 QY 61 FSGSGSGTETLTLSLSQSEDFAYVFCQHYSTWPLTFGGGKVEPK 106

RESULT 9
 ID W01278 standard; protein: 108 AA.
 AC W01278;
 DI 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b6.
 KW Heavy chain; light chain; variable region; VH: monoclonal antibody;

KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone:
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2

FT Misc_difference 116
 FT /note= "pro encoded by GTT (sic)"
 PN W09312232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U19228
 PR 10-DEC-1991; US-804652.
 PA (DAND) DANA FARBER CANCER INST INC
 PI (NEWSE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 DR WPI: 93-214174/26
 DR N-PSDB: Q42706.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Disclosure: Page 74-75; 109pp; English.
 CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
 CC other F105 VK sequences given elsewhere in the specification) was
 CC compared with germline gene Humv325 (Q42706), showing 97.7%
 CC similarity. By nucleotide sequence analysis, F105 appears to
 CC be derived from a member of the VK III subgroup gene family.
 SQ Sequence 129 AA;
 Query Match 79.9%; Score 596; DB 7; Length 129;
 Best Local Similarity 77.1%; Pred. No. 7.25e-33;
 Matches 81; Conservative 18; Mismatches 5; Indels 1; Gaps 1;
 Db 24 lqtsgptlslsgeratlsctasqssvssylawyyqgkqgqaprllygassratgipdrf 83
 QY 3 LTQSPATLSVSPGERASLSCASQSQSGNN-LAWYQKPKQAPRLIYSGNTRATGTPDRF 61
 Db 84 sgsgsgtdftltisrlepedfavyycqgsgsptyfgggtkleik 128
 QY 62 SGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106
 RESULT 5
 ID R54311 standard; protein: 107 AA.
 AC R54311.
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..107
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-275852.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DP, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAbs) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the F2
 CC gene clone, B20. A MAb containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ug of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAb
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 107 AA;
 Query Match 79.5%; Score 593; DB 19; Length 107;
 Best Local Similarity 77.4%; Pred. No. 1.18e-32;
 Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;
 Db 1 eltgspgtlslsgeratlsctasqssvssylawyyqgkqgqaprllygassratgipdr 50
 QY 2 ELTGSPATLSVSPGERASLSCASQSQSGNN-LAWYQKPKQAPRLIYSGNTRATGTPDR 60
 Db 61 fsgsgsgtdftltisrlepedfavyycqgsgsptyfgggtkleik 106
 QY 61 FSGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106

CC dicistronic vector to produce a library of fragments. E coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence #54311 is from a gp120-
 CC specific clone.
 SQ Sequence 107 AA;
 Query Match 79.5%; Score 593; DB 10; Length 107;
 Best Local Similarity 77.4%; Pred. No. 1.18e-32;
 Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;
 Db 1 eltgspgtlslsgeratlsctasqssvssylawyyqgkqgqaprllygassratgipdr 50
 QY 2 ELTGSPATLSVSPGERASLSCASQSQSGNN-LAWYQKPKQAPRLIYSGNTRATGTPDR 60
 Db 61 fsgsgsgtdftltisrlepedfavyycqgsgsptyfgggtkleik 106
 QY 61 FSGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106
 RESULT 6
 ID W01269 standard; Protein: 107 AA.
 AC W01269.
 DT 28-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAb, clone B20.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV, human immunodeficiency virus; glycoprotein gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 98..107
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-275852.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DP, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAbs) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the F2
 CC gene clone, B20. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ug of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAb
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 107 AA;
 Query Match 79.5%; Score 593; DB 19; Length 107;
 Best Local Similarity 77.4%; Pred. No. 1.18e-32;
 Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;
 Db 1 eltgspgtlslsgeratlsctasqssvssylawyyqgkqgqaprllygassratgipdr 50

```

RESULT 2
ID R50218 standard; Protein: 109 AA.
AC F50218;
DT 31-OCT-1994 (first entry)
DE HSV glycoprotein F binding MAB clone rsv23L VH/VL domain.
KW Complementarity determination region; CDR3: human; bronchiolitis.
KW monoclonal antibody; epitope: glycoprotein F; influenza virus;
KW respiratory syncytial virus; RSV; disease: rhinovirus; coronavirus;
KW lung; pneumonia.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FP1
FT Region 24..34
FT /label= CDR1
FT Region 35..49
FT /label= FP2
FT Region 50..56
FT /label= CDR2
FT Region 57..88
FT /label= FP3
FT Region 89..97
FT /label= CDR3
FT Region 98..109
FT /label= FP4
FT /label= FR4
PN W09406448-A.
PD 31-MAR-1994.
PF 15-SEP-1994; U09786.
PR 16-SEP-1992; US-945515.
PA (USRI ) SCRIPPS RES INST.
PA (USRI ) US DPT HEALTH & HUMAN SERVICES.
PI Barbas CF, Burton DR, Chanock PM, Crowe JE, Murphy BR.
DP WPI: 94-118147/14
PT Human neutralising monoclonal antibodies to respiratory syncytial
PI virus - for treatment prophylaxis and diagnosis of RSV and other
PI diseases of the respiratory tract
PS Disclosure: Fig 4; 104pp; English
CC The sequences given in R50215-19 represent the heavy and light chain
CC variable domains of various clones of a human monoclonal antibody
CC which binds to an epitope on glycoprotein F of respiratory syncytial
CC virus (RSV). These antibodies may be used as a reagent for the
CC diagnosis of RSV disease and other viral mucosal diseases, eg.
CC influenza virus, rhinovirus and coronavirus. They are particularly
CC useful in ameliorating RSV when delivered directly to the lungs, and
CC may also be used for treating pneumonia and bronchiolitis.
SQ Sequence 109 AA.

Query Match 81.5%; Score 608; DB 9; Length 109;
Best Local Similarity 75.5%; Pred No 1 03e-33;
Matches 80; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

Db 2 aeltspvltlsvspgervalsckasqndlnlwygkpgqaprllygassratatpdr 61
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
QY 1 AELTUSPAILSVSPGERASUSCFASQSVGNLAWYQKPGQAPRLIYGNTRATSTPDR 60
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

Db 62 fsgsgsgtftltlrlepfavvyccqygsgsptfsgqtkleik 107
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
QY 61 FSGSGSGTEFTLTISLSQSEDFAVYFCCHYSTWPLTFGGGKVEFK 106
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 3
ID R38593 standard; peptide: 107 AA.
AC R38593;
DT 28-OCT-1993 (first entry)
DE Human lambda light chain subgroup 3 (hL3).
KW Antibody: variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc difference 96
FT /note= "residue conserved in less than 50% of the
FT /note= "sequences of hL3"
PN W09311734-A.

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PD 24-JUN-1993.
PF 14-DEC-1992; U10906.
PR 13-DEC-1991; US-R08464.
PA (XOMA ) XOMA CORP.
PI Fishwild DM, Kohn FR, Little PG, Studnicka GM.
DS WPI: 93-213827/26.
PT Antibodies prep. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Claim 2; Page 93-94; 160pp; English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (hK1 - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 -
CC R38592, hL3 - R38593, hL6 - R38594, hK4 - R38595, hL4 - R38596,
CC and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
CC hH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 107 AA.

Query Match 80.2%; Score 508; DB 7; Length 107;
Best Local Similarity 76.9%; Pred. No. 5.24e-33;
Matches 80; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Db 4 ltgspgtlslspgeratlscrasqsvsylvaygkpgqaprllygassratatpdrfs 63
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
QY 3 LTQSPAILSVSPGERASUSCFASQSVGNLAWYQKPGQAPRLIYGNTRATSTPDRFS 62
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

Db 64 gsgsgtftltlrlepfavvyccqygsgsptfsgqtkleik 107
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
QY 63 GSGSGTEFTLTISLSQSEDFAVYFCCHYSTWPLTFGGGKVEFK 106
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 4
ID R38672 standard; Protein: 129 AA.
AC R38672;
DT 01-NOV-1993 (first entry)
DE Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS.
KW CDR4: receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide
FT Protein 21..129
FT /label= mat_protein
FT Region 1..116
FT /label= vk325
FT Region 117..129
FT /label= Jk2
FT Region 44..55
FT /label= CDR1
FT Region 71..77
FT /label= CDR2
FT Region 110..117
FT /label= CDR3
FT Misc difference 1
FT /note= "Met encoded by ATC (sic)"
FT Misc difference 35
FT /note= "Pro encoded by GCA (sic)"
FT Misc difference 99
FT /note= "Leu encoded by GTG (sic)"
FT Misc difference 113
FT /note= "Gly encoded by GAT (sic)"
FT Misc difference 114
FT /note= "Ser encoded by AAC (sic)"

```

WIRE

(TM)

Release 2 ID John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07 24 14 1998, Maspar time 6.61 Seconds
Tabular output not generated.
222,822 Million cell updates/sec

Title: >US-08-844-215-11
Description: (1-106) from US08844215 pep
Perfect Score: 746
Sequence: 1 AELTQSPATLSVSPGPRASL CQHYSTWPLTFCGGTKVEPK 106

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13880129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-generated30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 29.550; Variance 174.430; scale 0.169

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	635	85.1	234	9 R52951	Human anti-IgE MAB 11
2	608	81.5	109	9 R50218	HSV glycoprotein F bi
3	598	80.2	107	7 R38593	Human lambda light ch
4	596	79.4	129	7 P38472	vk325-JK2
5	593	79.5	107	10 P54311	Anti-HIV gp120 immuno
6	593	79.5	107	10 W01264	VL region of HIV neut
7	593	79.5	108	10 P54307	Anti-HIV gp120 immuno
8	593	79.5	108	19 W01265	VL region of HIV neut
9	591	79.2	108	19 W01278	VL region of HIV neut
10	591	79.2	108	9 R54316	Anti-HIV gp120 immuno
11	590	79.1	107	19 W01266	VL region of HIV neut
12	590	79.1	107	10 P54308	Anti-HIV gp120 immuno
13	589	79.0	349	2 P12128	IB1 IgG aberrant high
14	589	79.0	401	2 P12129	OFF 1 of IgG light ch
15	589	79.0	414	2 P13111	IB1 IgG aberrant high
16	589	79.0	414	2 P13018	IB1 IgG aberrant high
17	586	78.6	109	9 R50217	HSV glycoprotein F bi
18	581	77.9	111	10 R54377	Anti-HIV gp41 immunoq
19	581	77.9	111	19 W01322	VL of Fab, GL 41 1, b
20	580	77.7	109	19 W01320	VL of Fab, DL 41 19,

21	580	77.7	109	10 P54275	Anti-HIV gp41 immunoq
22	579	77.6	215	19 W07516	Ulcerative colitis-as
23	578	77.5	107	22 W08949	Kappa light chain var
24	576	77.2	127	22 W08946	Kappa light chain var
25	572	76.7	104	9 R54317	Anti-HIV gp120 immuno
26	572	76.7	104	19 W01279	VL region of HIV neut
27	572	76.7	107	7 P37612	HLIF Ab 1 chain V re
28	572	76.7	112	10 R54279	Anti-HIV gp41 immunoq
29	572	76.7	112	19 W01324	VL of Fab, SS 41 8, b
30	570	76.4	107	5 R35729	Humanised VL region o
31	570	76.4	107	22 W08948	Kappa light chain var
32	565	75.7	109	10 P56396	Light chain of Ab 31
33	564	75.6	124	22 W45399	Immunoglobulin F10-2
34	563	75.5	108	19 W01267	VL region of HIV neut
35	562	75.3	112	2 P81245	Anti-pseudomonas aeru
36	562	75.3	128	1 P91001	Anti-F. aeruginosa st
37	561	75.2	127	9 R50191	Light chain variable
38	560	75.1	129	7 P38673	F105VK-F105VK
39	560	75.1	129	7 R41286	F105 rearranged varia
40	557	74.7	214	19 W07515	Ulcerative colitis-as
41	555	74.4	127	9 R50187	Light chain variable
42	555	74.4	127	9 R50192	Light chain variable
43	554	74.3	134	20 W11155	Anti-lung tumour anti
44	551	73.9	108	19 W01289	VL region of HIV neut
45	551	73.9	108	23 W10895	CEA-specific antibody

ALIGNMENTS

RESULT 1
ID R52951 standard; Protein; 234 AA.
AC R52951.
DT 27-OCT-1994 (first entry)
DE Human anti-IgE MAB light chain.
KW Human IgE; CH4 region; triggers mediator release;
KW Mast cells; Monoclonal antibody; allergy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 21 128
FT /label= light chain variable region
FN EF-592230-A.
PD 13-APR-1994.
PF 07-OCT-1993; 308006.
PR 07-OCT-1992; JP-293800.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;
PI Yoshida T;
DR WPI: 94-120330/15.
DR N-PSDB: Q71872.
PT Human monoclonal anti-IgE peptide antibody - inhibits histamine
PT release from mast cells by allergen stimulation, useful for
PT preventing allergies
PS Claim 3; Page 12; 21pp; English.
CC R52951 shows the light chain of a human type anti-IgE peptide
CC monoclonal antibody which inhibits the signal transmission for
CC the release of chemical mediator from mast cells and basophils
CC stimulated with allergen. The antibody can be used for the
CC prophylaxis and the therapy of allergy.
SQ Sequence 234 AA:

Query Match 85.1%, Score 635, DB 9, Length 234.
Best Local Similarity 81.7%; Pred. No. 1,26e-35;
Matches 85, Conservative 14, Mismatches 5, Indels 0, Gaps 0;

Db	24	mqspatlsveqgrualscrasvsnlawyqkqkqaprllygastratgiparfs	84
QV	3	ELTQSPATLSVSPGPRASL.....CQHYSTWPLTFCGGTKVEPK	106
Db	84	qsgs2tdftlisslgsedfalyvcgqyswprtfqgatkvdik	127
QV	63	GS5SSTEFTLLISSLSQSDFAVYFCQHYSTWPLTFCGGTKVEPK	106


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CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/275,952
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA; 11956 MW; 63169 CN;

Query Match 77.9%; Score 581; DB 13; Length 111;
Best Local Similarity 75.7%; Pred. No. 2.42e-35;
Matches 81; Conservative 17; Mismatches 7; Indels 2; Gaps 2;

Db 2 AELTQSPGTLSPGERATLSQASVSNGYLAWYQKPGQAPRLIYGASTRATDIPD 61
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QY 1 AELTQSPAILSVSPGERASLSQASVSNN-LAWYQKPGQAPRLIYGGNTRATGTPD 59
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Db 62 RFGSGSGADFTLAISRLEPEDFAVYCCQYAG-SHTFCQGTKEIK 107
   |||||:||||:|||||:|||||:|||||:|||||:|||||:
QY 60 RFGSGSGTEFTLIISLSQSEDFAVYFCQRYSTWPLTFGGGKVEFK 106
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Search completed: Tue Feb 24 07:51:02 1998
Job time : 14 secs.

RESULT	14
ID	US-08-487-200-e6
XX	STANDARD; PRT; 109 AA.
AC	xxxxxx
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DT	01-JAN-1900
XX	
DE	Sequence 86, Application US/08487200.
XX	
CC	Sequence 86, Application US/08487200
CC	Patent No. 5693762
CC	GENERAL INFORMATION:
CC	APPLICANT: QUEEN, Cary L.
CC	APPLICANT: CO, Man Sung
CC	APPLICANT: SCHNEIDER, William P.
CC	APPLICANT: LANDOLFI, Nicholas F.
CC	APPLICANT: GOELINGH, Kathleen L.
CC	APPLICANT: SELICK, Harold E.
CC	TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

06 SUSGSGIDPILLISKLEPEDFAVYCQOYSLGRPGQGVKEIK 108
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62 SCSGSSTEFILTSLSQSEDFAVYCOHYSTWLTFGGKVVEFK 106

RESULT 15
ID PCT-US95-08743-149 STANDARD: PRF: 111 AA.
XX xxxxxx
XX XX
XX 01-JAN-1900
XX Sequence 149, Application PC/TUS9508743.
XX
XX Sequence 149, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC Best Application Number: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC Application Number: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC Application Number: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC Application Number: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:
SQ
Query Match 78.3% Score 584: DB 6: Length 108:
Best Local Similarity 76.2% Pred No 1.43e-75:
Matches 80: Conservative 17: Mismatches 7: Indels 1: Gaps 1:
Db 4 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQCAPPLLIYGASSPATGIPDRF 53
QY 3 LTSPATLSPGSRASLSCRASQSVGN-LAWYQKPGQAPPLLIYGGNTRATGTPDRF 61
Db 64 SGSGSGTDFLTLSRLEPEFAVYCOQYGLRGTGQGTKEIK 108
QY 52 SGSGSGTEFTLTISSLSQSEDFAVYFCWHYSTWELTGGGTRKEFK 106
RESULT 12
ID US-07-634-278-85 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 86, Application US/07634278.
XX Sequence 86, Application US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELING, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue

CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC Application Number: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC Application Number: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC Application Number: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:
SQ
Query Match 78.3% Score 584: DB 6: Length 108:
Best Local Similarity 76.2% Pred. No. 1.43e-35:
Matches 80: Conservative 17: Mismatches 7: Indels 1: Gaps 1:
Db 4 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQCAPPLLIYGASSPATGIPDRF 64
QY 3 LTSPATLSPGSRASLSCRASQSVGN-LAWYQKPGQAPPLLIYGGNTRATGTPDRF 61
Db 64 SGSGSGTDFLTLSRLEPEFAVYCOQYGLRGTGQGTKEIK 108
QY 62 SGSGSGTEFTLTISSLSQSEDFAVYFCWHYSTWELTGGGTRKEFK 106
RESULT 13
ID US-08-474-040-86 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 86, Application US/08474040.
XX Sequence 86, Application US/08474040
CC Patent No. 5693761
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELING, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew

CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178 302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA: US 07/954,148
CC APPLICATION NUMBER: 30-SEP-1992
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN:

Query Match 79.2%; Score 591; DB 7; Length 108;
Best Local Similarity 74.5%; Pred. No. 4.17e-36;
Matches 79; Conservative 19; Mismatches 7; Indels 1; Gaps 1;

Dd 1 ELTQSPGTLSPGEPATLSCPASQSVSNLYAWYQKPGCAPPLLIYGASNPATGIPDR 60
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Qy 2 ELTQSPATLSVSPGEPASLSCPASQSVGN-LAWYQKPGCAPPLLIYGNTATGTPDP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Dd 61 FSGSGSGTDFLTLSRLEPDAFYVYCOQYGTSPYTFGGTGOLDIK 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 FSGSGSGTEFTLTSSLOSEDAFYVFCQHYSTWPLTFGGGKVEFK 106
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RESULT 7
ID PCT-US95-08743-99 STANDARD: PRT: 108 AA.
XX xxxxxx
AC
XX 01-JAN-1900
DT
XX
XX

DE Sequence 99, Application PC/TUS9508743.
XX Sequence 99, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN:

Query Match 79.2%; Score 591; DB 13; Length 108;
Best Local Similarity 74.5%; Pred. No. 4.17e-36;
Matches 79; Conservative 19; Mismatches 7; Indels 1; Gaps 1;

Dd 1 ELTQSPGTLSPGEPATLSCPASQSVSNLYAWYQKPGCAPPLLIYGASNPATGIPDR 60
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Qy 2 ELTQSPATLSVSPGEPASLSCPASQSVGN-LAWYQKPGCAPPLLIYGNTATGTPDP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Dd 61 FSGSGSGTDFLTLSRLEPDAFYVYCOQYGTSPYTFGGTGOLDIK 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 FSGSGSGTEFTLTSSLOSEDAFYVFCQHYSTWPLTFGGGKVEFK 106
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RESULT 8
ID PCT-US95-08743-87 STANDARD: PRT: 107 AA.
XX xxxxxx
AC
XX 01-JAN-1900
DT

XX Sequence 87, Application PC/TUS9508743.
XX GENERAL INFORMATION:
CC APPLICANT:

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11654 MW: 62438 CN:

Query Match 79.1%; Score 590; DB 13; Length 107;
Best Local Similarity 78.3%; Pred. No. 4.97e-36;
Matches 83; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

Dd 1 ELTQSPGTLSPGEPATLSCPASQSVSNLYAWYQKPGCAPPLLIYGASNPATGIPDR 60
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Qy 2 ELTQSPATLSVSPGEPASLSCPASQSVGN-LAWYQKPGCAPPLLIYGNTATGTPDP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Dd 61 FSGSGSGTATFTLTSSQPEDVAIYYCOQYHSSPYTFGGGKLEIK 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 FSGSGSGTEFTLTSSLOSEDAFYVFCQHYSTWPLTFGGGKVEFK 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
ID US-08-276-852-87 STANDARD: PRT: 107 AA.
XX xxxxxx
AC
XX 01-JAN-1900
DT

XX Sequence 87, Application US/08276852.
XX Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

XX Sequence 86, Application PC/TUS9508743.
DE Sequence 86, Application PC/TUS9508743.
XX GENERAL INFORMATION:
CC APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25 (RPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65957 CN;
Query Match 79.5%; Score 593; DB 13; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.93e-36;
Matches 85; Conservative 11; Mismatches 9; Indels 1; Gaps 1;
Db 1 ELTQSPGTLISLSPGEPATISCRASQSVISNYLAWYQQRPGQAPRLLIYGVSNPATIGTDP 60
QY 2 ELTQSPATLSVSGEPASLSQASQSV-GNNLAWYQQRPGQAPRLLIYGVSNPATIGTDP 60
Db 61 FSGSGSGTDFLTISRLEPEDFVYSCQOYGTSPWTFGGTKVEIK 106
QY 61 FSGSGSGTEFTLTISLQSEDFVYFCQHYSTWPLTFGGTKVEIK 106
RESULT 5
ID US-08-276-852-86 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 86, Application US/08276852.
XX Patent No. 5652138
XX GENERAL INFORMATION:
XX APPLICANT: Burton, Dennis R
XX APPLICANT: Barbas, Carlos F
XX APPLICANT: Lerner, Richard A
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX NUMBER OF SEQUENCES: 170
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: The Scripps Research Institute, Office of
XX STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
XX CITY: La Jolla
XX STATE: CA
XX COUNTRY: USA
XX ZIP: 92037
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX OPERATING SYSTEM: IBM PC compatible
XX SOFTWARE: Patent in Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/276,852
XX FILING DATE: 18-JUL-1994

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65957 CN;
Query Match 79.5%; Score 593; DB 7; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.93e-36;
Matches 85; Conservative 11; Mismatches 9; Indels 1; Gaps 1;
Db 1 ELTQSPGTLISLSPGEPATISCRASQSVISNYLAWYQQRPGQAPRLLIYGVSNPATIGTDP 60
QY 2 ELTQSPATLSVSGEPASLSQASQSV-GNNLAWYQQRPGQAPRLLIYGVSNPATIGTDP 60
Db 61 FSGSGSGTDFLTISRLEPEDFVYSCQOYGTSPWTFGGTKVEIK 106
QY 61 FSGSGSGTEFTLTISLQSEDFVYFCQHYSTWPLTFGGTKVEIK 106
RESULT 6
ID US-08-276-852-99 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 99, Application US/08276852.
XX Patent No. 5652138
XX GENERAL INFORMATION:
XX APPLICANT: Burton, Dennis R
XX APPLICANT: Barbas, Carlos F
XX APPLICANT: Lerner, Richard A
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX NUMBER OF SEQUENCES: 170
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: The Scripps Research Institute, Office of
XX STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
XX CITY: La Jolla
XX STATE: CA
XX COUNTRY: USA
XX ZIP: 92037
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX OPERATING SYSTEM: IBM PC compatible
XX SOFTWARE: Patent in Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/276,852
XX FILING DATE: 18-JUL-1994

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 23L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
CC SEQUENCE 109 AA: 11959 MW: 64524 CN:

Query Match 81.5% Score 608; DB 11; Length 109;
Best Local Similarity 75.5% Pred No 2 0ae-37;
Matches 80; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

Db 2 AELTQSPVTLSPGEPVALSCRASQSNINNLAWYQKPGQAPPLLIYGASSPATGIDPP 61
QY 1 AELTQSPATLSVSGEPASLSQASQSVGNNAWYQKPGQAPPLLIYGNTATGTPDR 60
Db 62 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGGKLEIK 107
QY 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGGKLEIK 106

RESULT 2
ID US-08-276-852-90 STANDARD: PPT: 107 AA
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 90, Application US/08276852.
XX CC Patent No. 5652138
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Burton, Dennis F
XX CC APPLICANT: Barbas, Carlos F
XX CC APPLICANT: Lerner, Richard A
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: The Scripps Research Institute, Office of
XX CC ADDRESSEE: Patent Counsel
XX CC STREET: 10556 Nc 5652138th Torrey Pines Road, Suite 220.
XX CC STREET: Mail Drop 1068
XX CC CITY: La Jolla
XX CC STATE: CA
XX CC COUNTRY: USA
XX CC ZIP: 92037
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent In Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC CLASSIFICATION: 514
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/178,302
XX CC FILING DATE: 30-SEP-1993
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/954,148
XX CC FILING DATE: 30-SEP-1992
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Fitting, Thomas
XX CC REGISTRATION NUMBER: 34,163
XX CC REFERENCE/DOCKET NUMBER: SCF1452P
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 619-554-2937
XX CC TELEFAX: 619-554-6312
XX CC INFORMATION FOR SEQ ID NO: 90:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC CLONE: rsv 23L
CC SEQUENCE 107 AA: 11705 MW: 62938 CN:

Query Match 79.5% Score 593; DB 7; Length 107;
Best Local Similarity 77.4% Pred No 2.93e-36;
Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;

Db 1 ELTQSPCTLSLSPGERATLSGRASQSLNNYLAWYQKPGQAPPLLIYGSSSTPGTGIDPP 60
QY 2 ELTQSPATLSVSGEPASLSQASQSVGNNAWYQKPGQAPPLLIYGNTATGTPDR 60
Db 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGGKLEIK 106
QY 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGGKLEIK 106

RESULT 3
ID PCT-US95-08743-90 STANDARD: PPT: 107 AA
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 90, Application PC/TUS9508743.
XX CC Sequence 90, Application PC/TUS9508743
XX CC GENERAL INFORMATION:
XX CC APPLICANT:
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US95/08743
XX CC FILING DATE: 11-JUL-1995
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 09/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC INFORMATION FOR SEQ ID NO: 90:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 107 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 107 AA: 11705 MW: 62938 CN:

Query Match 79.5% Score 593; DB 13; Length 107;
Best Local Similarity 77.4% Pred No 2.93e-36;
Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;

Db 1 ELTQSPCTLSLSPGERATLSGRASQSLNNYLAWYQKPGQAPPLLIYGSSSTPGTGIDPP 60
QY 2 ELTQSPATLSVSGEPASLSQASQSVGNNAWYQKPGQAPPLLIYGNTATGTPDR 60
Db 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGGKLEIK 106
QY 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGGKLEIK 106

RESULT 4
ID PCT-US95-08743-86 STANDARD: PPT: 108 AA
XX AC xxxxxx
XX DT 01-JAN-1900
```

[W][O][R][D] (TM)

Release 2 1d John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:50:48 1998: MasPar time 2.95 Seconds
Tabular output not generated.
183.108 Million cell updates/sec

Title: >US-08-844-215-11
Description: (1-106) from US08844215.pep
Perfect Score: 746
Sequence: 1 AELTQSPATLSVSPGPRSL COHYSTWPLTRGGTKVEFK 106

Scoring table: PAM 150
GAP 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1-back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
10-PCR92 11-PCR93 12-PCR94 13-PCR95 14-PCR96

Statistics: Mean 27.204: Variance 140.039: scale 0.183
pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

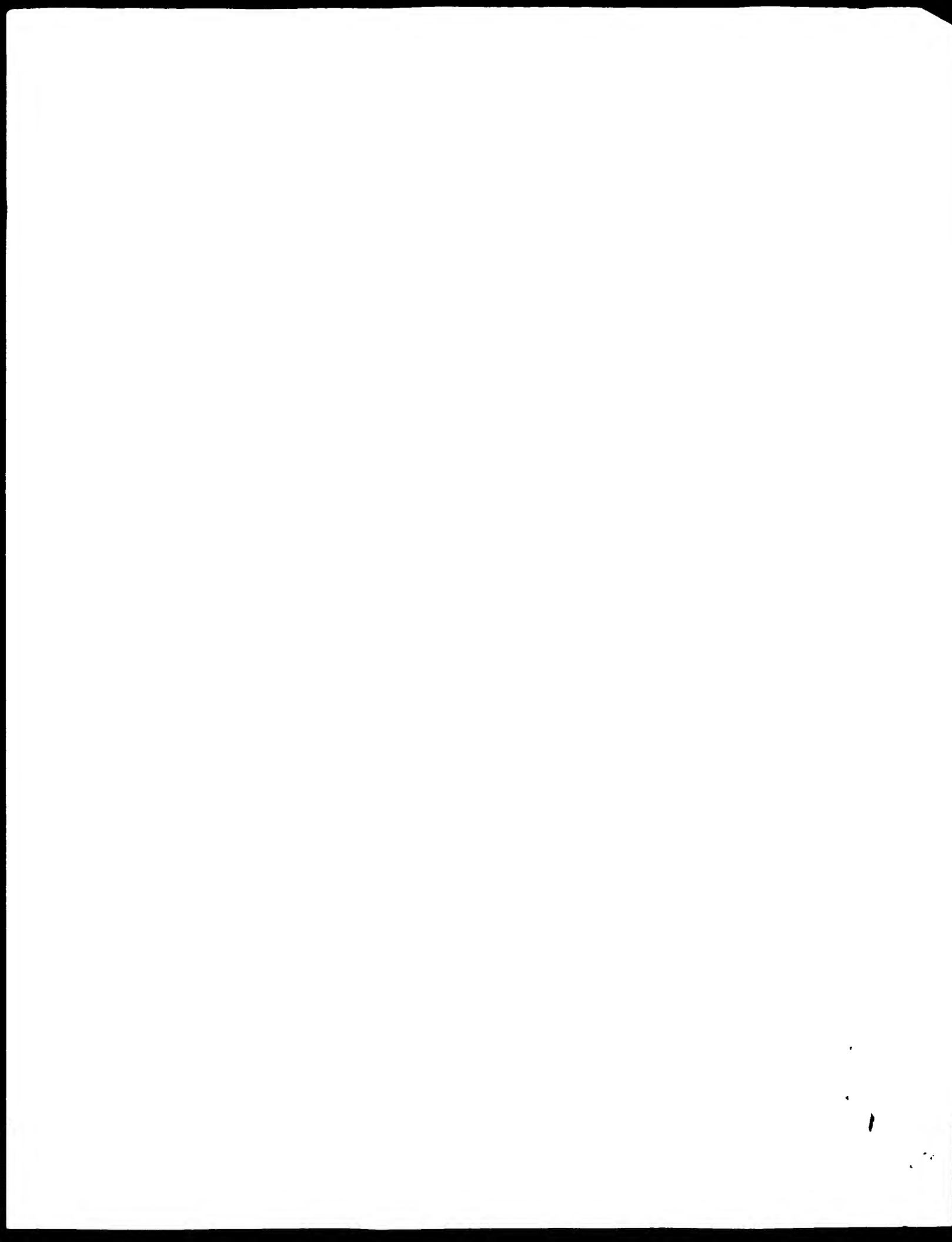
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3	593	79.5	107 13	PCT-US95-0	Sequence 90, Applicati	2 93e-36
4	593	79.5	108 13	PCT-US95-0	Sequence 86, Applicati	2 93e-36
5	593	79.5	108 7	US-08-276-	Sequence 86, Applicati	2 93e-36
6	591	79.2	108 7	US-08-276-	Sequence 99, Applicati	4 17e-36
7	591	79.2	108 13	PCT-US95-0	Sequence 99, Applicati	4 17e-36
8	590	79.1	107 13	PCT-US95-0	Sequence 87, Applicati	4 97e-36
9	590	79.1	107 7	US-08-276-	Sequence 87, Applicati	4 97e-36
10	586	78.6	109 11	PCT-US93-0	Sequence 23, Applicati	1 00e-35
11	584	78.3	108 6	US-08-477-	Sequence 86, Applicati	1 43e-35
12	584	78.3	108 7	US-07-634-	Sequence 86, Applicati	1 43e-35
13	584	78.3	108 7	US-08-474-	Sequence 86, Applicati	1 43e-35
14	584	78.3	108 7	US-08-487-	Sequence 86, Applicati	1 43e-35
15	581	77.9	111 13	PCT-US95-0	Sequence 149, Applicati	2 42e-35
16	581	77.9	111 7	US-08-276-	Sequence 149, Applicati	2 42e-35
17	580	77.7	109 7	US-08-276-	Sequence 147, Applicati	2 88e-35
18	580	77.7	109 13	PCT-US95-0	Sequence 147, Applicati	2 88e-35
19	572	76.7	104 7	US-08-276-	Sequence 100, Applicati	1 18e-34
20	572	76.7	104 13	PCT-US95-0	Sequence 100, Applicati	1 18e-34
21	572	76.7	112 7	US-08-276-	Sequence 151, Applicati	1 18e-34
22	572	76.7	112 13	PCT-US95-0	Sequence 151, Applicati	1 18e-34

23	570	76.4	107 7	US-08-487-	Sequence 63, Applicati	1 67e-34
24	570	76.4	107 7	US-08-487-	Sequence 87, Applicati	1 67e-34
25	570	76.4	107 6	US-08-477-	Sequence 87, Applicati	1 67e-34
26	570	76.4	107 6	US-08-477-	Sequence 63, Applicati	1 67e-34
27	570	76.4	107 7	US-08-474-	Sequence 63, Applicati	1 67e-34
28	570	76.4	107 7	US-08-474-	Sequence 87, Applicati	1 67e-34
29	570	76.4	107 6	US-07-634-	Sequence 87, Applicati	1 67e-34
30	570	76.4	107 6	US-07-634-	Sequence 53, Applicati	1 67e-34
31	563	75.5	108 13	PCT-US95-0	Sequence 88, Applicati	5 71e-34
32	563	75.5	108 7	US-08-276-	Sequence 88, Applicati	5 71e-34
33	551	73.9	108 7	US-08-276-	Sequence 110, Applicati	4 69e-33
34	551	73.9	108 13	PCT-US95-0	Sequence 110, Applicati	4 69e-33
35	549	73.6	115 7	US-08-053-	Sequence 179, Applicati	6 66e-33
36	547	73.3	108 13	PCT-US95-0	Sequence 96, Applicati	4 46e-33
37	547	73.3	108 7	US-08-276-	Sequence 96, Applicati	4 46e-33
38	546	73.2	107 7	US-08-474-	Sequence 34, Applicati	1 13e-32
39	546	73.2	107 7	US-08-487-	Sequence 34, Applicati	1 13e-32
40	546	73.2	107 6	US-08-477-	Sequence 34, Applicati	1 13e-32
41	546	73.2	107 6	US-07-634-	Sequence 34, Applicati	1 13e-32
42	545	73.1	116 7	US-08-053-	Sequence 183, Applicati	1 13e-32
43	544	72.9	105 7	US-08-276-	Sequence 93, Applicati	1 60e-32
44	544	72.9	105 13	PCT-US95-0	Sequence 93, Applicati	1 60e-32
45	543	72.8	107 13	PCT-US95-0	Sequence 118, Applicati	1 91e-32

ALIGNMENTS

RESULT 1
ID PCT-US93-08786-24 STANDARD: PPT: 100 AA
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 24, Application PC/TUS9308786.
XX
CC Sequence 24, Application PC/TUS9308786
CC GENERAL INFORMATION.
CC APPLICANT: Burton, Dennis P
CC APPLICANT: Barbas, III, Carlos F.
CC APPLICANT: Hancock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr, James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: IO RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1800 Century Park East, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM: disk
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA: PCT/US93/08786
CC APPLICATION NUMBER: PCT/US93/08786
CC FILING DATE: 16-SEP-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wetherell, Jr, Ph D, John P.
CC REGISTRATION NUMBER: 31,678
CC REFERENCE/DOCKET NUMBER: PD-2791
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid



DP HSP: P01607: 1DPR
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11630 MW: 8330044 CRC32:

 Query Match 75.2%, Score 561; DB 5; Length 109;
 Best Local Similarity 73.3%; Pred. No. 1.46e-104;
 Matches 77; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

 Db 4 ltqspatlsqgeratlsrcaallssrgylawyyqkqgqaprllymgyassratgipdrf 63
 QY 3 LTQSPATLSVSGERASLCRASQ-SVGNLAWYQKQPGQAPRLLYGGNTPATGTPDRF 61

 Db 64 gsgsdtdfllisrlepedfavyycqygsprsfqggtkveik 108
 QY 62 SGSGSGTEFTLISSLSQSEDFAVYFCQHYSTWPLTFGGTKVEEK 106

 RESULT 10
 ID KV31_HUMAN STANDARD: PRT: 129 AA.
 AC P06311:
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 EC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 PA KLOBECK H.G., MEINDL A., COMBIATO G., SOLOMON A., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: Z00021; G33179; -;
 DP PIR: A01899; K3H041.
 DR HSP: P01607; 3HEM
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41)
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 128 JKL SEGMENT.
 FT DISULFID 43 128
 FT NON_TER 129 128 BY SIMILARITY.
 SQ SEQUENCE 128 AA: 14070 MW: 318004F CRC32:

 Query Match 75.1%; Score 560; DB 5; Length 128;
 Best Local Similarity 74.0%; Pred. No. 2.57e-104;
 Matches 77; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

 Db 24 ltqspatlsqgeratlsrcaallssrgylawyyqkqgqaprllymgyassratgipdrfs 83
 QY 3 LTQSPATLSVSGERASLCRASQ-SVGNLAWYQKQPGQAPRLLYGGNTPATGTPDRFS 62

 Db 84 gsgsdtdfllisrlepedfavyycqygsprsfqggtkveik 127
 QY 63 SGSGSGTEFTLISSLSQSEDFAVYFCQHYSTWPLTFGGTKVEEK 106

 RESULT 11
 ID KV31_HUMAN STANDARD: PRT: 115 AA.
 AC P04433:
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT)
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 PA KLOBECK H.G., MEINDL A., COMBIATO G., SOLOMON A., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: Z00021; G33179; -;
 DP PIR: A01899; K3H041.
 DR HSP: P01607; 3HEM
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41)
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 128 JKL SEGMENT.
 FT DISULFID 43 128
 FT NON_TER 129 128 BY SIMILARITY.
 SQ SEQUENCE 128 AA: 14070 MW: 318004F CRC32:

 Query Match 75.1%; Score 560; DB 5; Length 128;
 Best Local Similarity 74.0%; Pred. No. 2.57e-104;
 Matches 77; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

 Db 24 ltqspatlsqgeratlsrcaallssrgylawyyqkqgqaprllymgyassratgipdrfs 83
 QY 3 LTQSPATLSVSGERASLCRASQ-SVGNLAWYQKQPGQAPRLLYGGNTPATGTPDRFS 62

 Db 84 gsgsdtdfllisrlepedfavyycqygsprsfqggtkveik 127
 QY 63 SGSGSGTEFTLISSLSQSEDFAVYFCQHYSTWPLTFGGTKVEEK 106

 RESULT 12
 ID KV31_HUMAN STANDARD: PRT: 108 AA.
 AC P01605:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (LAY).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 EC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 77038198
 PA CAPRA J.D., KLAPPER D.G.;
 PL SCAND. J. IMMUNOL. 5:677-684(1976).
 CC - THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
 CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
 CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC - THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR: A01871; K1HULY.
 DR HSP: P01607; 2FGW
 KW IMMUNOGLOBULIN V REGION.
 FT SIGNAL 1 23
 FT DOMAIN 24 34 FRAMEWORK 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA: 11834 MW: 222840C CRC32:

 Query Match 73.2%; Score 546; DB 5; Length 108;
 Best Local Similarity 65.7%; Pred. No. 5.56e-101;
 Matches 69; Conservative 21; Mismatches 15; Indels 0; Gaps 1;

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85087932.
 PA PECH M., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 12:9229-9236(1984).
 DR EMBL: X01668; -; NOT_ANNOTATED_CDS.
 DP PIR: A01400; K3HUVG.
 DR HSP: P01607; 1AAG.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (VG).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA: 12575 MW: 37E182FC CRC32:

 Query Match 73.6%; Score 549; DB 5; Length 115;
 Best Local Similarity 80.4%; Pred. No. 1.07e-101;
 Matches 74; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

 Db 24 ltqspatlsqgeratlsrcaallssrgylawyyqkqgqaprllymgyassratgipdrfs 83
 QY 3 LTQSPATLSVSGERASLCRASQ-SVGNLAWYQKQPGQAPRLLYGGNTPATGTPDRFS 62

 Db 84 gsgsdtdfllisrlepedfavyycqgqrsnwp 115
 QY 63 GSGSGTEFTLISSLSQSEDFAVYFCQHYSTWP 94

 RESULT 12
 ID KV31_HUMAN STANDARD: PRT: 108 AA.
 AC P01605:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (LAY).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 EC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 77038198
 PA CAPRA J.D., KLAPPER D.G.;
 PL SCAND. J. IMMUNOL. 5:677-684(1976).
 CC - THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
 CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
 CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC - THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR: A01871; K1HULY.
 DR HSP: P01607; 2FGW
 KW IMMUNOGLOBULIN V REGION.
 FT SIGNAL 1 23
 FT DOMAIN 24 34 FRAMEWORK 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA: 11834 MW: 222840C CRC32:

 Query Match 73.2%; Score 546; DB 5; Length 108;
 Best Local Similarity 65.7%; Pred. No. 5.56e-101;
 Matches 69; Conservative 21; Mismatches 15; Indels 0; Gaps 1;


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RESULT 2
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01624:
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RA KLAPPER D G, CAPRA J D:
RL ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01897; K3HUPM.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: A0C42C88 CRC32:

Query Match 82.0%; Score 612; DB 5; Length 109;
Best Local Similarity 79.0%; Pred. No. 9 44e-117;
Matches 83; Conservative 14; Mismatches 7; Indels 1; Gaps 1;

Db 4 mtqspgtlslspgeratlscrasqsvsnslawyqkpgqaprllygastatgiparf 63
QY 3 LTQSPATLSVSPGERASLSCRASQSVGN-LAWYQKPGQAPRLLYGNTATGTPDRF 61

Db 64 sgsqsgtftltisslgsedfavyqgqygnnwptfqqgtvveik 108
QY 62 SSGSGSTFTLTSSLOSDEFAVYFQCHYSTWPLTFGGGKVEFK 106

RESULT 3
ID KV3D_HUMAN STANDARD: PRT: 129 AA.
AC P18135:
DT 01-NOV-1990 (REL 16, CREATED)
DT 01-NOV-1990 (REL 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAH)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N/A
RX MEDLINE: 88171307
RA KIPPS T J, TOMHAVE E, CHEN P P, CAPSON D A:
RL J. EXP. MED. 167:840-852(1988)
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA
DR PIR: P10022; K3HUHA.
DR HSSP: P01607; 1AAG
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAH).
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 2C44B85E CRC32:

Query Match 80.8%; Score 603; DB 5; Length 129;
Best Local Similarity 79.0%; Pred. No. 1 36e-114;
Matches 83; Conservative 16; Mismatches 5; Indels 1; Gaps 1;

Db 4 mtqspgtlslspgeratlscrasqsvsnslawyqkpgqaprllygastatgiparf 63
QY 3 LTQSPATLSVSPGERASLSCRASQSVGN-LAWYQKPGQAPRLLYGNTATGTPDRF 61

Db 64 sgsqsgtftltisslgsedfavyqgqygnnwptfqqgtvveik 108
QY 62 SSGSGSTFTLTSSLOSDEFAVYFQCHYSTWPLTFGGGKVEFK 106

RESULT 4
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01620:
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D W, CAPRA J D:
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUSI.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 00B5DD5D CRC32:

Query Match 80.7%; Score 602; DB 5; Length 109;
Best Local Similarity 77.1%; Pred. No. 2 36e-114;
Matches 81; Conservative 18; Mismatches 5; Indels 1; Gaps 1;

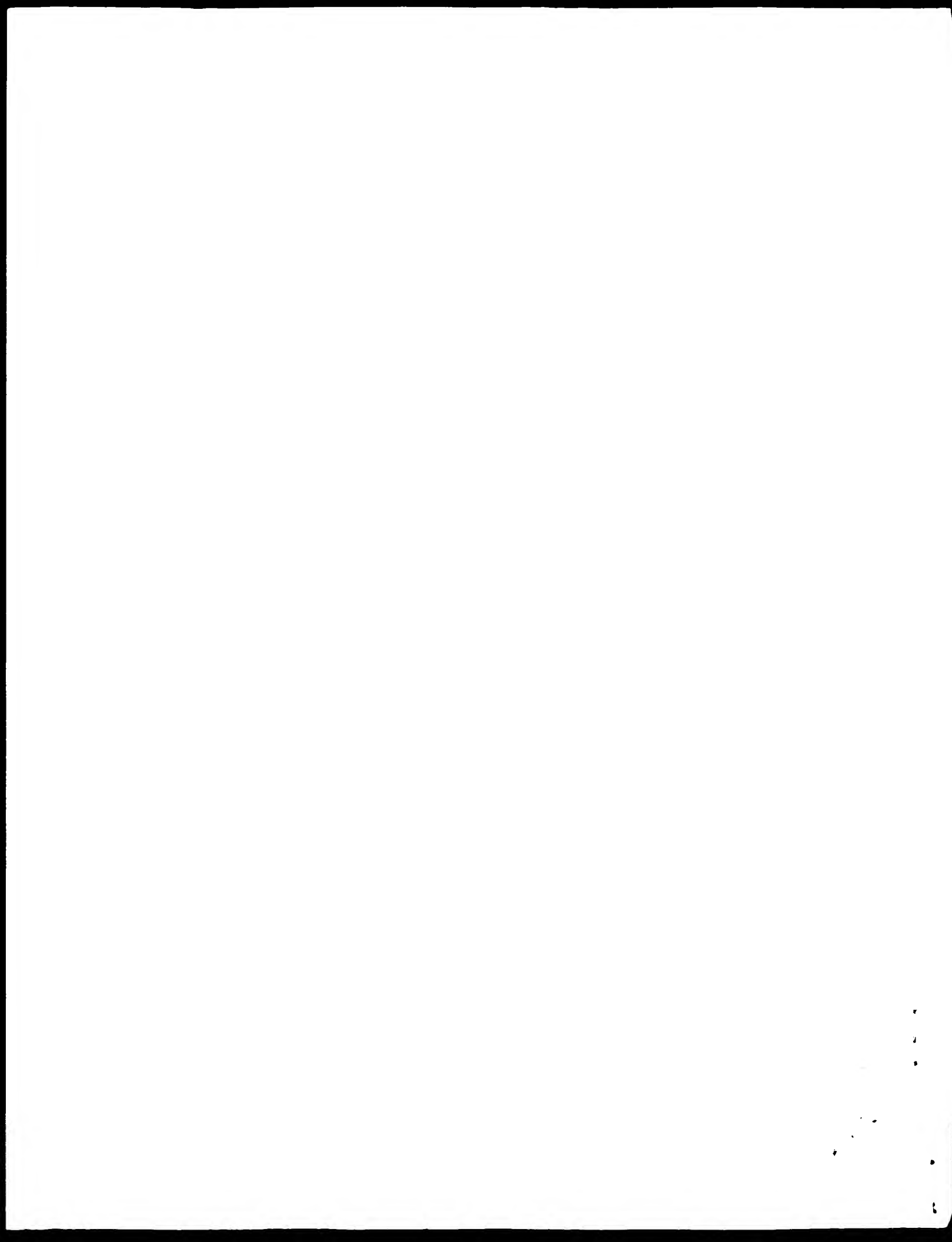
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QY 3 LTQSPATLSVSPGERASLSCRASQSVGN-LAWYQKPGQAPRLLYGNTATGTPDRF 61

Db 64 sgsqsgtftltisrlpddfavyqgqygnnwptfqqgskveik 108
QY 62 SSGSGSTFTLTSSLOSDEFAVYFQCHYSTWPLTFGGGKVEFK 106

RESULT 5
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01622:
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (T1).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 72188439.
RA SUTEP L, BARNIKOL H U, WATANABE S, HILSCHMANN N:
PL HOPPE-SEYLER S Z. PHYSIOL. CHEM. 353:189-208(1972).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HUTI.
DR HSSP: P01607; 2IMM.
KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: D03795B1 CRC32:

Query Match 79.6%; Score 594; DB 5; Length 109;
Best Local Similarity 78.1%; Pred. No. 1 94e-112;

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ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:89215279
#accession A30608
#status preliminary
#molecule_type protein
#residues 1-109 #label CON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6031

Query Match 81.6% Score 609; DB 7; Length 109;
Best Local Similarity 78.1% Pred. No. 1.38e-59;
Matches 82; Conservative 18; Mismatches 4; Indels 1; Gaps 1;

Db 4 ltspqtlslspgeratlsccrasgsvssylawyqkpgqaprlliygassratgipnrf 63
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Qy 3 LTQSPATLSVSPGERASLSCRASQSGNN-LAWYQKPGQAPRLIIYGGNTRATGTPDRF 61
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Db 64 sgsgsgtdftltisrlepedfavyycqyqyasspytfggqtkveik 108
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Qy 62 SGSGSGIEFTLTIISSQSEDFAVYFCQHYSTWPLTFGGGKVEFK 106
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RESULT 15
ENTRY B26555 #type complete
TITLE Ig kappa chain V-III region (Ger) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 16-Aug-1996
ACCESSIONS B26555
REFERENCE A92630
#authors Muddaugh, C.R.; Litman, G.W.
#journal J. Biol. Chem. (1987) 262:3671-3673
#title Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
#cross-references MUID:87137666
#accession B26555
#molecule_type protein
#residues 1-116 #label MID
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 116 #molecular-weight 12424 #checksum 5108

Query Match 81.2% Score 606; DB 7; Length 116;
Best Local Similarity 79.0% Pred. No. 3.29e-59;
Matches 83; Conservative 14; Mismatches 7; Indels 1; Gaps 1;

Db 4 mtqvpatlsvspgqatlsccrasgsvssylawyqkpgqaprlliyaastratgiparifs 63
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Qy 3 LTQSPATLSVSPGERASLSCRASQSGNN-LAWYQKPGQAPRLIIYGGNTRATGTPDRFS 62
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Db 64 sgsgsgtdftltisrlepedfavyycqyqyasspytfggqtkveik 108
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Qy 63 SGSGSGIEFTLTIISSQSEDFAVYFCQHYSTWPLTFGGGKVEFK 106
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Search completed: Tue Feb 24 07:23:57 1998
Job time : 36 secs.



Tue Feb 26 07:05:10 1998

US-08-844-215-22.rstb

Page 9

Query Match 7.08; Score 27; DB 37; Length 326;
Best Local Similarity 80.58; Pred. No. 9.46e-13;
Matches 33; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 77 ttgatatgagccaggaatccggtcaccgttctc 117
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QY 343 TTCAGGAGTGGGCTACGGTACCTTCATCTCTCTC 383

Search completed: Tue Feb 24 09:45:55 1998
Job time : 150 secs.

0: 50

997

to

ridae;

e, J. D.,

ne, L.D.,
N.S.,

Jr.,
K, J. M.,

ing, S.M.,
y, R.,

E. J.

sen H

ids, C.

patterns

an Gene

Site_1:

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL MEDLINE
Nature 377 (6547 Suppl), 3-174 (1995)

COMMENT
Other ESTs: THC166571
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse
Location/Qualifiers
1 279
/organism="Homo sapiens"
/note="Organ: testis; Vector: pBluescript SK-; Site: 1;
ECORI: Site: 2; XhoI:"
/clone_1lb="Testis tumor"
/sex="male"
/dev_stage="adult"
<1...>279
63 a 74 c 85 g 56 t 1 others

BASE COUNT
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Best Local Similarity 82.7%; Fred. No. 2.72e-186;
Matches 148; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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1 279
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/note="Organ: testis; Vector: pBluescript SK-; Site: 1;
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/clone_1lb="Testis tumor"
/sex="male"
/dev_stage="adult"
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63 a 74 c 85 g 56 t 1 others

LOCUS 2 AA377074 291 bp mRNA EST 21-APR-1997
DEFINITION EST89603 Small intestine I Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, VDJ regions (CB:214165).
ACCESSION AA377074
NID 92029413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Adams M.D., Kerlavage A.P., Fleischmann P.D., Fujimori P.A., Bult C.J., Lee N.H., Kirkness F.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon P.C., Man-Wai C., Clayton R.A., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D.,

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL MEDLINE
Nature 377 (6547 Suppl), 3-174 (1995)

COMMENT
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse
Location/Qualifiers
1 291
/organism="Homo sapiens"
/note="Organ: small intestine; Vector: pBluescript SK-;
Site: 1; EcorI: Site: 2; XhoI:"
/clone_1lb="Small intestine I"
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/dev_stage="adult"
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DEFINITION EST89660 Small intestine I Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, VDJ region.
ACCESSION AA377128
NID 92029456
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Adams M.D., Kerlavage A.P., Fleischmann P.D., Fujimori P.A., Bult C.J., Lee N.H., Kirkness F.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon P.C., Man-Wai C., Clayton R.A., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D.,

OS Homo sapiens (human)
 OC Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
 OC Vertebrata: Eutheria: Primates: Catarrhini: Homidae: Homo.
 RN [1]
 RP 1-292
 RA NCI-CGAP:
 RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 RT Tumor Gene Index";
 RL Unpublished.
 CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
 CC Robert_Strausberg@nih.gov This clone is available royalty-free
 CC through LHM; contact the IMAGE Consortium (info@image.lln.gov)
 CC for further information. Trace considered overall poor quality
 CC Possible reversed clone; similarity on wrong strand Seq primer:
 CC -28m13 rev2 ET from Amersham High quality sequence stop: 1.
 FH Key Location/Qualifiers
 FT source
 FT 1..292
 FT /organism="Homo sapiens"
 FT /note="Vector: p773D-Pac (Pharmacia) with a modified
 FT polylinker. Site_1: Not I, Site_2: Eco RI, 1st strand cDNA
 FT was prepared from human tonsillar cells enriched for
 FT germinal center B cells by flow sorting (CD20+, IgD-),
 FT provided by Dr. Louis M. Staudt (NCI). Dr. David Allman
 FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 FT primed with a Not I - oligo(dT) primer
 FT [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCAATTTTCTTTT-
 FT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (
 FT Pharmacia), digested with Not I and cloned into the Not I
 FT and Eco RI sites of the modified p773 vector. Library was
 FT through one round of normalization, and was constructed by
 FT Bento Soares and M. Fatima Bonaldo."
 FT /clone="685101"
 FT /clone_lib="NCI-CGAP_GCB1"
 FT /tissue_type="germinal center B cell"
 FT /lab_host="DH10B"
 FT <1..>292
 FT mRNA
 SQ Sequence 292 BP; 88 A; 76 C; 63 G; 65 T; 0 other;

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 Best Local Similarity 85.78; Prid. No. 2.18e-03;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 112 agaccctccacctaattgcagtctgt 139
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 QY 297 AGACCTCTCCACATATTGCAGTCTGT 324

Search completed: Tue Feb 24 09:48:51 1998
 Job time : 153 secs.

Ph	Key	Location/Qualifiers
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Ph		/note="Organ: ovary; Vector: p7173D (Pharmacia)
Ph		/note="Organ: ovary; Vector: p7173D (Pharmacia)
Ph		/modified polymer: Site_1: Not I; Site_2: Eco RI; 1st
Ph		strand cDNA was primed with a Not I - oligo(d) primer [5'
Ph		TGTTACCAATCTGAACTGGAGCGCCCGCTTTTCTTTTCTTTT 3'] ,
Ph		double-stranded cDNAs size selected, ligated to Eco RI
Ph		adapters (Pharmacia) , digested with Not I and cloned into
Ph		the Not I and Eco RI sites of a modified p7173 vector
Ph		(Pharmacia). Library constructed by Bento Soares and
Ph		M.Patma Ronaldo."
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Ph		/sex="Female"
Ph		/tissue.type="ovarian tumor"
Ph		/lab.host="DH10 (ampicillin resistant)"
Ph		<1..>266
Ph	mrna	
Ph	Sequence	266 bp; 54 A; 90 C; 70 G; 52 T; 0 other;

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Best Local Similarity 78.3%  Ped. No. 1,64e-44.
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Db      22  taaccagagaagaattccagaggaacgaatccctatgacggagaaacgctccacgaacactc 81
      |||||
Oy      181  TAGCGTACGAATAATCCGCGACACAGATCTCGATTTATCCGCGACCAATCCACGACGACGCG 240

Db      82  taacatgaagcgtgacgacgctctgaatctcgaagaacacgagcctcttatatcgtgcgaagaac 141
      |||||
Oy      241  TTCTATTGAGCTGACCACTTGATGATCTGTACACACAGCGGCGCTCTACTACTGTTGCGAGAAC 300

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RESULT	2	
LOCUS	AA505044	238 bp mRNA EST 02-JUL-1997
DEFINITION	aa63a01..1 NC1:CGAP:GCBI Homo sapiens cDNA clone 825648.5', similar to SW-HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;	
ACCESSION	AA505044	
NID	92241204	
KEYWORDS	EST	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryote; mitochondrial eukaryotes; Metazoa, Chordata, Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
REFERENCE	1 (bases 1 to 238)	
AUTHORS	NCI-CCAP	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT		

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbfp/image/image.html

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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -26m13 rev1 ET from Amer sham
High quality sequence stop: 1
    * Location/Qualifiers
FEATURES
    Source          1..238

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/organism="Homo sapiens"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
```

polymerase site_1: Not I; site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20⁺, IgD⁻), provided by Dr. Louis M. Staudt (NCI). cDNA synthesis was (NCI) and Dr. Gerald Martin (CBER). cDNA synthesis was primed with a Not I - oligo(dt) primer
15'-GTATCATTCAGTACGTTGGAGCGGCTGCTCATTTTTTTTTTT-3'. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRIT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Honalido.
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/lab_host="DH10B"
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57 a 69 c 66 g 46 t

[illegible]

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RESULT
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NI      G2241204
DT      04-JUL-1997 (rel 52, Created)
DT      04-JUL-1997 (rel 52, Last updated, Version 1)
DE      aa63801.r1 NCI-CGAP GCBI Homo sapiens cDNA clone 825648 5' similar
DE      to SW-HV05_MOUSE P01749. IS HEAVY CHAIN PEPCKP58R V REGION.
KW      EST
OS      Homo sapiens (human)
OC      Eukaryota, mitochondrial eukaryotes, Metazoa, Chordata:
OC      Vertebrata: Mammalia, Eutheria, Primates: Catarrhini: Homidae:
OC      Homo.
RN      [1]
RP      1-238
RA      NCI-CGAP;
RT      "National Cancer Institute, Cancer Genome Anatomy Project (CGAP)",
RT      "Tumor Gene Index",
RL      Unpublished.

```

CC Contact: Robert Strauszberg, Ph.D. Tel: (301) 466-1550 Email:
CC Robert.Strauszberg@nih.gov Tissue Procurement: Louis M. Staudt,
CC M.D., Ph.D. David Allman, Ph.D. Gerald Matli, M.D. cDNA library
CC Preparation: M. Benito Soares, Ph.D., M. Fatima Bonald, Ph.D. cDNA
CC Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by:
CC Washington University Genome Sequencing Center Clone distribution:
CC NIH-OSAP clone distribution information can be found through the
CC I M A G E Consortium at:
CC www.bio.ihl.gov/bhpf/image/image.htm Trace considered overall
CC poor quality possible reversed clone; similarity on wrong strand
CC Seq primer: -28m3 rev1 Et from Amer sham High quality sequence
CC stop: 1.

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EH
ET source 1..238
ET /organism="Homo sapiens"
ET /note="Vector: pT73-Pac (Pharmacia) with a modified
ET polylinker. Site_1: Not I; Site_2: Eco RI. 1st strand cDNA
ET was prepared from human tonsillar cells enriched for
```

FT germinal center B cells by flow sorting (CD20⁺, IgM⁺),
FT provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

Fitzpatrick, J. L., Fitzpatrick, W. M., Fitzchum, J., Gochaguen, N. S. M., Glodde, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, Jr, P. S., Kelley, J. M., Klimke, K. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M., Moreno-Palacios, P. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. W., Phillips, G. A., Pyder, S. E., Scott, J. L., Saudke, D. M., Shitley, R., Small, K. V., Spilgus, T. A., Utterback, T. R., Weidman, J. F., Li, Y., Rednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Nimke, D., Peng, P., Pette, A., Fischer, C., Hastings, G. A., He, W.-W., Hu, J. S., Greene, J. M., Gruber, C., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Ji, H., Li, H., Weissner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wang, J., Xu, C., Yu, G.-L., Ruben, S. M., Dillon, P. J., Fannon, R. S., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)



CC SOFTWARE: Patent Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053.131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEO ID NO: 61:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 813 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 241..285
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CC NAME/KEY: CDS
CC LOCATION: 373..678
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Query Match 41.7% Score 160; DB 7; Length 813;
Best Local Similarity 86.7% Pred. No. 1,93e-103;
Matches 260; Conservative 0; Mismatches 28; Indels 12; Gaps 4;
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DB 514 GGGCTTGAATGATGGGAAGATCATCCTATCCTTGT-----A-TA-GC---AAAC 561
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AC xxxxxx
DT 01-JAN-1900
DE Sequence 3, Application US/08217918.
CC Sequence 3, Application US/08217918.
CC Patent No. 5506132
CC GENERAL INFORMATION:
CC APPLICANT: LAKE, PHILIP
CC APPLICANT: OSTBERG, LARS
CC TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
CC TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS

CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/217,918
CC FILING DATE: 24-MAR-1994
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEO ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 441 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FEATURE:
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CC LOCATION: 1..441
CC SEQUENCE 441 BP: 89 A; 125 C; 135 G; 92 T; 0 other:
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Best Local Similarity 84.1% Pred. No. 1,32e-88;
Matches 248; Conservative 0; Mismatches 35; Indels 12; Gaps 4;
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66 TGAAGGACACTTCAGCAAGTTTTCATACATCAGTGGTGGTGGTGGTGGTGGTGGTGGT 125
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AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PCT/US9511235.
CC Sequence 1, Application PCT/US9511235.
CC GENERAL INFORMATION:
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGENIC PEPTIDE CHAINS

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
Sequence 2287 BP: 483 A, 752 C, 654 G, 398 T; 0 other.

Query Match 53.6%; Score 206; DB 14; Length 2287;
Best Local Similarity 84.6%; Pred No 115e-139;
Matches 325; Conservative 0; Mismatches 47; Indels 12; Gaps 4;

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RESULT 2
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AC xxxxxx
DT 01-JAN-1900
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CC Sequence 53, Application US/07834539A
CC Patent No. 5633425
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 77
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/834,539A
CC FILING DATE: 19920205
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 1443-5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Exon
LOCATION: 241..335
OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
FEATURE:
NAME/KEY: Exon
LOCATION: 372..677
OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
SO Sequence 812 BP: 204 A, 198 C, 223 G, 197 T; 0 other;

Query Match 41.7%; Score 160; DB 7; Length 812;
Best Local Similarity 86.7%; Pred No: 1.93e-103;
Matches 260; Conservative 0; Mismatches 28; Indels 12; Gaps 4;

DB 393 CTGGTGGACCTGCGGGCTGAGGTGAGAGAGCGCTGGGCTCTCTGGTGAAGGTCTCTGGAG 452
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RESULT 3
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AC xxxxxx
DT 01-JAN-1900
DE Sequence 53, Application PC/TUS9206185.
CC Sequence 53, Application PC/TUS9206185
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 75
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/06185
CC FILING DATE: 19910828
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.

DR WP1: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 immunodeficiency virus - used for diagnosis and immuno-therapy of
 HIV-induced disease
 PS Example 2, Page 193-197: 249pp. English.
 CC This sequence represents the expression vector, pPho-TT which is a
 modified version of the phagemid expression vector, pComb3 given in
 CC 092546. pPho-TT provides for the expression of soluble Fabs which are
 CC secreted into the periplasmic space which is regulated from the alkaline
 CC phosphatase (phoA) promoter. This plasmid was used within the scope of
 CC the invention to express various mutagenised human Fabs which comprise
 CC heavy and light variable regions which bind to HIV gp120. pPho-TT
 CC consists of a DNA molecule having two cassettes to express two soluble
 CC proteins a heavy chain and a light chain. The vector comprises:
 CC operatively linked 5' to 3', a first cassette consisting of the phoA
 CC promoter/operator sequences, an EcoRI restriction site, a ribosome
 CC binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer
 CC region, a cloning region bordered by 5' sacI and 3' XbaI restriction
 CC sites, an NcoI restriction site between the two cassettes, and a second
 CC cassette consisting of an expression control RBS, a PstI leader, a human
 CC consensus amino terminus spacer region comprising the sequence EVQDLE,
 CC a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
 CC followed by a SfiI site, expression control stop sequences and a NotI
 CC restriction site. The pPho-TT expression vector contains a light
 CC chain stuffer that is 1200 bp in length and a heavy chain stuffer that
 CC is 300 bp in length. The nucleotide sequences of the heavy and light
 CC chain stuffers encode the heavy and light chain variable domains of a
 CC tetanus toxin-specific Fab.
 CC Sequence 6166 BP: 1416 A: 1706 C: 1629 G: 1415 T:
 SO
 Query Match 35.98; Score 138; DB 16; Length 6166;
 Best Local Similarity 83.28; Pred. No. 1,06e-77;
 Matches 248; Conservative 0; Mismatches 38; Indels 12; Gaps 9;
 Db 5354 ctgcagagcctcgggagcgtgagtgaaagacccctggctcctggtagaggtcctcgcag 5413
 QY 1 ctgcagagcctcgggagcgtgagtgaaagacccctggctcctggtagaggtcctcgcag 60
 Db 5414 gctctgagagcagcctcagcaatctgcatcagctggtgagcagagcccttgacaa 5473
 QY 61 gctctgagagcagcctcagcaatctgcatcagctggtgagcagagcccttgacaa 120
 Db 5474 gggcttgagtgagtgagag-g-g-alc-t-tccct-ttccgttaa-tacag-caag- 5521
 QY 121 ggacttgactgactgactgactgactgactgactgactgactgactgactgactgactg 180
 Db 5522 tacgcaaacactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5581
 QY 181 tacgcttcgcaaacactcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
 Db 5582 tacatgagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5639
 QY 241 ttatttgccttcgcaaacactcagcagcagcagcagcagcagcagcagcagcagcagc 298
 RESULT 15
 ID 089329 standard: DNA: 294 BP.
 AC 089329;
 DT 26-SEP-1995 (first entry)
 DE OF7H1.2 VH-1 H chain gene.
 KW Graves ophthalmopathy associated immunoglobulin protein;
 KW orbital antigen; monoclonal antibody; heavy chain; H chain;
 KW variable region; autoimmunity; ss.
 OS Homo sapiens.
 PN MO9508336-A.
 PD 30-MAR-1995.
 PF 22-SEP-1994: U10756.
 PR 22-SEP-1993: U5-124469.
 PA (NICH-) NICHOLS INST DIAGNOSTICS.
 PI McLaughlan SM. Rapoport B.
 DR WP1: 95-139383/18.
 DR *PDB: R72070.
 PI Graves' ophthalmopathy-associated monoclonal antibody - produced

PT By molecular cloning of immunoglobulin genes by PCR
 PS Claim 25; Page 68; 94pp. English.
 CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained 13/15 clones of H chain (VH) genes
 CC showed homology to the closest germline genes, DP10 (Q89327) and
 CC hV1263 (Q8428). The LNA (Q8425) and corresp. amino acid
 CC (R72070) sequences of the VH region of a representative clone.
 CC OF7H1.2, are provided.
 CC Sequence 294 BP: 72 A: 68 C: 91 G: 63 T:
 SO
 Query Match 34.48; Score 132; DB 14; Length 294;
 Best Local Similarity 88.48; Pred. No. 1.89e-73;
 Matches 152; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Db 17 agtcggggagcgtgagtgagagacccctggctcctggtagaggtcctcgcag 76
 QY 8 agtcggggagcgtgagtgagagacccctggctcctggtagaggtcctcgcag 67
 Db 77 gaagcagccttcgaatacgtatgctatcctcctgggagcagcagcagcagcagcagc 146
 QY 68 gaagcagccttcgaatacgtatgctatcctcctgggagcagcagcagcagcagcagc 127
 Db 137 agtcggagtgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 188
 QY 128 agtcgagtgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 179
 Search completed: Tue Feb 24 09:38:31 1998
 Job time : 71 secs.

PD 14-MAR-1996.
 PF 01-SEP-1995: 011235.
 PR 02-SEP-1994: US-30038b.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-171625/17
 PT Oligonucleotide(s) for inducing mutagenesis in an Ig light chain
 PT gene CDR - useful for prodn. of Ig heavy and light chain
 PT combinatorial antibody libraries
 PS Example 1: Page 83; 125pp; English.
 CC 15262 and 15203 are the heavy and light chain variable domains of
 CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a pComb3
 CC based expression vector. The heavy and light chain variable domains
 CC are used in an example to demonstrate the prodn. of antibodies for
 CC an antibody library using mutagenic primers. Mutagenic primers of the
 CC invention have sequences at their 3' and 5' ends both capable of
 CC binding different framework regions linked by a sequence 6 to 50
 CC nucleotides long. Different immunoglobulins produced using the
 CC primers may be used to produce antibody libraries having diverse and
 CC novel immunospecificities and affinities. By using mutagenic ONS an
 CC extremely large population of different randomised binding sites can
 CC be created and use of the universal light chain increases the number
 CC of combinations which yield functional heterodimeric antibodies.
 SQ Sequence 687 BP; 155 A, 211 C, 135 G; 126 T;
 Query Match 35.9%; Score 138; DB 22; Length 687.
 Best Local Similarity 83.2%; Fred No. 1.06e-77;
 Matches 248; Conservative 0; Mismatches 38; Indels 12; Gaps 9;
 Db 1 ctgaagcagctcgtgagctgagagaaagcctgtgctcctcgtgagagctcctcagcag 60
 Uy 1 CTCGAGCAGCTCTGAGCTGAGAGAAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 60
 Db 61 gctctgagagcagctcagcaaatatgcatagcgtgagagagagagagagagagagag 120
 Uy 61 GCTCTGAGAGCAGCTCAGCAAAATATGCAATGATGATGATGATGATGATGATGATG 120
 Db 121 gggctcagctgagctgagagag-g-g-alc--t-tccct--ttccgtaa--taagc-caaa-g- 168
 Uy 121 GGACTGAGCTGAGCTGAGAGAGAGCATGCTGATCTGTTGTTGTTGTTGTTGTTGTTG 168
 Db 169 taagcacaacagctcagagagagagctacacattacagcagagagagagagagagagc 228
 Uy 181 TACGCTGAGAAATTCGAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATG 240
 Db 229 tacatgagagctgagagagagctgagagagagagagagagagagagagagagagag 286
 Uy 241 TTCATTGAGCTGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 298
 RESULT 13
 ID 092546 standard; DNA: 4691 BP.
 AC 092546;
 DT 11-MAR-1996 (first entry)
 DE pComb3 expression vector.
 KW pComb3; phagemid expression vector; bacteriophage; coat protein 3;
 KW Gene III; filamentous phage; minor phage coat protein; gpIII; cp3;
 KW bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120,
 KW combinatorial Fab library; cassette; fd/cp3; lacZ promoter/operator;
 KW ribosome binding site; RBS; pelb leader; spacer; tether sequence;
 KW MT4; pMT4-3; antibody; ss; cyclic.
 US Synthetic.
 PN WO9511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994: 011907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 95-170215/22
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immunotherapy of

PT HIV-induced disease.
 PS Example 1: Page 185-188; 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
 CC the 406 residue minor phage coat protein, gpIII (cp3), which is expressed
 CC prior to extrusion in the phase assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector was designed for the cloning
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, fd/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a
 CC pelb leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a pelb leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the MT4 Fab display phagemid expression vector. pMT4-3 (see also
 CC 032540) used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 SQ Sequence 4691 BP; 1170 A, 1171 C, 1232 G; 1118 T;
 Query Match 35.9%; Score 138; DB 16; Length 4691.
 Best Local Similarity 83.2%; Fred No. 1.06e-77;
 Matches 248; Conservative 0; Mismatches 38; Indels 12; Gaps 9;
 Db 3424 ctgagagagctcgtgagctgagagagagcctgtgctcctcgtgagagctcctcagcag 3483
 Uy 1 CTCGAGCAGCTCTGAGCTGAGAGAAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 60
 Db 3484 gctctgagagcagctcagcaaatatgcatagcgtgagagagagagagagagagagag 3543
 Uy 61 GCTCTGAGAGCAGCTCAGCAAAATATGCAATGATGATGATGATGATGATGATGATG 120
 Db 3544 gggctcagctgagctgagag-g-g-alc--t-tccct--ttccgtaa--taagc-caaa-g- 3591
 Uy 121 GGACTGAGCTGAGCTGAGAGAGAGCATGCTGATCTGTTGTTGTTGTTGTTGTTGTTG 180
 Db 3592 taagcacaacagctcagagagagagctacacattacagcagagagagagagagagagc 3651
 Uy 181 TACGCTGAGAAATTCGAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATG 240
 Db 3652 tacatgagagctgagagagagctgagagagagagagagagagagagagagagagag 3709
 Uy 241 TTCATTGAGCTGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 298
 RESULT 14
 ID 092547 standard; DNA: 6166 BP.
 AC 092547;
 DT 11-MAR-1996 (first entry)
 DE Expression vector, pPho-TT.
 KW Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3D1; 3D3; 3D4; 3D5; MT4; humanised; monoclonal antibody; MAb;
 KW immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;
 KW alkaline phosphatase; phoA; ss; cyclic.
 US Synthetic.
 PN WO9511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994: 011907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;


```

FT   misc_RNA      290..385
FT   /*tag- g
FT   /label= FR3
ET   misc_PNA      366..439
ET   /*tag- h
ET   /label= CDP3
FT   misc_RNA      440..472
ET   /*tag- i
ET   /label= FR4
FT   misc_RNA      473..763
ET   /*tag- j
ET   /label= CH1
FT   misc_RNA      764..811
ET   /*tag- k
ET   /label= HINGE
FT   misc_RNA      812..1141
ET   /*tag- l
ET   /label= CH2
FT   misc_RNA      1142..1462
ET   /*tag- m
ET   /label= CH3
FT   TATA_signal    1566..1571
ET   /*tag- n
PD   EP-523949-A.
PF   20-JAN-1993.
PF   14-JUL-1992; 306420.
PR   15-JUL-1991; GB-015284.
PR   01-AUG-1991; GB-016594.
PR   23-MAR-1992; GB-006284.
PA   (WELL ) WELLCOME FOUND LTD.
PI   Crowe JS Lewis AP.
DR   WPt: 93-019951/03.
P-PSDB: R31024.
PT   Prodn. of recombinant primate antibodies - useful for treating
PT   infections caused by hepatitis A, B and C, herpes,
PT   cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
PT   arthritis etc.
PS   Disclosure: Fig. 2: 35pp: English.
CC   The sequences given in G93069-100 encode the heavy and light chains
CC   of Antibody D respectively. Antibody D is a monoclonal antibody which
CC   was derived from peripheral blood lymphocytes from a hepatitis A virus
CC   (HAV) sero positive patient. Antibody D is closely related in nature
CC   to murine antibody B5H3. Total RNA was isolated from antibody D
CC   expressing cells and polyadenylated RNA was extracted. These polyA
CC   RNAs were used to prepare a cDNA library which was screened for human
CC   kappa light (L) chains and two positive clones were detected.
CC   Further heavy (H) chain clones were also isolated.
SQ   Sequence 1617 bp: 375 A; 526 C; 441 G; 275 T;

Query Match          38.8%; Score 149; DB 6; Length 1617;
Best Local Similarity 77.6%; Pred. No. 1,58e+85;
Matches 294; Conservative 0; Mismatches 73; Indels 12; Gaps 4;

Db       106 gaagtcggaggcgaagaataaaagacgcctgtgclcccgatgacgcgtctcccgcaagcatc 165
QY       5 GCAGTCCTGGGACTGAAGTCAATGAAACCGTTGTGCTGCTGCTGCAAGGCGTTC 65
        166 tggaggacccttgagacaactatgatcaagcgtggtgacaaagccccctggacaagacct 225
QY       56 TGGAAGGCACGCTTGAGGCGGCGCATGTAATCATTGATGATCTGTGATGAGTACGAGGACT 125
Db       226 tgattgatalgggaagagatcaccccctcttttgt-----gc-ac--taac-taac 273
        126 TGAGTAGGATGGAGAAGAGAGCATGCCCTTCCTTGTGTTGTCGCAAACTACGCTCAAAC 185
QY       274 acagaacctccaagggcagagtaaagtatccgcggagacaacatccacacacagaccacac 333
        186 TCAGAAATTCGGGACACAGAGATCTGCGATATCTGCGAACGAAATCCAAGACCAAGTGTGAT 245
Db       334 ggagtgctgactagacgttagagatctgagaaaagcgagcgatgctgtgtagaatcgcta 393
        246 TGAAGTGAAGCAACCTGAGATCTGAGCACACAGCGAGCGATGACAGTATGATGATGATGAT 305

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 M E S S E N G E R
 (TM)

Release 2.1F John F. Collins, Biocomputing Research Unit.
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Msrch_n n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 09:37:20 1998: Msrch time 63.74 Seconds
 639 605 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-22
 Description: (1-384) from US08844215.seq
 Perfect Score: 384
 N.A. Sequence: 1 CTCGACGACGCTGGCGCTCA.....CGCTGTCACGCTGCTGCTCA 384
 Comp: GAGCTGTGTAGAGCTGGCACT.....GGAGGAGAGTGG-AGAGAGAGT

Scoring table: TABLE default
 Gap 6

Mismatch STD: Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

n-geneseg30
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.070; Variance 4.671; scale 1.728

Pred. NO. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred No
1	206	53.6	2287	4 Q25443	Sequence encoding ant	1.76e-116
2	206	53.6	2287	28 T60739	IgG1 gene.	1.76e-116
3	163	42.4	294	14 D910	VH gene.	1.58e-95
4	160	41.7	812	3 Q22419	Human heavy chain V r	2.21e-93
5	160	41.7	812	7 Q44185	Human heavy chain V r	2.21e-93
6	150	40.9	294	14 T37243	DNA fragment VH4.8,	3.03e-91
7	157	40.9	294	14 T89352	VH1263 VH gene.	3.03e-91
8	149	38.8	325	5 Q29767	Gene for HV region of	1.58e-85
9	149	38.8	325	5 Q29767	Antibody D heavy chain	1.58e-85
10	141	36.7	369	33 T72151	CEA-specific antibody	7.82e-80
11	141	36.7	441	14 Q82750	33kD anti-Varicella	7.82e-80
12	138	35.9	687	22 T15202	PCARP13 anti-Varicella	1.06e-77
13	138	35.9	4691	16 Q92546	Promy expression vec	1.06e-77
14	138	35.9	6166	16 Q92547	Expression vector, pp	1.06e-77
15	132	34.4	294	14 Q89329	Optim 2 VH-1 H chain	1.89e-73

ALIGNMENTS

16	121	31.5	372	9 Q55663	Monoclonal antibody G	1.11e-65
17	122	31.5	439	31 T75422	Human anti tumor ant	1.11e-65
18	121	31.5	512	13 Q78940	Human immunoglobulin	1.11e-65
19	120	31.3	539	13 Q78956	Human immunoglobulin	5.59e-65
20	117	30.5	564	13 Q78946	Human immunoglobulin	7.19e-63
21	114	29.7	799	13 Q78984	Human immunoglobulin	9.18e-61
22	112	29.3	294	6 Q38635	SP2 IgG heavy chain c	2.31e-59
23	111	28.9	363	19 T10938	VHmu coding sequence	1.16e-58
24	106	27.6	466	13 Q78941	Human immunoglobulin	3.62e-55
25	105	27.3	360	33 T72132	CEA-specific antibody G	1.80e-54
26	105	27.3	378	9 Q55662	Monoclonal antibody G	1.80e-54
27	103	26.8	748	13 Q78983	Human immunoglobulin	4.46e-53
28	101	26.8	366	12 Q70085	DNA encoding MAb heavy	1.95e-51
29	99	25.8	595	33 T90022	DNA encoding heavy ch	2.60e-50
30	99	25.8	629	13 Q79046	Human immunoglobulin	2.60e-50
31	94	24.5	421	33 T73633	CDNA for humanised he	7.78e-47
32	94	24.5	421	33 T73624	CDNA for humanised he	7.78e-47
33	92	24.0	421	33 T73636	CDNA for humanised he	1.87e-45
34	92	24.0	587	13 Q78965	Human immunoglobulin	1.87e-45
35	86	23.2	234	17 T04653	Human derived heavy c	2.18e-43
36	86	22.4	372	16 Q92540	Encodes VH Fab M74 wh	2.50e-41
37	86	22.4	421	33 T73640	CDNA for humanised he	2.50e-41
38	85	22.1	600	13 Q78962	Human immunoglobulin	1.21e-40
39	84	21.9	336	9 Q51552	PBL3/Humanised heavy	5.84e-40
40	84	21.9	417	9 Q51555	PBL3/Humanised heavy	5.84e-40
41	84	21.9	417	12 Q73623	CY17489A VH region.	5.84e-40
42	84	21.9	417	12 Q73624	CY17489B VH region.	5.84e-40
43	84	21.9	417	12 Q73625	CY17489C VH region.	5.84e-40
44	84	21.9	451	10 Q66702	DP60-200 Humanized an	5.84e-40
45	84	21.9	660	13 Q78950	Human immunoglobulin	5.84e-40

RESULT 1
 ID Q25443; standard: DNA; 2287 BP.
 AC Q25443;
 DT 02-JAN-1992 (first entry)
 DE Sequence encoding antibody molecule IgG1.
 KW Antibody; immunoglobulin G1; ds.
 OS Homo sapiens
 FH Key
 FT exon Location/Qualifiers
 FT /atag- a 1..453
 FT /exon 1..372
 FT /atag- b 1361..1405
 FT exon 1524..1853
 FT /atag- d 1950..2273
 FT exon
 FT /atag- e
 FT exon
 PN W09209293-A.
 PD 11-JUN-1992.
 PF 18-NOV-1991; U08605.
 PR 23-NOV-1990; US-618314.
 PA (CEHD) GEN HOSPITAL CORP.
 PI Seed B, Walz G;
 DR WFI: 92-216789/26.
 DP P-FSDB: R2442.
 PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
 PT used in treating chronic inflammation, rheumatoid arthritis,
 PT psoriasis, etc.
 FS Disclosure: Fig 1; 46pp. English.
 CC The IgG1, in its nascent form, bears no staphylococcal side chains. The
 CC inventors designed a molecule including several such sites for
 CC attachment of staphylococcal side chains (see R2442, PT). The
 CC additional N-linked glycosylation sites are introduced at locations
 CC which impair complement fixing and Fc receptor binding ability. They
 CC are preferably located in the CH2 region of the Ig molecule.
 CC Antibodies bearing multiple staphylococcal determinants are useful for
 CC disrupting undesirable interactions between cells or proteins, for
 CC disrupting this interaction has therapeutic applications, for

ORGANISM

I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.

REFERENCE

Eukaryotes: Metazoa: Eumetazoa: Bilateria: Coelomata: Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes: Sarcopterygii, Chondata, Tetrapoda, Amniota, Mammalia, Theria, Eutheria: Archonta: Primates: Catarrhini: Hominoidea: Homo: 1 (bases 1 to 419)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, I., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

TITLE

The WashU-HMM EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-HMM EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence stops: 261
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
1..419
/organism="Homo sapiens"
/clone="214441"

BASE COUNT

91 a 100 c 116 g 102 t 10 others

ORIGIN

Query Match 17.6%; Score 65; DB 90; Length 419;
Best Local Similarity 63.1%; Pred. No. 1,64e-86;

Matches

157; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Db

27 ctgggggggctccctggaactcctctgcaagcgtcgaattcaactcgaatgaca 86

Qy

32 CTGGGCTCTCGTGAAGAGTCTCTGAGGTTTGTGAGACACCTTCACGATACACIA 91

Db

87 tgcactgggtcccgccagcgaagggcgtgagtgagtgacattacagatg 146

Qy

92 TTGAGTGTGGGACAGGCGCTTGACAGAGGCTGAGTGGATGGAAATATCATGCCCTG 151

Db

147 atggaagataataatcatcatcgaactccgtggaagggccgcatccatccagaagaca 206

Qy

152 TCTATATACACCAACTACCTGCGAGAGTTTCAGAGGAGACTCTGATACCGCGAGAG 211

Db

207 attccagaacacgctgtatctcaaatgacagcgtcgtgagcgtgagggacacgctgt 266

Qy

212 ATTCTGAGACACAGCTTACATGAACTGAGTACGATCTGAGTGGACGACGCGCTCT 271

Db

267 attactgt 275

Qy

272 ATTCTGTG 280

RESULT

LOCUS 5 AA170255 823 bp mRNA EST 16-FEB-1997

DEFINITION

ms87a10..r1 Soares mouse 3NBMS Mus musculus cDNA clone 618594 5'

ACCESSION

AA170255

KEYWORDS

EST

SOURCE

house mouse

ORGANISM

Mus musculus

Eukaryotes

Eukaryotes: Metazoa: Eumetazoa: Bilateria: Chordata:

REFERENCE

Vertebrata: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus: 1 (bases 1 to 823)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R.

TITLE

The WashU-HMM Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMM Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:379418
putative full length read
vector to vector length is 867
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 492.

FEATURES

source
1..823
/organism="Mus musculus"
/strain="C57BL/6J"

BASE COUNT

200 a 208 c 202 g 213 t

ORIGIN

Query Match 16.8%; Score 62; DB 196; Length 823;
Best Local Similarity 50.8%; Pred. No. 2,93e-80;

Matches

174; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Db

127 ctgtgtgagctctggggaagccttaagcgtggaagcctcgaacacccctctatgaca 186

Qy

1 CTGAGACAGCTGGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60

Db

187 gacctggaattcactcagatgacatgcatgcttgatgagtcgacacacccagaag 246

Qy

61 GTTTTGGAGACACCTTTAGAGATACATATTCAGTGGTGGAGAGAGAGAGAGAG 120

Db

247 agcgtggaatggtgcacatcatcagatgagtgagtgatcatcactactacgaacact 306

Qy

121 GGAGCTGAGTGGAGAGAGATATCATGCTCTGTATATACACCAATACAGCGAGAG 180

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Qy

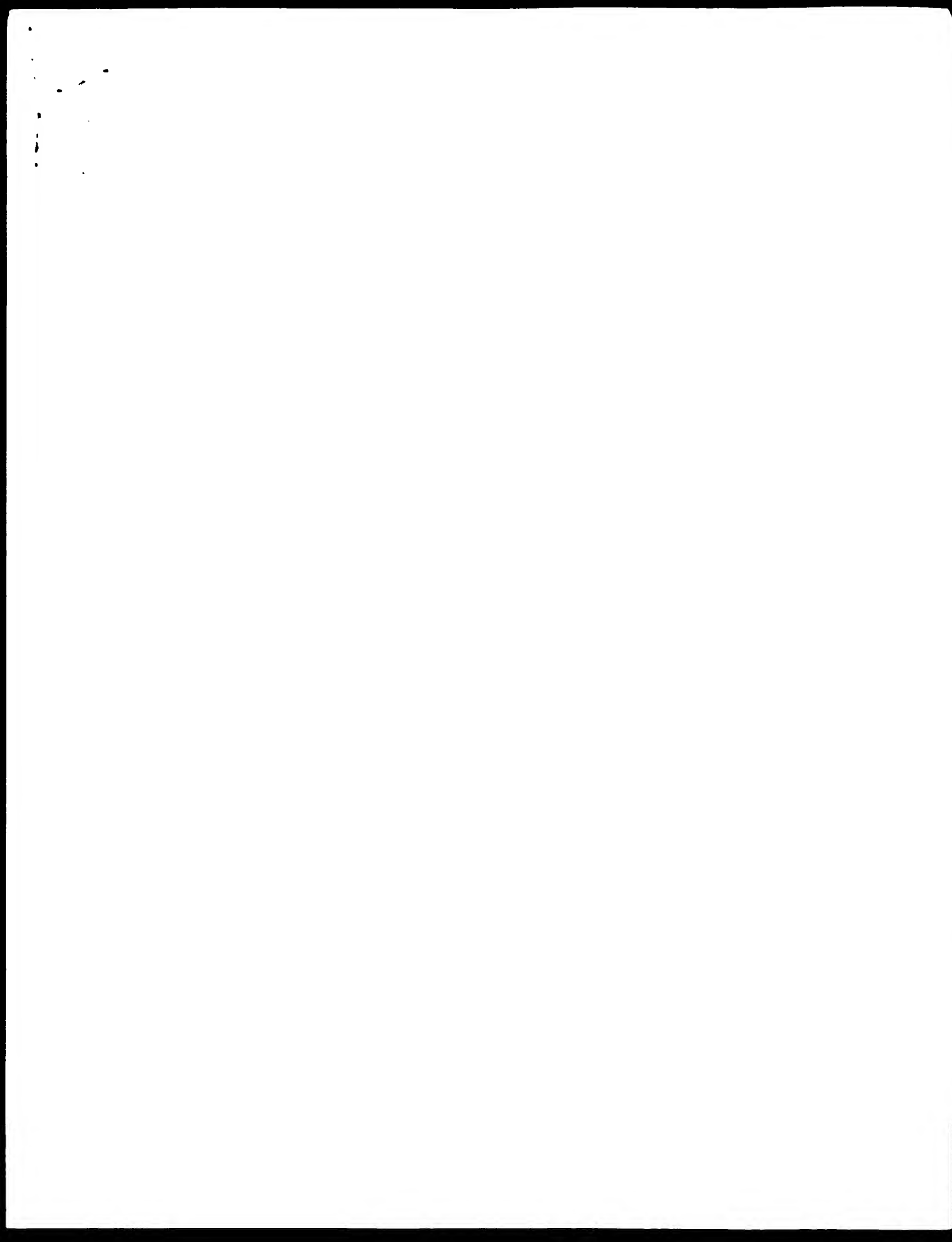
181 TTTCAGGAGTACAGCTCTGAGTAAACCGCGAGAGATTCAGAGAGAGAGAGAG 240

Db

367 agcagctggaatgagtcagacacacacacacacacacacacacacacacacacac 412

Qy

241 AGTAGGCTGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 286



COMMENT

Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:380026
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 391.
 Location/Qualifiers

FEATURES

source

1..420
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTCACATCTGAAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through
 three rounds of normalization, and was constructed by
 Bento Soares and M. Fatima Bonaldo."
 /clone="619202"
 /clone_1lb="Soares mouse 3NBMS"
 /sex="male"
 /tissue_type="Spleen"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
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MRNA
 BASE COUNT 107 a 119 c 99 g 95 t
 ORIGIN

Query Match 8.4%, Score 31, DB 1, Length 420,
 Best Local Similarity 84.4%, Pred. No. 5,19e-21;
 Matches 38, Conservative 0, Mismatches 7, Indels 0,

Db 99 tactttgactactgaggaagcaccactctcagctctctctca 143
 |||
 OY 325 TACTTGACTACTAGGGGCTAGGSAACCTGAGTCACTCTCTCA 369

Search completed: Tue Feb 24 10:06:13 1998
 Job time : 146 secs.

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.

REFERENCE 1 (bases 1 to 291)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brannon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitchugh, W.M., Fitchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kellley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

TITLE
JOURNAL
MEDLINE
COMMENT

CONTACT: Kerlavage, AR
Bioinformatics
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Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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/note="Organ: small intestine; Vector: pBluescript SK-";
Site_1: ECOM1; Site_2: Xho1"
/clone_lib="Small intestine I"
/dev_stage="adult"
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mRNA
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Best Local Similarity 72.9%; Pred. No. 2,16e-157;
Matches 153; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 81 ctgtgcaaatcttgagctggaagagccttgctctctgtgaagtntctgcaag 140
QY 1 CTCGAGCAGTGTGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 60
Db 141 gctatgatacacccttaccgattatacctaaccctgagtgagcagagccctgagca 200
QY 61 GTTTTGGAGACACCTTACGACAGATACACTATTCAGTGGTGGACAGGCGCTGGACAA 120
Db 201 ggaacttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 260
QY 121 GGGCTGAGTGGATGGAAATATCATCCCTCTCTATTAATACACCAATCACTGCGCAGAG 180
Db 261 ttgagggagagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 290
QY 181 TTTCAAGGAGACACTCTGCAATACCGCGCGAC 210

RESULT 4 AA377128 265 bp mRNA EST 21-APR-1997
LOCUS
DEFINITION EST89660 Small intestine 1 Homo sapiens cDNA 5' end similar to

similar to immunoglobulin heavy chain, VDJ region.

ACCESSION AA377128
MID g2029456
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.

REFERENCE 1 (bases 1 to 265)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brannon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitchugh, W.M., Fitchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kellley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

TITLE
JOURNAL
MEDLINE
COMMENT

CONTACT: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

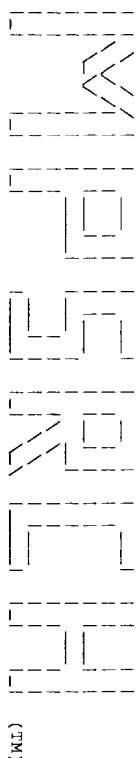
FEATURES
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/note="Organ: small intestine; Vector: pBluescript SK-";
Site_1: ECOM1; Site_2: Xho1"
/clone_lib="Small intestine I"
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Query Match 24.1%; Score 89; DB 58; Length 265;
Best Local Similarity 80.0%; Pred. No. 1.26e-135;
Matches 116; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 104 ctgtgcaaatcttgagctggaagagccttgctctctgtgaagtntctgcaag 163
QY 1 CTCGAGCAGTGTGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 60
Db 164 antctgttaccaccttaccacatacagatcagctgagtgagcagagccctgagca 223
QY 61 GTTTTGGAGACACCTTACGACAGATACACTATTCAGTGGTGGACAGGCGCTGGACAA 120
Db 224 gggcttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 248
QY 121 GGGCTGAGTGGATGGAAATATCA 145

RESULT 5 AA402547 266 bp mRNA EST 16-MAY-1997
LOCUS



Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 10:03:47 1998, MasPar time 133.36 Seconds

Tabular output not generated.

Title: >US-08-844-215-23

Description: (1-369) from US08844215.seq

Perfect Score: 369

N.A. Sequence:

Comp: 1 CTCGACGCTGAGAGCCGAGCT.....GCGTGTGACCGCTCTCTCA 369
GAGCTGCTGAGAGCCGAGCT.....GCGTGTGAGTGGCAGAGAGT

Scoring table:

Gap 6

Nmatch SMD:

Dbase 0: Query 0

Searched:

39746 seqs 1410104 bases x 2

Post-processing:

Minimum Match 0%

Database:

Listing first 45 summaries

EST-C

1:EST197 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202

7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208

13:EST209 14:EST210 15:EST211 16:EST212 17:EST213

18:EST214 19:EST215 20:EST216 21:EST217 22:EST218

23:EST219 24:EST220 25:EST221 26:EST222 27:EST223

28:EST224 29:EST225 30:EST226 31:EST227 32:EST228

33:EST229 34:EST230 35:EST231 36:EST232 37:EST233

38:EST234 39:EST235 40:EST236 41:EST237 42:EST238

43:EST239 44:EST240 45:EST241 46:EST242 47:EST243

48:EST244 49:EST245 50:EST246 51:EST247 52:EST248

53:EST249 54:EST250 55:EST251 56:EST252 57:EST253

58:EST254 59:EST255 60:EST256 61:EST257 62:EST258

63:EST259 64:EST260 65:EST261 66:EST262 67:EST263

68:EST264 69:EST265 70:EST266 71:EST267 72:EST268

73:EST269 74:EST270 75:EST271 76:EST272 77:EST273

78:EST274 79:EST275 80:EST276 81:EST277 82:EST278

83:EST279 84:EST280 85:EST281 86:EST282 87:EST283

88:EST284 89:EST285 90:EST286 91:EST287 92:EST288

93:EST289 94:EST290 95:EST291 96:EST292 97:EST293

98:EST294

Database:

EST-D

99:EST295 100:EST296 101:EST297 102:EST298 103:EST299

104:EST300 105:EST301 106:EST302 107:EST303 108:EST304

109:EST305 110:EST306 111:EST307 112:EST308 113:EST309

114:EST310 115:EST311 116:EST312 117:EST313 118:EST314

119:EST315

Statistics: Mean 9.793; Variance 1.717; scale 5.702

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	139	35.0	379	99	AA291381	ct44g02.r1 Soares ova	7.45e-230
2	111	30.1	279	26	AA300571	EST13661 Testis tumor	7.44e-189
3	97	26.3	291	58	AA377074	EST189603 Small Intest	2.10e-157
4	89	24.1	265	58	AA377128	EST189660 Small Intest	1.26e-139
5	75	20.3	266	80	AA402547	zu47h07.r1 Soares ova	5.02e-109
6	59	16.0	198	65	AA383972	EST197425 Thyms II Ho	4.20e-75
7	49	13.3	341	25	AA295703	EST1100902 Pancreas tu	9.56e-55
8	44	11.9	366	59	AA378312	EST100902 Synovial sar	6.46e-45
9	42	11.4	240	52	AA360289	EST64410 Lymph node,	4.58e-41
10	36	9.8	202	85	AA428970	zv44b02.r1 Soares ova	7.40e-30
11	34	9.2	273	26	AA300982	EST13869 Testis tumor	2.39e-26
12	33	8.9	280	37	AA326955	EST29467 Colon I Homo	1.74e-24
13	33	8.9	326	37	AA327241	EST140532 Colon I Homo	1.74e-24
14	32	8.7	256	26	AA300605	EST13453 Testis tumor	9.75e-23
15	31	8.4	420	1	AA175689	ms94c02.r1 Soares mou	5.19e-21
16	28	7.6	371	37	AA327565	EST10921 Colon I Homo	5.50e-16
17	26	7.0	267	52	AA360197	EST19376 Lymph node I	8.82e-13
18	25	6.8	294	31	AA314630	EST118648 Lung Homo sa	3.15e-11
19	24	6.5	455	22	AA146478	mr05g07.r1 Soares mou	1.03e-09
20	23	6.2	258	52	AA360195	EST69374 Lymph node I	3.08e-08
21	23	6.2	364	16	AA098195	mr86h06.r1 Striatagene	3.08e-08
22	21	5.7	287	37	AA327407	EST30739 Colon I Homo	2.01e-05
23	21	5.7	481	94	AA130659	z01h09.r1 Striatagene	2.01e-05
24	20	5.4	37	112	AA444863	ve75f02.r1 Soares mou	4.32e-04
25	20	5.4	170	79	AA400764	z17b05.r1 Soares tes	4.32e-04
26	20	5.4	181	72	AA342620	EST48174 Fetal spleen	4.32e-04
27	20	5.4	326	104	HUM095E11B	Human fetal brain CDN	4.32e-04
28	20	5.4	341	36	AA325281	EST38241 Striatagene	4.32e-04
29	20	5.4	312	75	AA349776	EST6674 Infant brain	4.32e-04
30	20	5.4	318	113	AA448258	z28g011.r1 Soares tes	4.32e-04
31	20	5.4	331	78	AA393400	z17b05.r1 Soares tes	4.32e-04
32	20	5.4	347	7	AA33719	z17b05.r1 Striatagene	4.32e-04
33	20	5.4	425	112	AA443899	z746d08.r1 Soares ova	4.32e-04
34	20	5.4	444	13	AA245100	mx08g10.r1 Soares mou	4.32e-04
35	20	5.4	455	85	AA427173	ve83g01.r1 Soares mou	4.32e-04
36	20	5.4	481	87	AA344169	z28b011.r1 Soares ova	4.32e-04
37	20	5.4	482	39	AA116281	EST181189 Jurkat T-ce	4.32e-04
38	20	5.4	503	1	AA178724	mp17h01.r1 Soares mou	4.32e-04
39	20	5.4	506	19	AA118377	mp17h01.r1 Soares mou	4.32e-04
40	20	5.4	509	1	AA177425	mx17d01.r1 Soares mou	4.32e-04
41	20	5.4	522	11	AA337580	mx17d01.r1 Soares mou	4.32e-04
42	19	5.1	278	98	CO1167	HUM6S0607856, Human G	8.14e-03
43	19	5.1	327	55	AA368203	EST19418 Placenta I H	8.14e-03
44	19	5.1	346	30	AA310626	EST181425 Jurkat T-ce	8.14e-03
45	19	5.1	406	81	AA411110	z17g08.r1 Soares ova	8.14e-03

ALIGNMENTS

RESULT 1
LOCUS AA291381 379 bp mRNA
DEFINITION ct44g02.r1 Soares ovari tumor NBHCT Homo sapiens cDNA clone 725234
5' similar to gb:U18512 IG HEAVY CHAIN PRECURSOR V-1 REGION
(HUMAN);

ACCESSION
NID AA291381
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Eukaryota; Eutheria; Primates; Catarrhini; Homidae;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae;
Homo.

REFERENCE 1 (bases 1 to 379)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubucq, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, R., Stepien, M., Tan, F., Theising, R., White, Y., Wyllie, T., Waterston, R. and Willson, R.
TITLE WashU-Merck EST Project 1997

Db	264	cgctcaaaagtgtaactccgaaggctgcacagggagagctctcagagtagaccgccaggtctac	323			
CP	92	cttttgaaagctccctccacagagccctctcagagagctctcagagtagaccgccaggtctac <td>33</td>	33			
Db	324	aaagctcccccagatctccacagcttgacgtc	355			
CP	32	acctcagagaccatctctccagacacgtccacgtc	1			
RESULT	6	AA507475	433 bp	mRNA	EST	15-JUL-1997
LOCUS	DEFINITION	nb6c05.s1 NCI-CCAP.Br1.1 Homo sapiens cDNA clone 964424 similar to				
ACCESSION		gb.X14584.1 G HEAVY CHAIN PREGNOROP V-111 PROTEIN (HUMAN)..				
NID		AA507475				
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SOURCE		EST				
ORGANISM		human.				
		Homo sapiens				
		Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;				
		Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,				
		Homo.				
REFERENCE		1 (bases 1 to 435)				
AUTHORS		NCI-CCAP.				
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
JOURNAL		Tumor Gene Index				
COMMENT		Unpublished (1997)				
		Contact: Robert Strausberg, Ph.D.				
		Tel: (301) 496-1550				
		Email: Robert.Strausberg@nih.gov				
		Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael P.				
		Emmert-Buck, M.D., Ph.D.				
		cDNA Library Preparation: M. Bento Soares, Ph.D.				
		cDNA Library Arrayed by: Greg Lennon, Ph.D.				
		DNA Sequencing by: Washington University Genome Sequencing Center				
		Clone distribution: NCI-CCAP clone distribution information can be				
		found through the I.M.A.G.E. Consortium/LLNL at:				
		www-bio.llnl.gov/bhrp/image/image.html				
		Insert length: 558				
		Std Error: 0.00				
		Seq primer: -40m13 fwd. ET from Amersham				
		High quality sequence stop: 131.				
FEATURES		Location/Qualifiers				
source		1. 435				
		/organism="Homo sapiens"				
		/note="Vector: p773b-Pac (Pharmacia) with a modified				
		polylinker; 1st strand cDNA was prepared from pooled bulk				
		breast tumor tissue, and was then primed with a Not I -				
		oligo(dT) primer. Double-stranded cDNA was ligated to Eco				
		RI adaptors (Pharmacia), digested with Not I and cloned				
		into the Not I and Eco RI sites of the modified p773				
		vector. Library is not normalized. (The normalized				
		version of this library is NCI-CCAP Br2.) Library was				
		constructed by Bento Soares and M. Fatima Bonaldo."				
		/clone="964424"				
		/clone_lib="NCI-CCAP.Br1.1"				
		/sex="female, pooled"				
		/tissue_type="breast"				
		/lab_host="DH10B"				
		<1..>435				
BASE COUNT		94 a 128 c 112 g 101 t				
ORIGIN						
Query Match		7.9%: Score 30; DB 40; Length 435;				
Best Local Similarity		66.3%: Pred. No. 2,73e-17;				
Matches		61: Conservative 0; Mismatches 31; Indels 0; Gaps 0;				
Db	264	ctgcctaaagtgtaactccgaaggctgcacagggagagctctcagagtagaccgccaggtctac	323			
CP	92	cttttgaaagctccctccacagagccctctcagagagctctcagagtagaccgccaggtctac	33			
Db	324	aaagctcccccagatctccacagcttgacgtc	355			

[illegible]

JOURNAL Unpublished (1997)

COMMENT

Contact: Wilson RK
Mashu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 414.

FEATURES

source

Location/Qualifiers
1..511
/organism="Homo sapiens"
/note="Organ ovary: Vector pT7T3 (Pharmacia) with a
modified polylinker: Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGAGCGCGCGTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonafide."
/clone="810397"
/clone_lib="Soares ovary tumor NBHOT"
/sex="female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
-1
-511
/db_xref="GDB:6040750"
BASE COUNT 105 a 169 c 124 g 112 t
ORIGIN

Query Match 6.3%; Score 24; DB 17; Length 511;
Best Local Similarity 85.3%; Pred. No. 1,720-08;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 387 ctggagccaaagagacatgctgacatctccca 420
|||||
OY 345 ctggggccagggactctgctaccccttcca 378

RESULT 11

ID HS1321118 standard: RNA; EST: 403 bp
AC AA531145;

NI 92273851
DT 24-JUL-1997 (Rel. 52, Created)

DT 24-JUL-1997 (Rel. 52, Last updated, Version 1)
DE n51b07.s1 NCI_CGAP_P19 Homo sapiens cDNA clone 995989 similar to
gb:U17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);..

KW EST.
OS Homo sapiens (human)
OC Eukaryota; Eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

OC Homo.
NC [1]
RN 1-403
RP 1-403

RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index";

RT Unpublished.

CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
Robert.Strausberg@nih.gov Tissue Procurement: W. Marston Linahan,

CC M.D., Rodrigo F. Chuquib, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CC cDNA Library Preparation: David R. Krizman, Ph.D. cDNA Library

CC Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington
CC University Genome Sequencing Center Clone distribution: NCI-CGAP
CC clone distribution information can be found through the I.M.A.G.E.
CC Consortium/LNL at: www.bio.llnl.gov/bhrp/image.html Trace

CC considered overall poor quality Seq primer: -40m13 fwd. ET from
CC Amersham High quality sequence stop: 1.

PH Key

PH Location/Qualifiers

FT 1..403
FT source

/organism="Homo sapiens"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells. cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on agarose
gels, average insert size 600 bp. Library made by D.
Krizman, NIH."

/clone="995989"
/clone_lib="NCI_CGAP_P19"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"

FT mRNA
FT Sequence 403 bp; 64 A, 136 C, 119 G, 93 T, 0 other,
11..>403

Query Match 5.6%; Score 21; DB 73; Length 403;
Best Local Similarity 74.4%; Pred. No. 1,460-04;

Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

DB 154 gttgcgacagcgcgagtgctgcaccagctgcgcacac 196
|||||

Cp 359 gttcccttggcccca359gctgcaactgaccccgacacatctccac 317

RESULT 12

LOCUS AA531145 403 bp mRNA EST 22-JUL-1997
DEFINITION n51b07.s1 NCI_CGAP_P19 Homo sapiens cDNA clone 995989 similar to
gb:U17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);..

ACCESSION AA531145
NID 92273851
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

Hom.
REFERENCE 1 (bases 1 to 403)

AUTHORS NCI-CGAP.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov
Tissue Procurement: W. Marston Linahan, M.D., Rodrigo F. Chuquib,

M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David R. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/bhrp/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers
1..403

/organism="Homo sapiens"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells. cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gels, average insert size 600 bp. Library made by
D. Krizman, NIH."

/clone="995989"
/clone_lib="NCI_CGAP_P19"
/sex="male"

/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"

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 ORIGIN
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 Best Local Similarity 74.4%; Pred. No. 1.46e-04;
 Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 154 gttcgcagacgagatgctgcacacagctgcgcgaactcagc 196
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 359 gttccctgacgagctgcgaacagcagcgcacacacacac 217
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
 ID HS1138859 standard; RNA: EST: 288 BP.
 AC AA078241;
 NI 91837717
 DT 13-FEB-1997 (Rel. 50, Created)
 DT 13-FEB-1997 (Rel. 50, Last updated, Version 1)
 DE 7H16206 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone
 DE 7H16206.
 KW EST.
 OS Homo sapiens (human)
 OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo
 RN [1]
 RP 1-288
 PA Touchman J.W., Bouffard G.S., Weintraub L.A., Idol J.P., Wang L.,
 Robbins C.M., Nisbaum J.C., Lovett M., Green E.D.;
 FT "2,006 Expressed-Sequence Tags Derived from Human Chromosome
 FT 7-Enriched cDNA Libraries";
 RL Genome Res. 7:0-0(0).
 CC Contact: Eric D. Green Genome Technology Branch National Human
 CC Genome Research Institute/NIH 49 Convent Dr., MSC4431, Building 49,
 CC Room 2A08, Bethesda, MD 20892 Tel: 3014020201 Fax: 3014024735
 CC Email: egreen@nhgri.nih.gov Plate: 16 row: G column: 06 Seq primer:
 CC -21M13 (AB1).
 FH Key
 FH Location/Qualifiers
 FT 1..288
 FT source
 FT /organism="Homo sapiens"
 FT /note="Vector: pAMP10; cDNA was generated from cytoplasmic
 FT RNA using a mixture of random DNA hexamers and oligo(dT).
 FT From this pool of cDNA, human chromosome 7-enriched cDNA
 FT was isolated by direct cDNA selection using chromosome 7
 FT genomic DNA (cosmids). The resulting direct-selected cDNA
 FT was cloned into a plasmid vector using a non-directional
 FT uracil DNA glycosylase (UDG)-mediated cloning strategy."
 FT /clone="7H16206"
 FT /clone_lib="Chromosome 7 HeLa cDNA Library"
 FT /sex="female"
 FT /cell_line="HeLa cell line: ATCC"
 FT /lab_host="E. coli strain DH5 alpha"
 FT <1 >288
 FT mRNA
 FT Sequence 288 BP; 75 A 87 C 72 G 53 T 1 other.
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 Best Local Similarity 80.5%; Pred. No. 2.42e-03;
 Matches 33; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Db 216 caaacactgcagacatagctgctgctgctgctgctgctgctg 256
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 302 CAAACATTGCATGCTGGAGG-ITCTGAGGCTGGTTCGA 341
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RESULT 14
 LOCUS HUMSWS3933 302 bp cDNA STS
 DEFINITION human chromosome 7 STS sws3933.
 ACCESSION G31805
 NID g1916530
 KEYWORDS STS sequence, primer, sequence tagged site.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.
 1 (bases 1 to 302)
 Bouffard G.S., Lovett M., Idol J.P., Braden V.V., Cunningham A.E.,
 Weintraub L.A., Mohr-Tidwell P.M., Peluso D.C., Fulton P.S.,
 Leckie M.P. and Green E.D.
 A collection of 18.4 human chromosome 7-specific STS
 Genome Res. 7 (1): 59-64 (1997)
 97189344
 2 (bases 1 to 302)
 Green E.D.
 Human chromosome 7 STS
 Unpublished (1997)
 Contact: Eric D. Green
 Genome Technology Branch
 National Human Genome Research Institute/NIH
 49 Convent Dr., MSC4431, Bldg 49, Rm 2A08, Bethesda, MD 20892
 Tel: 3014020201
 Fax: 3014024735
 Email: egreen@nhgri.nih.gov
 Primer A: CTACACCTTCATCTTC
 Primer B: CTAAGTTCATGTTATCACC
 STS size: 134
 PCR Profile:
 Presoak: 0 degrees C for 0.00 minute(s)
 Denaturation: 92 degrees C for 0.17 minute(s)
 Annealing: 55 degrees C for 1.00 minute(s)
 Polymerization: 72 degrees C for 1.00 minute(s)
 PCR Cycles: 35
 Thermal Cycler: PerkinElmer 9600
 Protocol:
 Template: 30-100 ng
 Primers: each 1 uM
 dNTPs: each 200 uM
 Tag Polymerase: 0.05 units/ul
 Total Vol: 10 ul
 Buffer:
 MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3
 The sequence for this STS was derived from a single sequencing
 read. For additional information about the NHGRI chromosome 7
 mapping project, see http://www.nhgri.nih.gov/STF/STF_CHR7/. Also
 see Genomics 11:548-64 (1997) (url:90128337).
 FEATURES
 source
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 /organism="Homo sapiens"
 /map="7"
 STS
 primer_bind 109..126
 primer_bind complement(221..242)
 BASE COUNT 95 a 70 c 70 g 67 t
 ORIGIN
 Query Match 53.8% Score 20; DB 11; Length 302;
 Best Local Similarity 75.0%; Pred. No. 2.42e-03;
 Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Db 128 gctgagccacagaaactcgaagaagccagcgcgaagg 167
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 197 GCAAGATCAATATTAAGGAGGAGGATGACAGGAGGAGG 236
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RESULT 15
 LOCUS HUMSWS3933 302 bp cDNA STS
 DEFINITION human chromosome 7 STS sws3933.
 ACCESSION G31805

Search completed: Tue Feb 24 13:44:30 1958
Job time : 374 secs.

NID g1916530
KEYWORDS STS sequence, primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
 Homo.

REFERENCE 1 (bases 1 to 302)
AUTHORS Bouffard,G.G., Iyer,L.M., Idol,J.P., Braden,V.V., Cunningham,A.F.,
 Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,
 Leckie,M.P. and Green,E.D.
TITLE A collection of 1814 human chromosome 7-specific STS
JOURNAL Genome Res. 7 (1), 59-64 (1997)
MEDLINE 97189344
REFERENCE 2 (bases 1 to 302)
AUTHORS Green,E.D.
TITLE Human chromosome 7 STS
JOURNAL Unpublished (1997)

COMMENT Contact: Eric D. Green
 Genentech Technology Branch
 National Human Genome Research Institute/NIH
 49 Convent Dr., MSC4431, Bldg. 49, Rm 2A06, Bethesda, MD 20892
 Tel: 3014020201
 Fax: 3014024735
 Email: edgreen@nhgri.nih.gov

Primer A: CTACACACCTTCATCTTC
Primer B: CTAAGTTGCATTCATTACACC
STS size: 134
PCR protocol:
 presoak: 0 degrees C for 0.00 minute(s)
 Denaturation: 92 degrees C for 0.17 minute(s)
 Annealing: 55 degrees C for 1.00 minute(s)
 Polymerization: 72 degrees C for 1.00 minute(s)
 PCR Cycles: 35
 Thermal Cycler: PerkinElmer 9600

Protocol:
 Template: 30-100 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3

 W O R L D
 (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MSearch_n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 15:01:27 1998; MasPar time 26.16 Seconds
 664,648 Million cell updates/sec

Tabular output not generated

Title: >US-08-844-215-27
 Description: (1-378) from US08844215.seq
 Perfect Score: 378
 N.A. Sequence: 1 GAGGTGACGTGCTGCTGAGTC CTCTGTACACGTGTGTTTA 378
 Comp: CTCACGCTGACGACGACGTCAG GAGACGACGTCGACAGAGT

Scoring table: TABLE default
 Gap 6

Mmatch STD: Dbase 0; Query 0

Searched: 97531 segs, 2295621 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: n-issued
 1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:PT90 9:PT91
 10:PT92 11:PT93 12:PT94 13:PT95 14:PT96

Statistics: Mean 7.735; Variance 4.122; scale 1.877

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	263	69.6	2287	14	PCT-US96-1 Sequence 8, Applicatio	8,686-184
2	263	59.0	912	7	US-07-834 Sequence 53, Applicatio	3,726-152
3	223	59.0	812	10	PCT-US92-0 Sequence 53, Applicatio	3,726-152
4	223	59.0	813	10	PCT-US92-1 Sequence 61, Applicatio	3,726-152
5	201	53.2	441	6	US-08-053 Sequence 61, Applicatio	3,726-152
6	201	53.2	441	6	US-08-217 Sequence 3, Applicatio	7,806-135
7	196	51.9	687	13	PCT-US95-1 Sequence 1, Applicatio	6,606-131
8	196	51.9	687	7	US-08-300 Sequence 1, Applicatio	6,606-131
9	196	51.9	687	12	PCT-US94-0 Sequence 1, Applicatio	6,606-131
10	172	45.5	363	7	US-08-264 Sequence 1, Applicatio	4,116-112
11	172	40.2	360	11	PCT-US93-0 Sequence 1, Applicatio	4,116-112
12	151	39.9	3282	13	PCT-US95-0 Sequence 154, Applicatio	9,256-96
13	151	39.9	3282	13	US-08-276 Sequence 154, Applicatio	9,256-96
14	151	39.9	3282	13	PCT-US95-0 Sequence 159, Applicatio	9,256-96
15	151	39.9	3282	7	US-08-276 Sequence 169, Applicatio	9,256-96
16	151	39.9	13254	7	US-08-276 Sequence 156, Applicatio	9,256-96
17	151	39.9	13254	13	PCT-US95-0 Sequence 156, Applicatio	9,256-96
18	151	39.9	13254	13	PCT-US95-0 Sequence 170, Applicatio	9,256-96
19	151	39.9	13254	7	US-08-276 Sequence 170, Applicatio	9,256-96

20	135	35.7	443	7	US-08-487 Sequence 9, Applicatio	2,246-83
21	135	35.7	443	5	US-07-634 Sequence 9, Applicatio	2,246-83
22	135	35.7	443	7	US-08-474 Sequence 9, Applicatio	2,246-83
23	135	35.7	443	6	US-08-477 Sequence 9, Applicatio	2,246-83
24	131	34.7	348	13	PCT-US95-0 Sequence 7, Applicatio	2,726-80
25	131	34.7	433	7	US-08-487 Sequence 18, Applicatio	2,726-80
26	131	34.7	433	7	US-08-474 Sequence 18, Applicatio	2,726-80
27	131	34.7	433	6	US-08-477 Sequence 18, Applicatio	2,726-80
28	131	34.7	433	6	US-07-634 Sequence 18, Applicatio	2,726-80
29	123	32.5	451	11	PCT-US93-1 Sequence 11, Applicatio	3,866-74
30	113	29.9	351	6	US-08-236 Sequence 10, Applicatio	1,746-66
31	113	29.9	351	13	PCT-US95-0 Sequence 10, Applicatio	1,746-66
32	113	29.9	366	13	PCT-US95-0 Sequence 8, Applicatio	1,746-66
33	113	29.9	366	6	US-08-236 Sequence 8, Applicatio	1,746-66
34	113	29.9	429	13	PCT-US95-0 Sequence 6, Applicatio	1,746-66
35	113	29.9	429	6	US-08-236 Sequence 6, Applicatio	1,746-66
36	111	29.4	357	7	US-08-467 Sequence 1, Applicatio	5,846-65
37	111	29.4	1572	7	US-08-353 Sequence 23, Applicatio	5,846-65
38	110	29.1	735	12	PCT-US94-1 Sequence 50, Applicatio	3,386-64
39	108	28.6	735	12	US-08-040 Sequence 1, Applicatio	1,136-62
40	108	28.6	735	12	PCT-US94-1 Sequence 54, Applicatio	1,136-62
41	107	28.3	348	13	PCT-US95-0 Sequence 3, Applicatio	6,496-62
42	107	28.3	360	12	PCT-US94-0 Sequence 1, Applicatio	6,496-62
43	107	28.3	499	4	US-07-916 Sequence 16, Applicatio	6,496-62
44	107	28.3	501	5	US-07-946 Sequence 23, Applicatio	6,496-62
45	106	28.0	366	7	US-08-040 Sequence 5, Applicatio	3,746-61

ALIGNMENTS

RESULT 1
 ID PCT-US96-10043-8 STANDARD: DNA; UNC: 2287 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 8, Application FC/TUS9610043.
 CC Sequence 8, Application FC/TUS9610043
 CC GENERAL INFORMATION:
 CC APPLICANT: The General Hospital Corporation
 CC TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
 CC TITLE OF INVENTION: AND METHODS
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESSES:
 CC ADDRESSEE: Fish & Richardson P.C.
 CC STREET: 225 Franklin Street
 CC CITY: Boston
 CC STATE: MA
 CC COUNTRY: USA
 CC ZIP: 02210-2804
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US96/10043
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 69/000,213
 CC FILING DATE: 14-JUN-1995
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Lech, Karen F.
 CC REGISTRATION NUMBER:
 CC REFERENCE/DOCKET NUMBER: 00756/284001
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 617/542-8906
 CC TELEFAX: 617/542-8906
 CC TELETYPE: 200154
 CC INFORMATION FOR SEQ ID NO: 8:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 2287 base pairs
 CC TYPE: nucleic acid

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1

QY 77 GAGGAGCTTCAGAACTACAAATTTCATTGGGTGCGACAGGCCCTGGACAGGCTTGTG 136
DB 128 AGTGGATGGAGGAGGATCTCTCCCTTCCGTAATACAGAAAGTACGACAACTTCCAGG 187
QY 137 AGTGGATGGAGGAGGATCTCTCCCTTCCGTAATACAGAAAGTACGACAACTTCCAGG 196
DB 188 GCAGAGCTACCACTTACCGGCGAGCAATCCAGGGGACGCTACATGAGCTGAGCGCC 247
QY 197 GCAGAGCTACCACTTACCGGCGAGCAATCCAGGGGACGCTACATGAGCTGAGCGCG 256
DB 248 TGAGATCTGAGGACAGCGGCAATATTTATTTGCGCA 283
QY 257 TGAGATCTGAGGACAGCGGCAATATTTATTTGCGCA 292

RESULT 9
ID PCT-US94-01258-1 STANDARD: DNA; UNC; 687 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9401258.
CC Sequence 1, Application PC/TUS9401258
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSEAL OF RANDOMIZED IMMUNOLOGICAL LIGHT
CC CHAINS
CC NUMBER OF SEQUENCES: 61
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01258
CC FILING DATE: 02-FEB-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,565
CC FILING DATE: 02-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 687 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
SQ Sequence 687 BP; 155 A; 211 C; 195 G; 126 T; 0 other;

Query Match 51.9%; Score 196; DB 12; Length 687;
Best Local Similarity 85.5%; Pred. No. 6.60e-131;
Matches 236; Conservative 0; Mismatches 40; Indels 0; Gaps 0.

DB 8 AGTCTGGGCTAGGTGAGAAAGCTGGGTCTCTGGTGAAGGCTCTCTGCAAGGCTTCTG 67
QY 17 AGTCTGGGCTAGGTGAGAAAGCTGGGTCTCTGGTGAAGGCTCTCTGCAAGGCTTCTG 76
DB 68 GAGGAGCTTCAGAACTTATGCTATCATGCTGGTGGCGAGGCGCTGGGAGAAAGGCTTG 127
QY 77 GAGGAGCTTCAGAACTTATGCTATCATGCTGGTGGCGAGGCGCTGGGAGAAAGGCTTG 136
DB 128 AGTGGATGGAGGAGGATCTCTCCCTTCCGTAATACAGAAAGTACGACAACTTCCAGG 187
QY 137 AGTGGATGGAGGAGGATCTCTCCCTTCCGTAATACAGAAAGTACGACAACTTCCAGG 196
DB 188 GCAGAGCTACCACTTACCGGCGAGCAATCCAGGGGACGCTACATGAGCTGAGCGCG 247
QY 197 GCAGAGCTACCACTTACCGGCGAGCAATCCAGGGGACGCTACATGAGCTGAGCGCG 256
DB 248 TGAGATCTGAGGACAGCGGCAATATTTATTTGCGCA 283

QY 257 TGAGATCTGAGGACAGCGGCAATATTTATTTGCGCA 292

RESULT 10
ID US-08-264-093-1 STANDARD: DNA; UNC; 363 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08264093.
CC Sequence 1, Application US/08264093
CC Patent No. 5639863
CC GENERAL INFORMATION:
CC APPLICANT: Michael D. Dan
CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CC TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ridout & Maybee
CC STREET: 2300 Richmond-Adelaide Centre
CC CITY: 101 Richmond Street West
CC STATE: Ontario
CC COUNTRY: Canada
CC ZIP: M5H 2T7
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: MS-DOS 6.00
CC SOFTWARE: ASCII Editor
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/264,093
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA: No. 5639863 applicable
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lake, James P.
CC REGISTRATION NUMBER: 31081
CC REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (416) 868-1482
CC TELEFAX: (416) 362-0823
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 363 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: linear
SQ Sequence 363 BP; 84 A; 97 C; 108 G; 74 T; 0 other;

Query Match 45.5%; Score 172; DB 7; Length 363;
Best Local Similarity 79.7%; Pred. No. 4.11e-112;
Matches 231; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

DB 2 AGTCTAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 61
QY 2 AGTCTAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 61
DB 52 CTGTGAGGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 121
QY 62 CTGTGAGGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 121
DB 122 CTGTGAGGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 181
QY 122 CTGTGAGGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 181
DB 182 CAGCAAACTTCCAGGCGAGAGTCTCCATGACGACAGCAATCCAGGACAGGCTTAC 241
QY 182 CAGCAAACTTCCAGGCGAGAGTCTCCATGACGACAGCAATCCAGGACAGGCTTAC 241
DB 242 TGAGATCTGAGGACAGCGGCAATATTTATTTGCGCA 283
QY 242 TGAGATCTGAGGACAGCGGCAATATTTATTTGCGCA 283

CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESSES:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 CC STREET: Mail Drop 7P08
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/279,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCRI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 154:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 3282 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 15..452
 CC Sequence 3282 BP, 710 A, 1109 C, 864 G, 599 T, 0 other:
 SQ
 Query Match 39.9%, Score 151, DB 7, Length 3282;
 Best Local Similarity 75.9%; Pred No 9, 26e-96;
 Matches 221, Conservative 0, Mismatches 70, Indels 0, Gaps 0;
 DB 73 AGCTTCAGCTGCTGATGTCGGGCTGAGGAGGAAGCCCTGGGCTCAGTGAAGTTT 132
 OY 2 AGCTGAGCTGCTGATGCTGGCTGAGGTGAAGAAACCTGGGCTTCGCTGAGGTTCT 61
 DB 133 CTGTGAGGCTTGTGATACAGATCAGTACCTTGTATTCATTTGGTGGCGGCC 192
 OY 62 CCGGAGGCGCTCTGAGGAGGAGCTTACAGACCTCAATTTCAATTTGGGTGGAGGCC 121
 DB 193 CCGGAGGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 252
 OY 122 CTGGAGAAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 181
 DB 253 CAGCGAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 312
 OY 182 CACAGAGAGGTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
 DB 313 TGGAGTTTCAAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
 OY 342 TGGAGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 292

RESULT 14
 ID PCT-US95-08743-169 STANDARD; DNA; UNC; 3282 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 169, Application PC/TUS9508743.
 CC Sequence 169, Application PC/TUS9508743.
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPC)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
 CC INFORMATION FOR SEQ ID NO: 169:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 3282 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC Sequence 3282 BP, 599 A, 864 C, 1109 G, 710 T, 0 other:
 SQ
 Query Match 39.9%, Score 151, DB 13, Length 3282;
 Best Local Similarity 75.9%; Pred No 9, 26e-96;
 Matches 221, Conservative 0, Mismatches 70, Indels 0, Gaps 0;
 DB 2920 TCGCAATATATAAAGCCGCTCTGCAAGCTGAGGCTGCAAGCTGAGGCTG 2979
 CP 292 TCGCAATATATAAAGCCGCTCTGCAAGCTGAGGCTGCAAGCTGAGGCTG 233
 DB 2960 TGTTCGGGAGTGTCCCGGTAAGGAGTGTCTGTCTGAGGAGGAGGAGGAGGAGG 3039
 CP 232 TGGCGGTGATGCTGCGCGTAATGTGTGACGTGCTGAGGAGGAGGAGGAGGAGG 173
 DB 3440 TGTTCGGTGAAGAT 3099
 CP 172 CTGTTCGAGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 113
 DB 3100 GCACCAATGATATACAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 3159
 CP 112 GCACCAATGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 53
 DB 3160 CTGAGGCGCCGAGGCTTCTTCACTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 3210
 CP 52 CGAAGAGCCAGGCTTCTTCACTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2
 RESULT 15
 ID US-08-276-852-169 STANDARD; DNA; UNC; 3282 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 169, Application US/08276852.
 CC Sequence 169, Application US/08276852.
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:

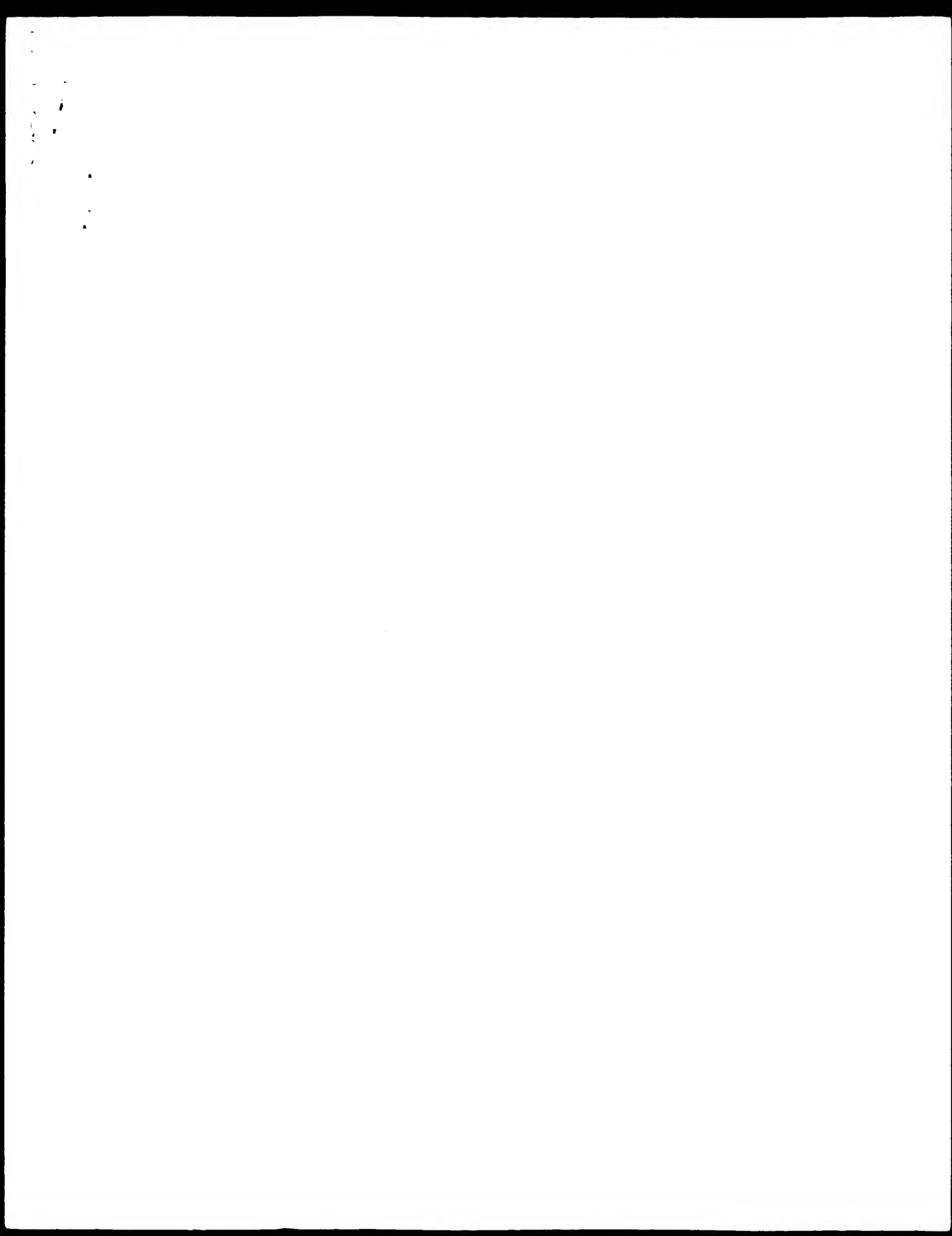
Thu Feb 26 07:05:49 1998

US-08-844-215-27.rni

Page 9

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CC ADDRESS: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop 1PC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178, 302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCP1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 169:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3282 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 3282 BP; 599 A; 864 C; 1109 G; 710 T; 0 other;
SQ
Query Match 39.9%; Score 151; DB 7; Length 3282;
Best Local Similarity 75.9%; Pred. No. 9.26e-96;
Matches 221; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
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Search completed: Tue Feb 24 16:02:43 1998
Job time : 76 secs.




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FT /number-1 373..812
FT exon
FT /*tag- c
FT /number-2 241..689
FT CDS
FT /*tag- d
FT /note- "CDS is interrupted by intron #1: the
FT last three codons of the CDS are not
FT translated in the amino acid sequence
FT R38623"
FT PN
FT WO312227-A.
FT 24-JUN-1993: U10983.
FT 17-DEC-1992: US-810279.
FT 17-DEC-1991: US-810279.
FT 18-MAR-1992: US-853408.
FT 23-JUN-1992: US-904068.
FT (GENP-) GENPHARM INT INC.
FT PA
FT Kay RM, Lomborg N;
FT WPI: 93-214169/26.
FT DR
FT P-PSDB: R38623.
PT Transgenic non-human animals contg. immunoglobulin heavy chain
PT trans gene - used to produce useful antibodies by isotype
PT switching
PS Example 12: Page 96; 196pp; English.
CC A human placental genomic DNA library cloned into the phage vector
CC lambda fix II was screened with the human VH1 family specific
CC oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a
CC 6.1kb XbaI fragment containing the variable segment VH49.8 was
CC subcloned into pNN03 to generate plasmid pVH49.8. An 800bp
CC region of this insert was sequenced (Q44185) and VH49.8 found to
CC have an open reading frame and intact splicing and recombination
CC signals, indicating that the gene is functional.
SQ Sequence 812 BP; 204 A; 188 C; 223 G; 197 T;

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Query Match 59.0%; Score 223; DB 7; Length 812;

Best Local Similarity 88.3%; Pred. No. 9,29e-137;

Matches 257; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

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Db 385 aggtccagctgtgcaagctctgaggtgagtggaagagcctggtcctggaaggtct 444
QY 2 AGGTCCAGCTGCTGCAAGCTCTGAGTGTGAGTGAAGAAAGCTGGTCTTCGGTAAAGTCT 61
Db 445 cctgcaaggtcttgaagagccttcagcagctatgctatcagctggtgagcaagccc 504
QY 62 CCTGCAAGGCTCTGAGGAGCTTCAGAACTCAATTTCAATTGGCTCGACAGGCC 121
Db 505 ctggacaaggtctgagtgatggaagagatcaccatccctatccttgatagcaactacg 564
QY 122 CTGGACAAGGCTTGTAGTGGATGGAGGCATCATCCCTATGTTGGAAACGCAAACTACG 181
Db 565 cacaagaagttccagagcagagatcagatcaccgagacaatccacagagacagactaca 624
QY 182 CACAGAAGTTTCAGGAGAGTTCACAAATTACCCGCGAGCAATCCAGCCACAGGCTACA 241
Db 625 tggagctgagcagctgagatcctgagagcaagccgtgtattactgagca 675
QY 242 TGGAGCTGAGCAGTCTGAGATCTGACAGACAGCGCCGTTATTACTGTGCGA 292

```

RESULT 7

ID 023419 standard; DNA: 912 BP.
AC 022419; 17-AUG-1992 (first entry)
DE Human heavy chain V region gene VH49.8.
KW Heavy chain; variable region; VH1 family; ss.
OS Homo sapiens.
FH Key
FT exon Location/Qualifiers
FT /*tag- a 1..286
FT Intron 287..373
FT /*tag- b
FT exon 373..812
FT /*tag- c

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FT CDS 241..689
FT /*tag- d
FT misc_recomb 678..686
FT /*tag- e
FT /note- "recombination signal"
FT misc_recomb 709..718
FT /*tag- f
FT /note- "recombination signal"
FT PN
FT WO320318-A.
FT 19-MAR-1992: U06185.
FT 28-AUG-1991: US-574748.
FT 29-AUG-1990: US-574748.
FT 31-AUG-1990: US-575963.
FT (GENP-) GENPHARM INT INC.
FT PA
FT Lomborg N, Kay R;
FT WPI: 92-113962/14.
FT DR
FT P-PSDB: R22358.
PT Immunoglobulin trans:genes - for prodn. of heterologous
PT non-rearranged and/or rearranged ig chains
PS Example 14: Page 87; 172pp; English.
CC The human placental genomic DNA library cloned into the phage
CC vector lambda fix II was screened with the human VH1 family
CC specific oligonucleotide (see Q22418). Phage clone lambda
CC 49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable
CC segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
CC An 800 bp region of this insert was sequenced. VH49.8 was found
CC to have an open reading frame and intact splicing and recombination
CC signals, thus indicating that the gene is functional.
SQ Sequence 812 BP; 204 A; 189 C; 222 G; 197 T;

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Query Match 59.0%; Score 223; DB 3; Length 812;

Best Local Similarity 88.3%; Pred. No. 9,29e-137;

Matches 257; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Db 385 aggtccagctgtgcaagctctgaggtgagtggaagagcctggtcctggaaggtct 444
QY 2 AGGTCCAGCTGCTGCAAGCTCTGAGTGTGAGTGAAGAAAGCTGGTCTTCGGTAAAGTCT 61
Db 445 ccttcaaggtcttgaagagccttcagcagctatgctatcagctggtgagcaagccc 504
QY 62 CCTGCAAGGCTCTGAGGAGCTTCAGAACTCAATTTCAATTGGCTCGACAGGCC 121
Db 505 ctggacaaggtctgagtgatggaagagatcaccatccctatccttgatagcaactacg 564
QY 122 CTGGACAAGGCTTGTAGTGGATGGAGGCATCATCCCTATGTTGGAAACGCAAACTACG 181
Db 565 cacaagaagttccagagcagagatcagatcaccgagacaatccacagagacagactaca 624
QY 182 CACAGAAGTTTCAGGAGAGTTCACAAATTACCCGCGAGCAATCCAGCCACAGGCTACA 241
Db 625 tggagctgagcagctgagatcctgagagcaagccgtgtattactgagca 675
QY 242 TGGAGCTGAGCAGTCTGAGATCTGACAGACAGCGCCGTTATTACTGTGCGA 292

```

RESULT 8

ID 029767 standard; cDNA: 325 BP.
AC 029767; 18-MAR-1993 (first entry)
DE Gene for Hb region of human rheumatoid factor antibody.
KW Heavy chain; variable region; YES8C; arthritis; ss.
OS Homo sapiens.
FH Key
FT CDS Location/Qualifiers
FT /*tag- a 7..19
FT /*tag- b
FT /note- "leader sequence"
FT misc_feature 93..105
FT /*tag- c
FT /note- "encodes CDR1"
FT misc_feature 150..198

PR 22-SEP-1994: U10756.
 PR 22-SEP-1993: US-124469.
 PA (NICH-) NICHOLS INST DIAGNOSTICS.
 PI McLachlan SM. Rapoport B:
 DR WPI: 95-139383/18.
 DR P-PSDB: R72070.
 PT Graves' ophthalmopathy-associated monoclonal antibody - produced
 PT by molecular cloning of immunoglobulin genes by PCR
 PS Claim 25: Page 68: 94pp: English.
 CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 13/15 clones of H chain (IgG1) genes
 CC showed homology to the closest germline genes, DP10 (Q88327) and
 CC hvi163 (Q89328). The DNA (Q89328) and correspons. amino acid
 CC (R72070) sequences of the VH region of a representative clone,
 CC OFH1.2, are provided.
 SQ Sequence 294 BP: 72 A: 68 C: 91 G: 63 T:

Query Match 52.6%, Score 199, DB 14, Length 294:

Best Local Similarity 84.2%, Pred. No. 1,256,119:

Matches 245: Conservative 0, Mismatches 46, Indels 0, Gaps 0:

Db 2 agtgaagatcgtcagatcgtcagaggtgaggtgaaagccctggtcctcgtgaggtct 61
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 QY 2 AGGTGAGCTGCTCGACGCTCGCTCGCTCGAGCTGAGAGCCCTGGGCTCGCTGAGAGTCT 61
 Db 62 cctgcaaggctcctggaagaccctcaataatcctatcctcgtggtgcaactgccc 121
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 62 CCTGCAGGCGCTCTGAGAGCCCTCAAGAGCTCAAGATTTCATTTGGGTGCGAGAGGCC 121
 Db 122 cggagcaaggactgagtgagtgaggaagatcctcctcctcgtgtaagcaactcag 181
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 122 CTGGAGAAAGCTCTTGAATGATGATGAGAGGATATCCCTATGTCGAGACAGCAAACTACG 181
 Db 182 taacagaagttcagtgatgagatcagattaccgtgataaatccagaggaagactaca 241
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 QY 182 CACAGCAAGCTTACAGGAGCTGAGAGCTCAAGATTACCCGCGCAACAACTCCAGCCCTACA 241
 Db 242 tggagctgagcagagctgagatcctaggaagagagccctctctctctctcag 292
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 242 TGGAGCTTACAGAGCTTGAAGATCTGAAGACAGCGGCGGTTATTAATGTGCGA 292

RESULT 13

ID 055662: standard; cDNA: 378 BP.

AC 055662: 22-JUL-1994 (first entry)
 DE Monoclonal antibody GP44 heavy chain (V H 1) coding sequence.
 KW HIV: Human Immunodeficiency Virus; gp120; glycoprotein;
 KM envelope protein; monoclonal antibody, Mab, vaccine, therapy, ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc-feature 91 105
 FT /*tag- a
 FT /*note- "Encodes CDR 1."
 FT misc-feature 148..198
 FT /*tag- b
 FT /*note- "Encodes CDR 2."
 FT misc-feature 295..336
 FT /*tag- c
 FT /*note- "Encodes CDR 3."
 FT misc-feature 337..378
 FT /*tag- d
 FT /*note- "Framework IV, JH4 segment."
 PN EP-58133-A.
 PD 02-FEB-1994.
 PR 05-JUL-1993: 201959.
 PR 03-JUL-1992: FF-202032.
 PA (NEM-) NEDERLANDEN, MIN WELZIJN.
 PI Osterhaus ADME:
 DR WPI: 94-036603/05.
 DR P-PSDB: R45605.
 PT Monoclonal antibodies to HIV-1 - directed against glycoprotein

PT gp120, useful for passive immunotherapy or prodn of
 PT anti-idiotypic vaccines
 PS Claim 11: Page 21-22: 34pp: English.
 CC The monoclonal antibodies (Mab's) designated GP13, GP44 and GP68
 CC react with HIV-1 gp120 glycoprotein variants containing the amine
 CC acids Asn88, Lys117, Asn252 and Tyr 435 but exhibit at least 50%
 CC reduced reaction with gp120 variants in which these amino acids
 CC have been deleted or substituted. The Mab's are useful for passive
 CC immunotherapy and their anti-idiotypic antibodies can be used in the
 CC production of vaccines.
 SQ Sequence 378 BP: 93 A: 93 C: 112 G: 80 T:

Query Match 51.9%, Score 196, DB 9, Length 378:

Best Local Similarity 77.2%, Pred No 1,726,117:

Matches 292: Conservative 0, Mismatches 94, Indels 2, Gaps 2:

Db 2 agtgaagctggtcagatcgtcagatcgtgaggaagaccctgagcctcagtgaaatt 61
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 QY 2 AGGTGAGCTGCTCGACGCTCGCTCGCTCGAGCTGAGAGCCCTGGGCTCGCTGAGAGTCT 61
 Db 62 cctgcaaggctcctggaagaccctcaccacctctatacactggtgtgtgtgtgtgtgt 121
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 QY 62 CCTGCAGGCGCTCTGAGAGCCCTCAAGAGCTCAAGATTTCATTTGGGTGCGAGAGGCC 121
 Db 122 cggagcaaggactgagtgagtgaggaagatcctcctcctcgtgtaagcaactcag 181
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 QY 122 CTGGAGAAAGCTCTTGAATGATGATGAGAGGATATCCCTATGTCGAGACAGCAAACTACG 181
 Db 182 caacaaacttccagagcagagatcagatcagaccagaggaagctccagagagacttaca 241
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 QY 182 CACAGCAAGCTTACAGGAGCTGAGAGCTCAAGATTACCCGCGCAACAACTCCAGCCCTACA 241
 Db 242 tggagctgagcagagctgagatcctaggaagagagccctctctctctcag 301
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 QY 242 TGGAGCTTACAGAGCTTGAAGATCTGAAGACAGCGGCGGTTATTAATGTGCGA 300
 Db 302 gccaatgttatttacttcttgaagagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
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 QY 302 CCAAAACATTCAGATCGTGGAGAGTGTGGGAGTGTGGGAGTGTGGGAGTGTGGGAGT 360
 Db 361 cgtggtcagcgttccctca 378
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 QY 361 CTGCTCACCGCTGCTTCA 378

RESULT 14

ID T15202: standard; cDNA: 687 BP.

AC T15202: 23-OCT-1996 (first entry)
 DE PC3A933 anti-tetanus toxoid Ig heavy chain variable domain cDNA.
 KW Complementarity determining region; light; heavy chain; PCR;
 KM Polymerase chain reaction; antibody library; diversity; affinity;
 KW immunospecificity; ss.
 OS Synthetic.
 PN WO9607754-A1.
 PD 14-MAR-1996.
 PR 01-SEP-1995: U11235.
 PR 02-SEP-1994: US-500386.
 PA (SCRI) SCRIPPS RES INST.
 PI Bairdas CF, Burton DR, Lerner RA:
 DR WPI: 96-171625/17
 PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
 PT gene CDR - useful for prodn. of Ig heavy and light chain
 PT combinatorial antibody libraries
 PS Example 1: Page 83: 125pp: English.
 CC T15202 and T15203 are the heavy and light chain variable domains of
 CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a comb3
 CC based expression vector. The heavy and light chain variable domains
 CC are used in an example to demonstrate the prodn. of antibodies for
 CC an antibody library using mutagenic primers. Mutagenic primers of the
 CC invention have sequences at their 3' and 5' ends both capable of
 CC binding different framework regions linked by a sequence 5 to 50

CC nucleotides long. Different immunoglobulins produced using the
 CC primers may be used to produce antibody libraries having diverse and
 CC novel immunospecificities and affinities. By using mutagenic ONS an
 CC extremely large population of different randomised binding sites can
 CC be created and use of the universal light chain increases the number
 CC of combinations which yield functional heterodimeric antibodies.
 SQ Sequence 687 BP; 155 A; 211 C; 195 G; 126 T;

Query Match 51.9%; Score 196; DB 22; Length 687;
 Best Local Similarity 85.5%; Pred. No. 1.72e-117;
 Matches 236; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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 QY 17 AGCTGGGCTCTGAGGTGAGAGAGCCTGGGTTTGGTGAAGGTTCTCTGAGAGGCTCTG 76
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 Db 68 gaggcaccttaacaatattgccatcagctggtgacagagcccttgacaagagcttg 127
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 QY 257 TGAGATCTGAGAGACAGCGCCCTTTATTACTGTGCGA 292

RESULT 15
 ID 092546 standard; DNA: 4691 BP.
 AC 092546;
 DT 11-MAR-1996 (first entry)
 DE pComb3 expression vector.
 KW pComb3; phagemid expression vector; bacteriophage; coat protein 3;
 KW Gene III; filamentous phage; minor phage coat protein; cpIII; cp3;
 KW bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120;
 KW combinatorial Fab library; cassette; Fd/cp3; lacZ promoter/operator;
 KW ribosome binding site; RBS; PelB leader; spacer; tether sequence;
 KW MT4; pMT4-3; antibody; ss; cyclic.
 OS Synthetic.
 PN MO9511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994; U11907.
 PR 19-OCT-1993; US-139409.
 PR 26-APR-1994; US-233619.
 PR 19-SEP-1994; US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT Immunodeficiency virus - used for diagnosis and Immunotherapy of
 PT HIV-induced disease
 PS Example 1; Page 185-188; 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
 CC the 406 residue minor phage coat protein, cpIII (cp3), which is expressed
 CC prior to extrusion in the phage assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector was designed for the cloning
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, Fd/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked, 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a

CC PelB leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cpI followed by a stop codon, a NotI restriction site
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a PelB leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the MT4 Fab display phagemid expression vector, pMT4-3 (see also
 CC 092540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 SQ Sequence 4691 BP; 1170 A; 1171 C; 1232 G; 1118 T;

Query Match 51.9%; Score 196; DB 16; Length 4691;
 Best Local Similarity 85.5%; Pred. No. 1.72e-117;
 Matches 236; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Search completed: Tue Feb 24 13:18:47 1998
 Job time : 105 secs.

JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
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Db 419 cgtcacccctcctca 435
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 QY 362 TGGTCAACGCTGCTTCA 378

RESULT 6
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 DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 202-G8).
 ACCESSION Z47260
 NID 9619471
 KEYWORDS immunoglobulin; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Lebecque, S.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
 Schering-Plough, Laboratory for Immunological Research, 27, Chemin
 des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
 2 (bases 1 to 522)
 REFERENCE
 AUTHORS Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jeffers, R.,
 Banchereau, J. and Lebecque, S.
 TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
 express unmutated immunoglobulin genes with intrachain heavy chain
 isotype variability
 JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
 MEDLINE 95220422
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BASE COUNT 99 a 141 c 177 g 105 t
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Query Match 65.3%; Score 247; DB 87; Length 522;
 Best Local Similarity 82.8%; Pred. No. 1,41e-193;
 Matches 312; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Db 59 aggtcagctggtcagctcgtgagctgaagcctcgtgctcgtgagctc 118
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 Db 119 cctgcaagctctcgtgagcaccctcagcagctatcgtcctcgtgagcagcc 178
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 QY 62 CCTGCAAGGCTCTGAGGACCTTCAGAGCTACATTTCATTGGGTGCGACAGGCC 121
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 Db 179 ctgcaagagggcttgagtgatgagagagatcaccctcctcctcttggtacagcaactacg 238
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Db 419 cgtcacccctcctca 435
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RESULT 7
 LOCUS HUMIGH3AE 475 bp mRNA PRI 03-MAY-1996
 DEFINITION Human (clone MAB57) Ig H-chain (IGH) mRNA, partial cds, VH-1
 subgroup.
 ACCESSION L08086
 NID 91294809
 KEYWORDS V-region; immunoglobulin heavy chain; variable region subgroup
 VH-1.
 SOURCE Homo sapiens cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Ikematsu, H., Harindranath, N., Tekl, Y., Nozkins, A. I. and Casali, P.
 TITLE Clonal analysis of a human antibody response. II. Sequences of the
 VH genes of human IgM, IgG, and IgA to rabies virus reveal
 hypermutational utilization of VHII segments and somatic
 hypermutation
 JOURNAL J. Immunol. 150 (4), 1325-1337 (1993)
 MEDLINE 9316357
 REFERENCE
 AUTHORS Ikematsu, H.
 TITLE Direct Submission
 JOURNAL Submitted (18-FEB-1993) Hideyuki Ikematsu, Department of General
 Medicine, Kyushu University Hospital, Kyushu University, Fukuoka,
 812 Japan

FEATURES Location/Qualifiers
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0y	62 CCTGAGAGGCCCTCTGAGACGACAGCTTCAAAAGGTACAAATTTTCAATTTGGGTGGAGAGGCC 121	
Db	179 ctggaacaagggtctgaatggaatgggaagatcatccctctcttgatcaagcaactacg 238	
0y	122 CTGGACAAAGGCTTTAGTGTGATGGAGAGCATCATCTCATGTTCGGAACAGCAAACTACG 181	
Db	239 cacagaagttcccaaggcagagatcacgattlaccgcgagcaagaaaccacaagcaacagctaca 298	
0y	182 CACAGAAAGTTTCA35GCGAGTCAACAATTAACGGCGAGAAATCCAGGCCCAAGAGCTTCA 241	
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0y	302 CAAAACATTGCGTGTGTGAAGTTGCTTGAGGCGTGGTTTGACCCCTCGGGGCCAAGGAATC 361	
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0y	362 TGGTCAACCGTGTCTTCA 378	

LOCUS	RESULT	10
DEFINITION	HS203M5	483 bp RNA
ACCESSION	H.sapiens mRNA for immunoglobulin variable region (clone 203-M5).	PRI 03-AUG-1995
NID	Z47272	
KEYWORDS	g619483	
SOURCE	immunoglobulin: variable region.	
ORGANISM	human.	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	
TITLE	Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
JOURNAL	1 (bases 1 to 483)	
REFERENCE	Lebecque, S.	
AUTHORS	Direct Submission	
TITLE	Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,	
JOURNAL	Scherling-Plough, Laboratory for Immunological Research, 27, Chemin	
REFERENCE	des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE	
AUTHORS	2 (bases 1 to 483)	
TITLE	Gabbert, L., Van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,	
JOURNAL	Banchereau, J. and Lebecque, S.	
REFERENCE	Anti-CD40 plus interleukin-4-activated human naive B cell lines	
AUTHORS	express unmutated immunoglobulin genes with interactional heavy chain	
TITLE	isotype variability	
JOURNAL	Eur. J. Immunol. 25 (3), 733-737 (1995)	
FEATURES	95220422	
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Best Local Similarity 98.9%   P-Id No. 6,882-190;
Matches 319; Conservative 0; Mismatches 58; Indels 3; Gaps 3

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Qy	242	tggagagctgaacacatctgacacatttgaagacacagagccgcttttttactgttgsgaat-gccctat	300
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Qy	301	ccaaacacattgcagctgtgtgaagatttgc-tggag-cttgcttggagcccttggagcttggagaa	358
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LOCUS       HS203E7             510 bp            RNA
DEFINITION  H sapiens mRNA for immunoglobulin variable region (clone 203-E7).
ACCESSION   H247266
KEYWORDS    9619477
SOURCE      immunoglobulin; variable region.
            human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Carnivora; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 510)
AUTHORS     Lebecque,S.
TITLE       Direct Submission
JOURNAL     Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
            Schering-Plough, Laboratory for Immunological Research, 27, Chemin
            des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69592, FRANCE
REFERENCE   2 (bases 1 to 510)
AUTHORS     Galibert,L., van Dooren,J.J., Durand,I., Rousset,F., Jefferis,R.,
            Barchetead,J. and Lebecque,S.
TITLE       Anti-CD40 plus interleukin-4-activated human naive B cell lines
            express unmutated immunoglobulin genes with intracellular heavy chain
            isotype variability
JOURNAL     Eur. J. Immunol. 25 (3), 733-737 (1995)
FEATURES
MEDLINE
FEATURES
SOURCE      Location/Qualifiers
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NID        9619478
KEYWORDS
SOURCE     Immunoglobulin: variable region.
ORGANISM   human.
REFERENCE  Homo sapiens
            Eukaryotic, mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS    1 (bases 1 to 510)
            Lebecque,S.
TITLE      Direct Submission
REFERENCE  Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
            Schering-Plough, Laboratory for Immunological Research, 27, Chemin
            des Peupliers, B P 11 CEDEX, Dardilly, Phone, 69572, FRANCE
AUTHORS    2 (bases 1 to 510)
            Galibert,L., van Dooren,J., Durand,J., Roussel,F., Jefferts,R.,
            Bancheureau,J. and Lebecque,S.
TITLE      Anti-CD40 plus interleukin-4-activated human naive B cell lines
            express unmutated immunoglobulin genes with intracellular heavy chain
            isotype variability
            Eur. J. Immunol. 25 (3), 733-737 (1995)
FEATURES   95220422
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BASE COUNT 105 a      142 c      155 g      108 t
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RESULT	13
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NID	9619475
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SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Ekayotocae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Carnivora; Homiidae; Homo.
TITLE	1 (bases 1 to 510)
AUTHORS	Lebecque,S
TITLE	Direct Submission
JOURNAL	Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology, Scheering-plough, laboratory for Immunological Research, 27, Chemin des Penilliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE	2 (bases 1 to 510)
AUTHORS	Galbrier,L., van Dooren,J., Durand,I., Foussat,F., Joffe,S.R., Bancherreau,J. and Lebecque,S.
TITLE	Anti-CD40 plus interleukin-4 activated human naive B cell lines express unmutated immunoglobulin genes with intrachain heavy chain isotype variability
JOURNAL	Eur J Immunol 25 (3), 733-737 (1995)
MEDLINE	95220422
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Best Local Similarity 83.9%:					Prod No 6 R2e-140;
Matches 319; Conservative					0; Mismatches 58; Indels 3; Gaps 4;
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Db	179	ctcggacaaagggtctgaatgagatggagaggatcatccctacatcttctgttacacagcaactacg	238		
Qy	122	CTGGACAAAGCTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	181		
Db	239	cacagaagttccagagcaagctacagatctcccgagcaatctccagagcaacagacagcttaca	298		
Qy	182	CACAGAAGCTTTCAGAGCAAGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	241		
Db	299	tggagctggagcagcctggagatctgaagagcacagcagcagctgtatcgttgaggagagggagag	358		
Qy	242	TGGAGTGGAGTATCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	300		
Db	359	ctaaagtcgaatttctggagagatctcagctcagctcagctcagctcagctcagctcagctcagctcag	418		
Qy	301	CTAAAGTCAATTCTGGAGAGATCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG	358		
Db	419	ccctggtccagcagctctctctcca	438		

Release 2.0 John F. Collins, Biocomputing Research Unit
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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

```
Run on: Tue Feb 24 12:51:02 1998; MASPAr time 125.47 Seconds
760.063 Will be updated
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Tabular output not generated.

Title:	Description	Perfect Score:
>US-08-844-215-26 (1:378) from US08844215 seq	1 GAAGTGCACCTGCTGGAGTC CTCCACGCTGGACGACGTGAG	378

Scoring table: TABLE default

62

```

Nimatchn  STD :  Dbase 0;  Query 0

```

[illegible]

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: STS

1: STS1 2: STS2 3: STS3 4: STS4 5: STS5 6: STS6 7: STS7 8: STS8
9: STS9 10: STS10 11: STS11 12: STS12 13: STS13 14: STS14
15: enEST2 16: enEST3 17: enEST4 18: enEST5 19: enEST1
20: enEST2 21: enEST8 22: enEST9 23: enEST10 24: enEST11
25: enEST12 26: enEST13 27: enEST14 28: enEST15 29: enEST16
30: enEST17 31: enEST18 32: enEST19 33: enEST20 34: enEST21
35: enEST22 36: enEST23 37: enEST24 38: enEST25 39: enEST26
40: enEST27 41: enEST28 42: enEST29 43: enEST30 44: enEST31
45: enEST32 46: enEST1 47: enEST2 48: enEST3 49: enEST4
50: enEST5 51: enEST6 52: enEST7 53: enEST8 54: enEST9
55: enEST10 56: enEST11 57: enEST12 58: enEST13 59: enEST14
60: enEST15 61: enEST16 62: enEST17 63: enEST18 64: enEST19
65: enEST20 66: enEST21 67: enEST22 68: enEST23 69: enEST24
70: enEST25 71: enEST26 72: enEST27 73: enEST28 74: enEST29
75: enEST30 76: enEST31 77: enEST32 78: enEST33 79: enEST34
80: enEST35 81: enEST36 82: enEST37 83: enEST38 84: enEST39
85: enEST40 86: enEST41 87: enEST42 88: enEST43 89: enEST44
90: enEST45 91: enEST46 92: enEST47 93: enEST48 94: enEST5
95: enEST1 96: enEST2

Statistics: Mean 10.030; Variance 1.934; scale 5.186

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	47	12.4	511	17	AA64794	zx83h07.r1	Soares ova	4.21e-45
2	47	12.4	511	63	HS1259634	zx83h07.r1	Soares ova	4.21e-45

C	3	43	11.4	435.80	AS07475	HS12605.s1	NC1_CGAP_B	4.71e-38
C	4	43	11.4	435.40	AS07475	h756c05.s1	NC1_CGAP_B	4.71e-38
C	5	37	9.8	266.54	AS1002338	h756c05.s1	NC1_CGAP_B	4.71e-38
C	6	36	9.5	262.54	AS1002338	z478c07.r1	Soares_Cv3	5.54e-28
C	7	36	9.5	252.69	HS1297932	h957b11.s1	NC1_CGAP_L	3.77e-28
C	8	34	9.0	597.83	MM1263658	h957b11.s1	NC1_CGAP_L	3.77e-28
C	9	34	9.0	597.24	AA122093	h108c05.r1	Soares mod	5.45e-23
C	10	33	8.7	230.57	HS1227079	h108c05.r1	Soares mod	5.45e-23
C	11	22	5.8	400.10	G31619	z478b02.r1	Soares_Cv3	1.83e-05
C	12	21	5.6	264.5	G13690	human STS SHGC-225175	Soares_Cv3	1.83e-05
C	13	21	5.6	335.75	HS1333	human STS SHGC-11910	Soares_Cv3	3.16e-04
C	14	21	5.6	515.15	AA461207	EST105623	Homo sapiens	3.16e-04
C	15	21	5.6	516.15	HS126187	z478b07.s1	Soares tot	3.16e-04
C	16	21	5.5	516.63	HS126187	z478b07.s1	Soares tot	3.16e-04
C	17	21	5.5	536.57	HS126187	z478b07.s1	Soares tot	3.16e-04
C	18	21	5.6	586.87	MM1304724	h613c05.r1	Soares mod	3.16e-04
C	19	21	5.3	586.35	AA511100	h613c05.r1	Soares mod	3.16e-04
C	20	20	5.3	207.81	MM1222221	v558b06.r1	Beddington	4.88e-03
C	21	20	5.3	228.69	HS1300441	a653c01.r1	NC1_CGAP_G	4.88e-03
C	22	20	5.3	328.35	AA505094	a653c01.r1	NC1_CGAP_G	4.88e-03
C	23	20	5.3	331.46	AA504845	z478c07.r1	NC1_CGAP_G	4.88e-03
C	24	20	5.3	337.8	G25003	z478c07.r1	NC1_CGAP_G	4.88e-03
C	25	20	5.3	397.9	G37866	human STS FC7274715	Soares tot	4.88e-03
C	26	20	5.3	415.68	HS1200498	human STS FC7274715	Soares tot	4.88e-03
C	27	20	5.3	415.37	AA4934472	h554c02.s1	NC1_CGAP_L	4.88e-03
C	28	20	5.3	418.9	HS1237168	h554c02.s1	NC1_CGAP_L	4.88e-03
C	29	20	5.3	420.66	HS1276219	z172c02.r1	Soares NhH	4.88e-03
C	30	20	5.3	446.61	HS1280075	z172c02.r1	Soares NhH	4.88e-03
C	31	20	5.3	514.78	HS1280075	z172c02.r1	Soares tot	4.88e-03
C	32	20	5.3	589.15	AA461335	z478b06.r1	Soares tot	4.88e-03
C	33	20	5.3	589.15	AA461335	z478b06.r1	Soares tot	4.88e-03
C	34	20	5.3	589.15	AA461335	z478b06.r1	Soares tot	4.88e-03
C	35	19	5.0	189.15	AA458884	z478b06.r1	Soares tot	4.88e-03
C	36	19	5.0	383.21	AA279076	z478b06.r1	Soares tot	4.88e-03
C	37	19	5.0	407.93	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	38	19	5.0	407.18	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	39	19	5.0	407.18	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	40	19	5.0	407.18	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	41	19	5.0	537.93	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	42	19	5.0	537.93	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	43	19	5.0	537.93	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	44	19	5.0	537.93	TCGMC106	z478b06.r1	Soares tot	4.88e-03
C	45	19	5.0	537.93	TCGMC106	z478b06.r1	Soares tot	4.88e-03

ALIGNMENTS

RESULT	1				
LOCUS	AA664794	511 bp	MRNA	EST	10-JUN-1997
DEFINITION	z883607.r1 Soares ovary tumor NBH1 Homo sapiens cDNA clone 810397				
DESCRIPTION	5' similar to gb:121564 IG HEAVY CHAIN V-I I REGION (JHMAN)...				

ACCESSION	AA464/94
NID	92189678
KEYWORDS	EST.

SOURCE	ORGANISM
human.	human.
Homo sapiens	Homo sapiens
Eukaryotes; mitochondrion	eukaryotes; Mitochondria
Eukaryotes; Mitochondria	Eukaryotes; Mitochondria
Vertebrata; Mammalia	Vertebrata; Mammalia
Eutheria	Eutheria
Primates	Primates
Catarrhini	Catarrhini
Hominidae	Hominidae
Homo.	Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 511)	Hillier, L., Allen, M., Rowles, I., Publique, T., Catal, G., Jon, S., Kicab, T., Lacy, M., Le, N., Lenton, G., Maria, F., Martin, J., Moore, B., Schellenberg, K., Stephens, M., Tan, F., Theising, B., White, Y., Wyle, T., Waterston, P. and Wilson, P.	Washu-Merck EST Project 1997		Unpublished (1997)

WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Contact: Pichard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 415/7259687
 Fax: 415/7259689
 Email: myerseshgc.stanford.edu

Primer A: TGCCCTCGAGTGTCCAC
 Primer B: AGCCTCCAGACAGTGTACGSA
 STS size: 167
 PCR Profile:
 Initial incubation: 94 degrees C for 90 seconds
 Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600
 Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Tag Polymerase: 0.05 units/uL
 Total Vol: 10 uL

Buffer:
 MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

Plasmid subclones, generated from flow-sorted chromosome 4 (Human Genome Center, Los Alamos National Laboratory), constructed and sequenced at the Stanford Human Genome Center.
 Location/Qualifiers
 1..400
 /organism="Homo sapiens"
 /map="4"
 STS
 primer_bind
 primer_bind
 complement(236..255)
 BASE COUNT 82 a 101 c 115 g 82 t 20 others

ORIGIN
 Query Match 5.8%; Score 22; DB 10; Length 400;
 Best Local Similarity 75.2%; Pred. No. 1,876-75;
 Matches 32; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 69 gccacgtcacacagagagcttgcctgcgaatttcacagca 110
 ||||| | ||||| ||||| | ||||| ||||| |||||
 Cp 252 GCTCAGCCTCAGSAGACTGATGTTGACATTGTTCACGCA 211

RESULT 12
 LOCUS G13630 264 bp DNA STS 04-JAN-1996
 DEFINITION human STS SHGC-11910.
 ACCESSION G13630
 NID 91129369
 KEYWORDS STS sequence; primer: sequence tagged site.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
 Tetrapoda; Amniota; Mammalia; Theria, Eutheria, Archonta; Primates;
 Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 264)
 Myers, R.M.
 Unpublished (1995)

REFERENCE
 AUTHORS
 JOURNAL
 COMMENT
 Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine

Page 7

CC Research 932 Clopper Road, Catthetersburg, MD 20878 Tel. 3018693056

Query Match	5.68
-------------	------

Query Match	5.6%	Score 21:	DB 15:	Length 515
Best Local Similarity	83.9%	Pred. No.	3.16e-04:	

Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 53 ctgttgccttgacttcttaagaagatgaag 83
 ||| ||||| ||||| ||||| ||||| |||||
 Cp 234 CTGGTCTTGACTTGCTTACAGACATGAAG 204

RESULT 15

ID HS1256187 standard; RNA; EST; 516 BP.

AC AA461207;

NI 92186327

DT 13-JUN-1997 (Rel. 52, Created)

DT 13-JUN-1997 (Rel. 52, Last updated, Version 1)

DE ZX70H07.s1 Soares total fetus NB2HF8 9w Homo sapiens cDNA clone

DE 796861 3' similar to gb:X04217 PORPHOBILINOGEN DEAMINASE (HUMAN);.

KW EST.

OS Homo sapiens (human)

OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN 111

RP 1516

RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,

RA Kucaba T., Lacy M., Le N., Lennon G., Maria M., Martin J.,

RA Moore B., Scheinberg K., Steptoe M., Tan F., Theising B.,

RA White Y., Wylie T., Waterston P., Wilson R.;

RT "Washu-Merck EST Project 1997";

RL unpublished

CC Contact: Wilson RK Washu-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@watsn.wustl.edu This clone is available royalty-free through

CC LNL; contact the IMAGE Consortium (info@image.llnl.gov) for

CC further information. Seq primer: -41m3 fwd. Et from Amersham High

CC quality sequence stop: 316.

FH Key

FT source

FT 1..516

FT /organism="Homo sapiens"

FT /note="Vector: pT73D-Pac (Pharmacia) with a modified

FT polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

FT was prepared from mRNA obtained from pooled 8-9 week

FT (total) fetus material with a Not I-oligo(dT) primer [5'

FT TGTTCACATCTGAGTGGAGCGCGCTTAATTTTCTTTT 3'].

FT Double-stranded cDNA was ligated to Eco RI adaptors

FT (Pharmacia), digested with Not I and cloned into the Not I

FT and Eco RI sites of the modified pT73 vector. Library wen

FT t

FT through one round of normalization, and was constructed by

FT Bento Soares and M. Fatima Bonaldo.

FT /clone="796861"

FT /clone_lib="Soares total fetus NB2HF8 9w"

FT /dev_stage="8-9 weeks"

FT /lab_host="DH10B"

FT /lab_host="DH10B"

FT complement(<1 >516)

FT mRNA

FT Sequence 516 BP; 119 A; 132 C; 141 G; 124 T; 0 other,

SO

Query Match 5.68; Score 21; DB 63; Length 516;

Best Local Similarity 83 94; Prnd. No 3 16e-04;

Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 53 ctgttgccttgacttcttaagaagatgaag 83

||| ||||| ||||| ||||| ||||| |||||

Cp 234 CTGGTCTTGACTTGCTTACAGACATGAAG 204

Search completed: Tue Feb 24 12:58:36 1998

Job time : 454 secs.

KEYWORDS EST.
SOURCE human primer-M13 Reverse Library-Human Testis.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, P.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.P.S., Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M., Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Wiley, R., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, F., Dink, D., Feng, P., Fertile, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, G.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Venter, J.C.
The Institute for Genomic Research
932 Clippert Rd. Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

FEATURES
source location/Qualifiers
1..299
/organism="Homo sapiens"
BASE COUNT
61 a 84 c 82 g 68 t 4 others
ORIGIN

Query Match 35.2% Score 133; DB 58; Length 299;
Best Local Similarity 84.4%; Pred. No. 1,58e-218;
Matches 178; Conservative 0; Mismatches 30; Indels 3; Gaps 2;

Db 80 aggcagacgtccagagatcgccagagactggtgaagccttcgagaccctccctca 139
|||
QY 2 AGGTGCAGCTCTCGATCGGCGCCAGAGACTGCTGAAGCTTGGGACCTCTCCCTCA 61
|||
Db 140 cctgcactgtctcgtgctcctccatcagtagt--t-actactgagactgagtcggcagc 196
|||
QY 62 CCTGCACGTCTCTGCTGCTGCTCATCAGAGCAGCTCAGTGTGAGTGGTCCGCCAGC 121
|||
Db 197 ccccaagagagagagacagtgatggtatgatactcattcagtgagacacccactaca 256
|||
QY 122 CCCAGGAGGAGGAGGAGTGTGAGAGAGCTTTTGTAGTGAAGACCATCTACA 181
|||
Db 257 acccttccctcaagacagtcagtcacatc 287
|||
QY 182 ACCCATCTCTTAACATGATCGAGTCTCATGTC 212
|||

RESULT 4
LOCUS 127715 331 bp mRNA EST 06-SEP-1995
DEFINITION EST13381 Homo sapiens cDNA 5' end similar to immunoglobulin gamma heavy chain V region (GB:M97921) (HT:3789).
ACCESSION 127715
NID 4509813
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens

REFERENCE
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, P.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.P.S., Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M., Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Wiley, R., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, F., Dink, D., Feng, P., Fertile, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, G.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Venter, J.C.
The Institute for Genomic Research
932 Clippert Rd. Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

FEATURES
source location/Qualifiers
1..331
/organism="Homo sapiens"
BASE COUNT
62 a 90 c 91 g 80 t 8 others
ORIGIN

Query Match 33.9% Score 128; DB 58; Length 331;
Best Local Similarity 77.7%; Pred. No. 5,80e-208;
Matches 192; Conservative 0; Mismatches 52; Indels 3; Gaps 3;

Db 81 aggcagacgtccagagatcgccagagactggtgaagccttcgagaccctccctca 140
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QY 2 AGGTGCAGCTCTCGATCGGCGCCAGAGACTGCTGAAGCTTGGGACCTCTCCCTCA 61
|||
Db 141 cctgcactgtctcgtgctcctccatcagtagt--t-actactgagactgagtcggcagc 200
|||
QY 62 CCTGCACGTCTCTGCTGCTGCTCATCAGAGCAGCTCAGTGTGAGTGGTCCGCCAGC 118
|||
Db 201 aggcagagagagagagacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 260
|||
QY 119 AGCCGCCAGGAGGAGGAGTGTGAGAGAGCTTTTGTAGTGAAGACCATCTACA 178
|||
Db 261 acacccctccagagagacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 320
|||
QY 179 ACAACGCTATCTCTTAACATGATCGAGTCTCATGTC 239
|||
Db 321 cccctgag 327
|||
QY 239 CCTGAG 245
|||

RESULT 5
LOCUS HS053085 346 bp mRNA EST 18-APR-1996
DEFINITION Human clone 7/24 mRNA sequence.
ACCESSION 053085

NID	91272484
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 346)
JOURNAL	Frohme, M. and Hoheisel, J.
	Direct Submission
	Submitted (29-MAR-1996) Marcus Frohme, Moleculargenetic Genome
	Analysis, German Cancer Research Center, Im Neuenheimer Feld 506,
	Heidelberg 69120, Germany
FEATURES	Location/Qualifiers
source	1..346
	/organism="Homo sapiens"
	/note="Identified by cDNA-RDA: similar to human Ig
	rearranged gamma-3 chain mRNA, GenBank Accession Number
	L01412"
	/clone="7/24"
	/tissue-type="pancreatic tumor"
BASE COUNT	65 a 113 c 98 g 67 t 3 others
ORIGIN	
Query Match	31.0%; Score 117, DB 116; Length 346.
Best Local Similarity	82.1%; Pred. No. 7.56e-185;
Matches 147:	Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Db	3 tcgcagacgccccgaaggaaaggaactgtgttgatcttcgaagcagcatgatgtggagc 62
QY	113 TCGCCAGGCCGCGCAGGAAGGAGCTGGAGTGTGAGAGACTTTTAGTGGAAGCA 172
Db	63 ccaactacaatccgtccctctaagantcgagtcaaccatcctcagttagaacagctccaagaac 122
QY	173 CCATCTTCACAAACCCTATCCCTCAACGATGCAGTCTTCATGCTGTGTAGACAAGTCGAAGGAC 212
Db	123 agctccccttgagccttgagacctgtgagccgccgtggaacagcgtgtgatttcgcgcgc 181
QY	233 AGGTCCTCCTGAGGCGCTGACGCTGTGTGACGCGCGCGGACACAGCGCGCTGTATTACTGTGCG 291
RESULT	6 HSU53086 437 bp mRNA EST 18-APR-1996
LOCUS	
DEFINITION	Human clone 8/24 mRNA sequence.
ACCESSION	U53086
NID	91272485
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 437)
JOURNAL	Frohme, M. and Hoheisel, J.
	Direct Submission
	Submitted (29-MAR-1996) Marcus Frohme, Moleculargenetic Genome
	Analysis, German Cancer Research Center, Im Neuenheimer Feld 506,
	Heidelberg 69120, Germany
FEATURES	Location/Qualifiers
source	1..437
	/organism="Homo sapiens"
	/note="Identified by cDNA-RDA: similar to human Ig gamma
	4b mRNA, GenBank Accession Number S64477"
	/clone="8/24"
	/tissue-type="pancreatic tumor"
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Best Local Similarity	78.3%; Pred. No. 6.22e-162;
Matches 144:	Conservative 0; Mismatches 38; Indels 2; Gaps 2;
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QY	113 TCGCCAGGCCGCGCAGGAAGGAG-AC TGAGATGTGATTTGAGAAGACTTTTAGTGGA-AG 170

Db 63 caccagctacgagcccccctcctaagaagtccagatcaccatcaatgcagacacgttccaaga 122
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Cy 171 CACCATTTAAACAACCATCCCTCAAGCATTGAGTGTTCATGTGTGTAGAAAGTCCAAGA 230
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Db 123 ccatttcctcgtagtgagctctgtgaacggctgcagacacgccagctctttmmnnn 182
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Cy 211 CCAGGTTCCCTGAGGCTGAGCTCTGTGACCGCGCGGAGAACAGAGATATATATGAGC 290
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Db 183 nana 186
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Cy 291 GACA 294

RESULT 7
LOCUS EST11989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, V region (GB:U12364) (Ht:3115).
DEFINITION T27730
ACCESSION g609828
NID
KEYWORDS EST.
SOURCE Human primer-MJ3 Reverse library-Human Testis.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygia; Channata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 180)
Adams,M.D., Keplavage,A.P., Frieschmann,P.N., Fuldner,P.A.,
Bull,C.J., Lee,N., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chin,M.-W.,
Clayton,F.A., Cline,R.T., Cotton,M.P., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., FitzHugh,W.M., Flitchman,J.I., Georgagen,N.S.M.,
Glodek,A., Guem,C.L., Hanna,M.C., Hedblow,E., Hinkle Jr.,P.S.,
Kellley,J.M., Klink,K.M., Kelley,J.C., Liu,L.Y., Maizuro,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.B.,
Sandek,D.M., Shirley,F., Small,K.V., Spriggs,T.A., Thierbach,T.R.,
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Fertile,A.,
Fischer,C., Hastings,G.A., He,M.-W., Hu,J.-S., Greene,J.M.,
Gruber,T., Hudson,P., Kim,A., Kozak,D.L., Kunisch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wel,Y.-F., Wang,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fanmon,M.P., Rosen,C.A.,
Raseltine,W.A., Fields,C., Friser,I.C. and Venter,J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL Unpublished (1995)

COMMENT Contact: Venter, JC
The Institute For Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

FEATURES
source Location/Qualifiers
1..180 /organism="Homo sapiens"
BASE COUNT 33 a 49 c 54 g 39 t 5 others

ORIGIN

Query Match 23.5%; Score 89; DB 58; Length 180;
Best Local Similarity 80.6%; Pred. No. 5,12e-127;

Matches 15; Conservative 0; Mismatches 30; Indels 5; Gaps 3;

Db 1 tncaggctcagagagctcgcgtcagagactgtgaagcctcanagaacctgtccctaacct 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cy 5 TGCAAGTGGCTGAATGAGAGGCAAGAACTATATTAATGTTGGTGAGAGGCTGACT 64
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NID	9661858	EST.	human cJone79452 library=Stratagene lung (#97210)
KEYWORDS	vector-BLuescript-SK+ host-SOLR cells (Kanamycin resistant)		
SOURCE	primer-M13p1 PsIpe1-EcoRI PsIpe2-XhoI Normal lung tissue from a 7 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb, Uni-ZAP XR Vector. 5' adaptor sequence: 5'-GATTCGCGCAGAG-3', 3' adaptor sequence: 5'-CTCGAGTTTCTTTTTTTTTTTT-3'.		
ORGANISM	Homo sapiens		
	Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia		
REFERENCE	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 367)		
	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,W., Hultman,M., Kucaba,T., Le-M., Lennon,G., Merra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevisks,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.		
TITLE	Washu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 243 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.		
FEATURES	Location/Qualifiers 1..367 /organism="Homo sapiens" /clone="79452"		
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Best Local Similarity	89.6%; Prid NO. 1,59e-71;		
Matches	69; Conservative 0; Mismatches 8; Indels 0; Gaps 0;		
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Db	61 tatactactgtcgaga 77		
OY	278 TGTATTACTGTGCGAGA 294		
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DEFINITION	EST894449 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, VDJ regions (GB:214165) (HT:3116).		
ACCESSION	729661		
NID	9611759		
KEYWORDS	EST.		
SOURCE	human primer-M13 Reverse library-Human Small intestine.		
ORGANISM	Homo sapiens		
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcosteyali; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 253)		
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.G., Chitt,M.W., Clayton,R.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Frichman,J.L., Georhagen,N.S.M., Glock,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klimke,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,		

TITLE
JOURNAL
COMMENT

Contact: Venter, JC
The Institute for Genomic Research
932 Colpper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tldb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tldb.tigr.org).

FEATURES
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Location/Qualifiers
1..253
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BASE COUNT
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52 a 72 c 65 g 60 t 4 others

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Best Local Similarity 70.8%; Pred. No. 2,87e-56;
Matches 114; Conservative 0; Mismatches 44; Indels 3; Gaps 2;

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QY 217 GACAAAGCCGAAGAGGACCAAGCTCCTCCACAGCCGTGGTGTGGAGCGCGCGGACACCGGC 276

Db 61 gttattactgtgcaggcgttaagaagcagcatgtg-agc--aggtagtaccttgatgct 117
QY 277 GTGATATTACTGTGCGAGATCCGCCATMAAATAAGATCATGGGAAAGATGATGTTTGATGCC 336

Db 118 tttnatatctgcggagacaagacaatgctgcacgclctctc 158
QY 337 TTGTATATCTGTGGSGGCGAGSGGACACTTCGTGTCATCTGTCCTTC 377

RESULT 12
LOCUS AA170256 823 bp mRNA EST 16-FEB-1997
DEFINITION MS87810.1 Scores mouse 3kbms Mus musculus cDNA clone 618594.5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-IT1 PEPTIDE (HUMAN); db:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the C-terminalus (MOUSE);.

ACCESSION
MIMD AA170256
KEYWORDS g1748794
SOURCE EST.
ORGANISM house mouse.
Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (Bases 1 to 823)
AUTHORS Maria M., Hillier,L., Allen,M., Bowles,N., Dietrich,P.N., Dubouque,T., Geisel,S., Kunoza,T., Lacy,M.M., Le,M., Martin,J., Morris,M., Scheinberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The Masnu-HMMI Mouse EST Project
JOURNAL Unpublished (1996)

COMMENT Contact: Maria M/Mouse EST Project
Masnu-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

WORLDWIDE
(TM)

Release 2.1D John F. Collins, BioComputing Research Unit,
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

Mpsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 15:51:53 1998: MaxPar time 23 03 Seconds

Tabular output not generated. 754.842 Million Cell Updates/sec

Title: >US-08-844-215-26

Description: (1-378) from US08844215.seq

Perfect Score: 378

N A Sequence: 1 GAGGTGCAAGTGTGCTGAGTCCACTGCTCATGCTGCTGCTTTC 378

Comp: CTGCAAGTGTGCAAGTGTGAG

Scoring table: TABLE default

Nmatch STD: Dbase 0: Query 0

Searched: 87531 seqs, 22956021 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-issund

1 back: 2 51 3 52 4 53 5 54 6 55 7 56 8 PCT90 9 PCT91

10 PCT92 11 PCT93 12 PCT94 13 PCT95 14 PCT96

Statistics: Mean 7.812: Variance 4.313: scale 1.811

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	176	46.6	402	7	US-08-468- Sequence 5, Applicatio	5.88e-111
2	176	46.6	402	7	US-08-468- Sequence 5, Applicatio	5.88e-111
3	176	46.6	420	7	US-08-478- Sequence 107, Applicat	5.88e-111
4	176	46.6	423	7	US-08-379- Sequence 19, Applicat	5.88e-111
5	176	46.6	423	7	US-08-481- Sequence 19, Applicat	5.88e-111
6	89	23.5	798	11	PCT-US93-0 Sequence 71, Applicat	2.14e-46
7	89	23.5	798	11	PCT-US93-0 Sequence 71, Applicat	2.14e-46
8	89	23.5	830	11	PCT-US93-0 Sequence 99, Applicat	2.14e-46
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10	75	19.8	402	11	PCT-US92-0 Sequence 15, Applicat	2.36e-36
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12	75	19.8	402	6	US-08-111- Sequence 15, Applicat	2.36e-36
13	75	19.8	402	7	US-08-211- Sequence 15, Applicat	2.36e-36
14	75	19.8	826	7	PCT-US93-0 Sequence 27, Applicat	2.36e-36
15	75	19.8	826	7	PCT-US93-0 Sequence 27, Applicat	2.36e-36
16	75	19.8	826	6	US-08-111- Sequence 27, Applicat	2.36e-36
17	74	19.6	357	13	PCT-US95-1 Sequence 61, Applicat	3.18e-34
18	72	19.0	357	7	US-08-467- Sequence 61, Applicat	3.18e-34
19	72	19.0	357	7	US-08-467- Sequence 61, Applicat	3.18e-34

20	70	18.5	923	7	US-08-401- Sequence 25, Applicat	8.25e-33
21	70	18.5	1289	7	US-08-401- Sequence 36, Applicat	8.25e-33
22	70	18.5	1952	7	US-08-401- Sequence 16, Applicat	8.25e-33
23	70	18.5	3664	6	US-08-148- Sequence 1, Applicat	4.18e-32
24	69	18.3	3691	2	PCT-US93-1 Sequence 37, Applicat	4.18e-32
25	69	18.3	4322	5	US-08-026- Sequence 1, Applicat	4.18e-32
26	68	18.0	363	7	US-08-275- Sequence 8, Applicat	2.12e-31
27	68	18.0	363	7	US-08-211- Sequence 19, Applicat	2.12e-31
28	68	18.0	363	11	PCT-US93-0 Sequence 19, Applicat	2.12e-31
29	68	18.0	363	6	US-08-111- Sequence 19, Applicat	2.12e-31
30	68	18.0	369	6	US-08-275- Sequence 15, Applicat	2.12e-31
31	68	18.0	369	6	US-08-122- Sequence 7, Applicat	2.12e-31
32	68	18.0	414	7	US-08-487- Sequence 32, Applicat	2.12e-31
33	68	18.0	414	7	US-08-474- Sequence 32, Applicat	2.12e-31
34	68	18.0	414	6	US-08-477- Sequence 32, Applicat	2.12e-31
35	68	18.0	414	6	US-07-634- Sequence 32, Applicat	2.12e-31
36	67	17.7	294	11	PCT-US93-1 Sequence 47, Applicat	1.07e-30
37	67	17.7	334	7	US-08-467- Sequence 3, Applicat	1.07e-30
38	67	17.7	334	13	PCT-US95-1 Sequence 1, Applicat	1.07e-30
39	67	17.7	334	7	US-08-470- Sequence 1, Applicat	1.07e-30
40	67	17.7	334	7	US-08-470- Sequence 5, Applicat	1.07e-30
41	67	17.7	334	7	US-08-470- Sequence 3, Applicat	1.07e-30
42	67	17.7	334	7	US-08-467- Sequence 5, Applicat	1.07e-30
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45	67	17.7	729	1	Patent No. 5455030-16	1.07e-30

ALIGNMENTS

RESULT 1

ID US-08-468-671-5 STANDARD: DNA: UNC: 402 BP.

AC xxxxxx

DT 01-JAN-1900

DE Sequence 5, Application US/08468671.

CC Sequence 5, Application US/08468671

CC Patent No. 5648077

CC GENERAL INFORMATION:

CC APPLICANT: OLSBERG, LAIS G.

CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

CC NUMBER OF SEQUENCES: 16

CC CORRESPONDENCE ADDRESS:

CC ADDRESS: Townsend and Townsend and Crew LLP

CC STREET: Two Embarcadero Center, Eighth Floor

CC CITY: San Francisco

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 94111-3834

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent in Release #1 0, Version #1 10

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/468,671

CC FILING DATE: 06-JUN-1995

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/259,372

CC FILING DATE: 14-JUN-1994

CC APPLICATION NUMBER: US 07/897,426

CC FILING DATE: 21-APR-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/676,036

CC FILING DATE: 27-MAR-1991

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/538,796

CC FILING DATE: 15-JUN-1990

CC PRIOR APPLICATION DATA: US 07/192,754

CC APPLICATION NUMBER: US 07/192,754

CC FILING DATE: 11-MAY-1988

Thu Feb 26 07:05:40 1998

US-08-844-215-26.rni

Page 2

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CC      PRIOR APPLICATION DATA: US 06/925,196
CC      APPLICATION NUMBER: US 06/925,196
CC      FILING DATE: 31-OCT-1986
CC      PRIOR APPLICATION DATA: US 06/904,517
CC      APPLICATION NUMBER: US 06/904,517
CC      FILING DATE: 05-SEP-1986
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Smith, William M
CC      REGISTRATION NUMBER: 30,223
CC      REFERENCE/DOCKET NUMBER: 11823-50-7
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (415) 326-2400
CC      TELEFAX: (415) 576-0300
CC      INFORMATION FOR SEQ ID NO.: 5.
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 402 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: unknown
CC      TOPOLOGY: unknown
CC      MOLECULE TYPE: cDNA
CC      HYPOTHETICAL: NO
CC      ANTI-SENSE: NO
CC      ORIGINAL SOURCE:
CC      ORGANISM: Homo sapiens
CC      CELL TYPE: Hybridoma
CC      CELL LINE: ZM1-2
CC      FEATURE:
CC      NAME/KEY: CDS
CC      LOCATION: 1..402
CC      Sequence 402 BP, 67 A, 119 C, 124 G, 92 T, 0 other;
SQ
Query Match          46.6%; Score 176; DB 7; Length 402;
Best Local Similarity 82.6%; Pred. No 5,886-111;
Matches 242; Conservative 0; Mismatches 48; Indels 3; Gaps 3;

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Qy 62 CTTGACACTGTCTCTGTGCTGCTTCAATAGAGAGAGTCACTGATGAGATGGATGGCGGCGAGC 121
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Db 176 CCGGGGGGAGAGCCCTCGAGAGTGGGTGGGGCGGTGCTTATACAGAGGAGAGTGTGAGATTACA 235
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Qy 122 CCCGAGGGAAGGAGCTCGAGAGTGGATTTGGAGAGATCTTTTTTAACTGGAGACCATCTTACA 181
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Db 236 ACCGCTCCCTCGAGAGCTGAGTTCACCGTGTGATGTGAGTGAACAGCTCCCAAGAGACAGTTCC 295
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Qy 182 ACCGATCCCTCGAACATTCAGATTCAGATGTCTGTAGACAACTCCCAAGACACAGATCTCC 241
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Db 296 TGAAGCTGACACTGTGTGACCGCTCGCGGAGACAGCCCGCTATATTATTTGGCAGAGA 348
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Qy 242 TGAAGCTGACACTGTGTGACCGCTCGCGGAGACAGCCCGCTATATTACTGTGCGAGA 294
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RESULT 2
ID US-08-259-372A-5 STANDARD; DNA: UNC; 402 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 5, Application US/08259372A.
CC Sequence 5, Application US/08259372A
CC Patent No. 5565354
CC GENERAL INFORMATION:
CC APPLICANT: Osiberg, Lars G.
CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
CC N
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco

```

```
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/259,372A
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196
CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 118,23-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 402 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: cDNA
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC CELL TYPE: Hybridoma
CC CELL LINE: ZM1-2
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..402
CC Sequence 402 BP, 67 A, 119 C, 124 G, 92 T, 0 other.
Cc
Cc
Query Match 46.6% Score 176; DB 6; Length 402;
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Db 119 CTCGCACTGTCTCCGCTGGCTCCTTCCAGT-G-ATT-ACTTTGGAAATTGGTTCCGGGCAGC 175
Gy 62 CTCGCACTGTCTCTGTGTGCTCACATCGAGGAGCAATCACTGGTAATGATGATGAGTGGTGG 121
Db 176 CCAGCGGGAAGGAGCCTTGGAGATGGCTTGGGCGTGTCTATACAGAGTGAAGTGTGCACTACA 235
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Qy      62 CCGGACATGTGTGTGGTGGCTGCATCAGGAGCATCTGCTGGTAGGTTGGGTCCGCCAGC 121
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Dh      182 CGCCAGAGAAAGTACTGTGAATGGATGGATGCTATCATATATGGTAAATGGTAAATAATT 241
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Qy      122 CGCCAGAGAAAGTACTGTGAATGGATGGATGCTATCATATATGGTAAATGGTAAATAATT 178
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Dh      302 CCCTGAAACTGAGGCTGTGTGAATGGTGGGAGCAAGCGCTGTATTACTGTGGAG 356
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AC       xxxxxx
DT       01-JAN-1900
DE       Sequence 19, Application US/08379072A.
CC       Sequence 19, Application US/08379072A
CC       Patent No. 5658570
CC       GENERAL INFORMATION:
CC       APPLICANT: NEMMAN, Roland A.
CC       APPLICANT: HANNA, Nabli
CC       TITLE OF INVENTION: PEROMYXIN ANTIBODIES FOR HUMAN THERAPY
CC       NUMBER OF SEQUENCES: 20
CC       CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Burns, Doane, Swecker & Mathis
CC       STREET: P.O. Box 1404
CC       CITY: Alexandria
CC       STATE: Virginia
CC       COUNTRY: United States
CC       ZIP: 22313-1404
CC       COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: Patent Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/379,072A
CC       FILING DATE: 25-JAN-1995
CC       CLASSIFICATION: 424
CC       PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 07/912,292
CC       FILING DATE: 10-JUL-1992
CC       PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 07/856,281
CC       FILING DATE: 23-MAR-1992
CC       PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 07/735,064
CC       FILING DATE: 25-JUL-1991
CC       ATTORNEY/AGENT INFORMATION:
CC       NAME: Rea, Teresa Stanek
CC       REGISTRATION NUMBER: 30,427
CC       REFERENCE/DOCKET NUMBER: 012712-067
CC       TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (703) 836-6620
CC       TELEFAX: (703) 836-2021
CC       INFORMATION FOR SEQ ID NO: 19:
CC       SEQUENCE CHARACTERISTICS:

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CC FILING DATE: 25 JUL 1991
CC ATTORNEY/AGENT INFORMATION:

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1 402
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AC xxxxxx
DT 01-JAN-1900
DE Sequence 14, Application PC/TUS9207111.
CC Sequence 14, Application PC/TUS9207111
CC GENERAL INFORMATION:
CC APPLICANT: Ohno, Tsuneya
CC TITLE OF INVENTION: HIV Immunotherapeutics
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESS: Bicknell
CC STREET: Two First National Plaza, 20 South Clark
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/07111
CC FILING DATE: 19920824
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/748,562
CC FILING DATE: 22-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31016
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 346-5750
CC TELEFAX: (312) 384-9740

CC TELEX: 25-3856
CC INFORMATION FOR SEQ. ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 402 base pairs
CC TYPE: Nucleic Acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..402
SQ Sequence 402 BP; 107 A; 113 C; 88 G; 94 T; 0 other;
Query Match 19.8%; Score 75; DB 10; Length 402;
Best Local Similarity 65.2%; Pred. No. 2,366-36;
Matches 193; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
Db 1 GAGGTCCAGCTGTGAGAGAGTGTGATCATCAAGTAGTAGTATGCTGGACATGATCCGC 60
1 GAGGTCCAGCTGTGAGAGAGTGTGATCATCAAGTAGTAGTATGCTGGACATGATCCGC 60
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Db 121 CAGCCCCAGAGAGAGGAGTATGAGTGTGAGAGAGAGTATGATGATGAGTTCATAGAC 180
QY 118 CAGCCCCAGAGAGAGGAGTATGAGTGTGAGAGAGAGTATGATGATGAGTTCATAGAC 177
Db 181 TATAGTCATTCATCAAAAGCCGAGAGACCATCTCCAGAGACATCTCTGAACAGATTC 240
QY 178 TACAAACCATCCCTCAAGATGAGTGTCTCATGCTGTGATCAAGTCCAGAGCCAGGTC 237
Db 241 TTATCCAGCTAGTCTGTGACAAATGAGAGACATCCCATGATGATGATGATGATGATG 296
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RESULT 12
ID US-08-111-080-15 STANDARD; DNA; UNC; 402 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 15, Application 08/111080.
CC Sequence 15, Application 08/111080
CC Patent No. 5558865
CC GENERAL INFORMATION:
CC APPLICANT: Ohno, Tsuneya
CC TITLE OF INVENTION: HIV Immunotherapeutics
CC NUMBER OF SEQUENCES: 38
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESS: Borun
CC STREET: 6300 Sears Tower, 233 S. Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: 08/111,080
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/748,562
CC FILING DATE: 22-AUG-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/07111
CC FILING DATE: 24-AUG-1992
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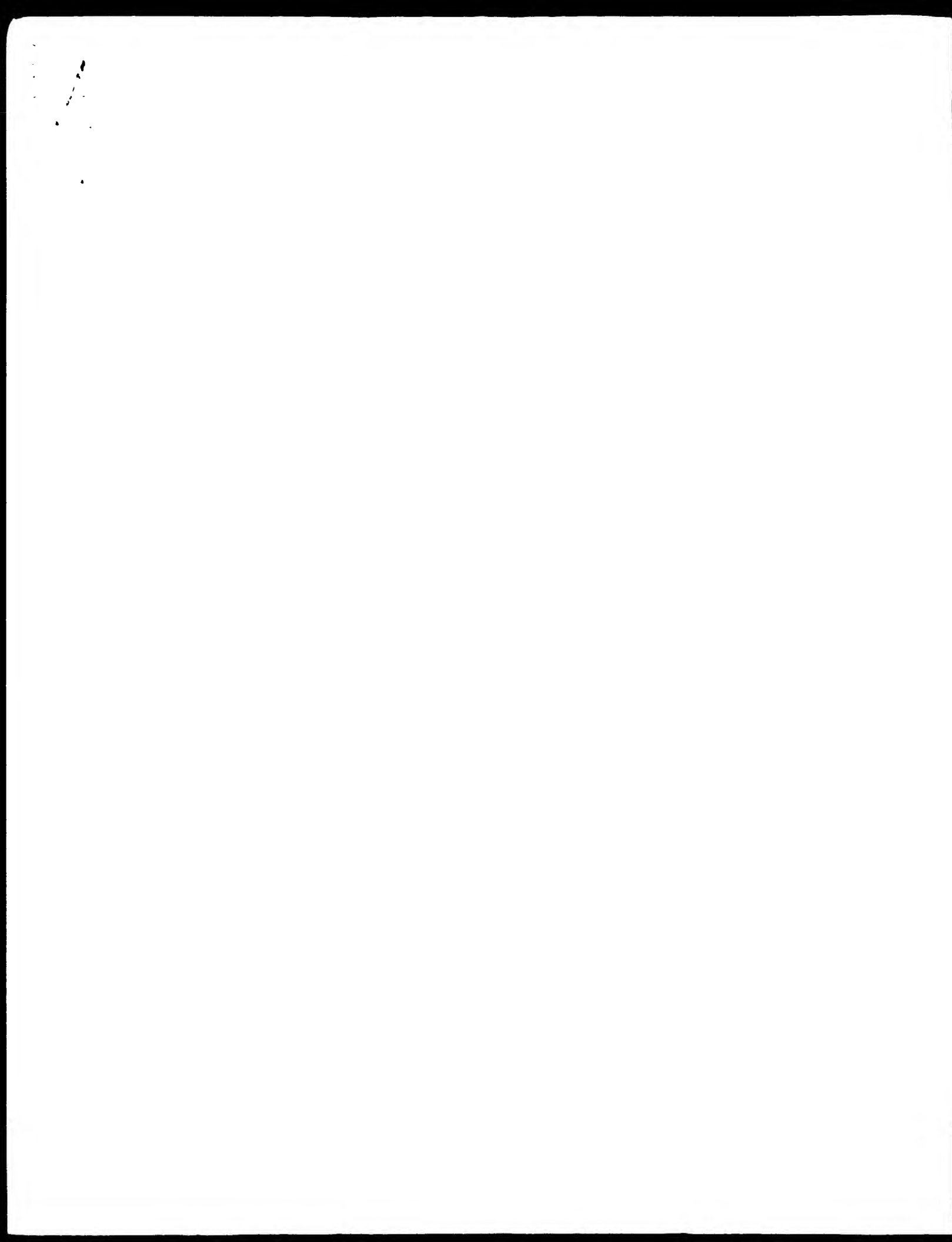
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CC FILING DATE:
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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/07111
CC FILING DATE: 24-AUG-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/039,457
CC FILING DATE: 22-APR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Borun, Michael F.
CC REGISTRATION NUMBER: 25,447
CC REFERENCE/DOCKET NUMBER: 31629
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ. ID NO.: 27:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 826 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 261..620
CC Sequence 826 BP: 217 A; 202 G; 206 G; 201 T; 0 other.
CC
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CC Query Match 19.8%; Score 75; DB 7; Length 826;
CC Best Local Similarity 65.2%; Pct. No. 2,36e-36;
CC Matches 193; Conservative 0; Mismatch 109; Indels 3; Gaps 2
Cc
Cc
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Cc QY 239 CCTGAGAGCTGAGGCTCTGTAGCCCGCGAGACAGCGCGGTATGCTGTGGAGA 294
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Cc DE Sequence 27. Application PC/TUS9407967.
Cc CC Sequence 27. Application PC/TUS9407967.
Cc GENERAL INFORMATION:
Cc APPLICANT: Ohno, Tsuneya
Cc TITLE OF INVENTION: HIV Immunotherapeutics
Cc NUMBER OF SEQUENCES: 38
Cc CORRESPONDENCE ADDRESS:
Cc ADDRESSEE: Marshall, C'Toole, Gerstein, Murray &
Cc ADDRESS: Borun
Cc STREET: 6300 Sears Tower, 233 S. Wacker Drive

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CC CITY : Chicago  
CC STATE : Illinois  
CC COUNTRY : USA  
CC ZIP : 60606  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER : IBM PC compatible  
CC OPERATING SYSTEM : PC-DOS/MS-DOS  
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CC APPLICATION NUMBER : PCT/US82/07111  
CC FILING DATE : 24-AUG-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER : US 08/039,457  
CC FILING DATE : 22-APR-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME : Borum, Michael F.  
CC REGISTRATION NUMBER : 25,447  
CC REFERENCE /DOCKET NUMBER : 31629  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE : (312) 474-6300  
CC TELEFAX : (312) 474-0448  
CC TELEX : 25-3856  
CC INFORMATION FOR SEQ ID NO.: 27:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 826 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: GDS  
CC LOCATION: 261..620  
SS Sequence 826 BP: 217 A; 202 C; 206 G; 201 T; 0 other;  
  
Query Match 19.8%; Score 75; DB JI; Length 826;  
Best Local Similarity 65.2%; Pred.No. 2,38e+86;  
Matches 193, Conservative 0, Mismatches 100, Indels 3, Gaps 2
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Search completed: Tue Feb 24 15:53:30 1998
Job time : 97 secs.




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ACCESSION AA360196
NID 92012574
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 239)
AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A.,
White,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
Blatt,C.E., Sutton,G., Blake,J.A., Brandon,R.C., Wang,Wai.C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
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Dimke,D., Feng,D.-F., Ferrier,A., Fischer,C., Hastings,S.A.,
He,W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
JOURNAL Initial assessment of human gene diversity and expression patterns
MEDLINE based upon 83 million nucleotides of cDNA sequence
COMMENT Nature 377 (6547 Suppl), 3-174 (1995)
96026280

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018599056
Fax: 3018599423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Matches 147; Conservative 0; Mismatches 31; Indels 3; Gaps 2;

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Db 179 agccnccagggaaggaactngatggatcggaattttctatnaccagnggatccnccanct 238
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ACCESSION AA098196
NID 91643751
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 364)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,P.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
MGI:331795
Seq primer: -28ml3 rev1 ET from Amersham.
Location/Qualifiers
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mRNA
BASE COUNT 99 a 95 c 77 g 93 t
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Best Local Similarity 69.8%; Pred. No. 6.28e-156;
Matches 206; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

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QY 121 CCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180

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QY 181 AACCATCTCTCAACGATCGAGTCTTCTATCTCTGTACACAAGTTCGAAGGACGACAGTCTCT 240

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	52 a	69 c	79 g	72 t	6 others
BASE COUNT					
OPIGIN					
Query Match	23.3%	Score 88:	DB 60:	Length 278:	
Rest Local Similarity	83.8%	Pred NO 6	64e-127:		
Matches	124:	Conservative	0:	Mismatches 21:	Indels 3: Gaps 1:
Ddb	52	adgtcgacgtcgagagtcggggcccgacgactggtgaagccctcgagacactgtccctna	111		
2	AGGTGCAGCTGCTCGAGTCGGGGCCGAGACTGSGFAGAGCTTCGGSGACCCCTGTCCTCA	61			
QY					
Ddb	112	tttgcactgtctctactgtgtccatcagatcaactatnactgg---	adttggaattcgacagt	168	

		Query Match	15.1%	Score 61:	DB 24:	Length 158:	
		Best Local Similarity	89.5%	Pred. NO.	8.95e-73:		
		Matches	68;	Conservative	0;	Mismatches	8; Indels 0; Gaps
Db	82	gtacgcctgacagatcgaggccaccagacttgtagaaccttcaactgaacctgacccgctcgcataacc	141				
QY	4	GTGAGATGGTCGACCTGGAGTGGCAAGACTTGGTAAGAGCCTCGAGAGCCGTGTGCACAC	63				
Db	142	tggcaactgatctctgag	157				

	Query Match	12.2%;	Score 46;	DB 100;	Length 306;	
	Best Local Similarity	62.7%;	Pred No. 1.73e-44;			
	Matches	175;	Mismatches 99;	Indels 5;	Gaps 5;	
D b	25	gagctgggtcctacagtggagaanaacacagaaacccacaggatgcacacttcctt	83			
Q y	16	GAGTCGGCCGACAGAACTGTTGAAGTATTGGGAGCAATGTGCTCATCTGCACITGCTCT	75			
D b	84	ggctttccactcacacttgattggaatggatggctggatccctcagccccagaaaaag	143			
Q y	76	GGTGCGTCTCATAAGACAGACACTG-ACATGG-TG-GACTGTGGTCTGCCAACGCCCCAGGGAAG	132			
D b	144	gccctgggaatggctggaactcatctactgggatgaatgaaaagcgctacagcccactct	203			

Query Match 9.58; Score 36, DB 52; Length 240;

```

Best Local Similarity 68.3%; Pred. NO. 6.58e-27;
Matches 56; Conservative 0; Mismatches 30; Indels 0; Gaps 0.

Db      73  cdaatccaccatctccagagacaacgcccaagcaactcgtatctgcgaagaaagacacgcctg 132
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      199  CTAAGTCTTCATCTCTGTGTGTGTGAATAGTCCCAAGTACAGTCTCTCTCTGAGTGTGATCTTGTG 248

Db      133  acagccacacacacacgcgtgtgtattactctgtcgagaa 168
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      259  ACGCGCGGGACACGCGCGTGTATTACTGTGCGGAGA 294

```

RESULT	15
LOCUS	AA175689 420 bp mRNA EST 16-FEB-1997
DEFINITION	ms94c02.r1 Soares mouse 3BMS Mus musculus cDNA clone 619202 5' similar to gb:X70423 M.musculus mRNA for monoclonal antibody heavy chain gamma (MOUSE);.
ACCESSION	AA175689
NID	gl756810
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrate; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 420) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geiseli,S., Kucaba,T., Lacy,M., Le M., Martin,J., Morris,M., Schellenger,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,I., Lennon,G , Soares,R , Wilson,P. and Waterston,R.
TITLE	The WashU-HMI Mouse EST Project
JOURNAL	Unpublished (1996)

Contact: Marra M/Mouse EST Project
Washington Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:380026
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 391.

FEATURES	Source
Location/Qualifiers	
1..420	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/note="Vector: pT73D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTAACCAATCTGAATGGAGCCGCCGCGTGTTTTTTTIIIIIIIIIII 3']; double-stranded cDNA was ligated to Eco RI adaptors. (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaído."	
/clone="619202"	
/clone_lib="Soares mouse 3NbMS"	
/sex="male"	
/tissue_type="Spleen"	
/dev_stage="4 weeks"	
/lab_host="DH10E"	
<1..>420	
107 a	119 c 99 g 95 t
mRNA	
RACE COUNT	
ORIGIN	

Query Match	93%	Scores	35	DB 1	Length	420
Best Local Similarity	75.4%	pred. No.	3.12e-25			
Matches	52	Conservative	0	Mismatches	17	Indels
				Gaps	0	

WATERMAN

(TM)

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MPsrch_nn n.a. - n.a database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 13:40:16 1998; MasPar time 127.67 seconds

Tabular output not generated. 746 944 Million cell updates/sec

Title: >US-08-844-215-27
Description: (1-378) from US08844215 seq
Perfect Score: 378
N.A. Sequence: 1 GAGGTGCGAGTCGCGAGTC.....CTTGGTCACCGTGTCTTCA 378
Comp: CTCACGTCGACGAGCTCAG.....GAGACGAGTCGACAGAGT

Scoring table: TARTLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 33443 seqs, 12143548 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
1 STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19 20:STS20
21:STS21 22:STS22 23:STS23 24:STS24 25:STS25 26:STS26
27:STS27 28:STS28 29:STS29 30:STS30 31:STS31 32:STS32
33:STS33 34:STS34 35:STS35 36:STS36 37:STS37 38:STS38
39:STS39 40:STS40 41:STS41 42:STS42 43:STS43 44:STS44
45:STS45 46:STS46 47:STS47 48:STS48 49:STS49
50:STS50 51:STS51 52:STS52 53:STS53 54:STS54
55:STS55 56:STS56 57:STS57 58:STS58 59:STS59
60:STS60 61:STS61 62:STS62 63:STS63 64:STS64
65:STS65 66:STS66 67:STS67 68:STS68 69:STS69
70:STS70 71:STS71 72:STS72 73:STS73 74:STS74
75:STS75 76:STS76 77:STS77 78:STS78 79:STS79
80:STS80 81:STS81 82:STS82 83:STS83 84:STS84
85:STS85 86:STS86 87:STS87 88:STS88 89:STS89
90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95 96:STS96

Statistics: Mean 9.902; Variance 1.885; scale 5.254
Pred No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES				
Result	Query	ID	Description	Pred. No
No.	Score	Match Length		
1	78	20.6	256 54 HS1202138	247th07.r1 Soares ova 9.34e-106
2	45	11.9	230 57 HS1227079	247th07.r1 Soares ova 1.35e-42

3	38	10.1	238	69	HS1300461	aa63901.r1 NCI_CGAP_G	2.39e-30
4	38	10.1	238	35	AA505044	aa63901.r1 NCI_CGAP_G	2.39e-30
5	30	7.9	435	80	HSAA7475	na76605.s1 NCI_CGAP_B	2.73e-17
6	30	7.9	435	40	AA507475	na76605.s1 NCI_CGAP_B	2.73e-17
7	27	7.1	597	24	AA472093	va10a05.r1 Soares mcn	9.34e-13
8	27	7.1	597	83	WM1263658	va10a05.r1 Soares mcn	9.34e-13
9	24	6.3	511	63	HS1258634	2483b07.r1 Soares ova	1.72e-08
10	24	6.3	511	17	AA454794	2483b07.r1 Soares ova	1.72e-08
11	21	5.6	403	73	HS121118	n51b07.s1 NCI_CGAP_P	1.46e-04
12	21	5.6	403	44	AA531145	n51b07.s1 NCI_CGAP_P	1.46e-04
13	20	5.3	288	95	HS1138859	7H16G06 Chromosome 7	2.42e-03
14	20	5.3	302	11	HUMSWS3933	human chromosome 7 ST	2.42e-03
15	20	5.3	302	12	HUMSWS3933	human chromosome 7 ST	2.42e-03
16	20	5.3	374	58	HS1252283	247d12.s1 Soares ova	2.42e-03
17	20	5.3	397	50	HS1177148	2486e04.r1 NCI_CGAP_G	2.42e-03
18	20	5.3	397	19	AA255889	2486e04.r1 NCI_CGAP_G	2.42e-03
19	20	5.3	412	75	HS8381	EST03727 Homo sapiens	2.42e-03
20	20	5.3	454	23	AA459598	2327g08.r1 NCI_CGAP_G	2.42e-03
21	20	5.3	454	62	HS1254438	2327g08.r1 NCI_CGAP_G	2.42e-03
22	20	5.3	1023	4	HS10618	human STS SHGC35785	2.42e-03
23	20	5.3	2775	9	HS08615	human STS SHGC35785	2.42e-03
24	19	5.0	259	30	AA488043	3012f07.r1 Stratagene	3.55e-02
25	19	5.0	334	50	HS1174298	2425b12.r1 NCI_CGAP_G	3.55e-02
26	19	5.0	324	20	AA037099	2435b1.r1 NCI_CGAP_G	3.55e-02
27	19	5.0	344	16	AA461658	2435b1.r1 NCI_CGAP_G	3.55e-02
28	19	5.0	349	81	WM1239198	2423b04.s1 Knowles So	3.55e-02
29	19	5.0	396	91	TC250	2423b04.s1 Knowles So	3.55e-02
30	19	5.0	400	9	GS8421	human STS SHGC35787	3.55e-02
31	19	5.0	416	37	AA503753	na50906.s1 NCI_CGAP_C	3.55e-02
32	19	5.0	442	90	PMMA35257	va49a02.s1 Knowles So	3.55e-02
33	19	5.0	444	90	MMAA35322	va49a02.s1 Knowles So	3.55e-02
34	19	5.0	445	18	AA465902	va62b10.s1 Knowles So	3.55e-02
35	19	5.0	444	50	HS1173165	7422f04.r1 NCI_CGAP_G	3.55e-02
36	19	5.0	451	76	HSAA10659	2401b03.s1 Stratagene	3.55e-02
37	19	5.0	460	75	HSAA10659	2401b03.s1 Stratagene	3.55e-02
38	19	5.0	496	26	AA477595	2444e07.r1 Soares mcn	3.55e-02
39	19	5.0	498	84	WM1246515	2444e07.r1 Soares mcn	3.55e-02
40	19	5.0	501	23	AA286927	2456a05.r1 NCI_CGAP_G	3.55e-02
41	19	5.0	524	57	HS1226054	2474e07.r1 Soares ova	3.55e-02
42	19	5.0	538	30	AA495574	2461e08.s1 Stratagene	3.55e-02
43	19	5.0	542	73	HS122042	n13b10.s1 NCI_CGAP_P	3.55e-02
44	19	5.0	558	25	AA475554	2413g05.r1 Soares mcn	3.55e-02
45	19	5.0	577	73	HS1219244	na87c01.s1 NCI_CGAP_B	3.55e-02

ALIGNMENTS

RESULT 1

IC HS1202138 standard. RNA, EST. 266 BP.

AC AA02847,

NI G2056386

DT 01-MAY-1997 (Ref. 51, Created)

RT 22-MAY-1997 (Ref. 52, Last updated, Version 2)

DE 247th07.r1 Soares ovary tumor NCHOT Homo sapiens cDNA clone 741181

EE 5' similar to gi 587789 TG SAMMA-1 CHAIN C REGION (HUMAN);

KW EST.

QS Homo sapiens (human)

CC Eukaryotic, mitochondrial eukaryotes; Metazoa, Chordata,

CC Vertebrata, Eutheria, Primates, Catarrhini, Hominoidea, Homo.

RN [1]

PP 1-266

RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,

PA Kuraba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,

PA Moore B., Schellenberg K., Stroppe W., Tan F., Theising B.,

PA White Y., Wylie T., Waterston P., Wilson R.;

RT "Washu-Merck EST Project 1997";

RL Unpublished.

CC Contact: Wilson RK Washu-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 268 1400 Fax: 314 268 1410 Email:

CC est@wustl.wustl.edu This clone is available royalty-free through

CC EMBL; contact the IMAGE Consortium (info@image.llnl.gov) for

CC further information. Seq primer 26m13 rev2 ET from Amersham.

 WIRE (TM)

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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
 Run on: Tue Feb 24 12:25:57 1998; MacStar time 55.47 Seconds
 786.410 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-844-215-26
 Description: (1.378) from US08844215.seq
 Perfect Score: 378
 N.A. Sequence: 1 GAGGTGACGCTGCTGAGTC
 Comp: CTCGACGCTGACGCTGAG

Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0; Query 0
 Searched: 159651 seqs, 5769962 bases x 2
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: n-genes30
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.204; Variance 4.969; scale 1.551
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	225	59.5	372	28	Human lung cancer spe	1.41e-133
2	223	59.0	624	13	Human immunoglobulin	3.42e-132
3	222	58.7	800	13	Human immunoglobulin	1.69e-131
4	208	55.0	348	7	VH415	8.18e-122
5	204	55.0	348	7	VH411	8.15e-122
6	207	54.8	1212	13	Human immunoglobulin	4.00e-121
7	205	54.5	348	7	VH71-4	1.96e-120
8	206	54.5	348	7	VH416	1.96e-120
9	206	54.5	622	13	Human immunoglobulin	1.96e-120
10	205	54.2	351	7	AS26	9.62e-120
11	204	54.0	650	13	Human immunoglobulin	4.71e-119
12	203	53.7	799	13	Human immunoglobulin	2.31e-118
13	200	52.9	408	32	Immunoglobulin rB6B7	2.72e-116
14	198	52.4	366	5	MAB 1-3-1 variable re	6.51e-115
15	198	52.4	372	2	Anti-human PHD PAG-1	6.51e-115

16	196	51.9	384	2	Q11951	Anti-human RHD FOM-1	1.56e-113
17	194	51.3	348	7	Q42698	F105Vh.	3.72e-112
18	194	51.3	426	7	Q43154	F105 rearranged varia	3.72e-112
19	194	51.3	685	13	Q78972	Human immunoglobulin	3.72e-112
20	194	51.3	1431	20	T18059	Monoclonal antibody 2	3.72e-112
21	193	51.1	631	13	Q78969	Human immunoglobulin	1.82e-111
22	191	50.5	369	22	T26870	Anti-rhesus D monoclo	4.33e-110
23	191	50.5	1418	22	T26889	Anti-rhesus D monoclo	4.33e-110
24	190	50.3	403	33	T73440	Human immunoglobulin	2.12e-109
25	189	50.0	363	2	Q11952	Anti-human PHD FOM-A	1.04e-108
26	188	49.7	404	33	T73438	Human immunoglobulin	5.04e-108
27	187	49.5	291	3	N50188	Sequence of human im	2.46e-107
28	187	49.5	357	33	T72126	CEA-specific antibody	2.46e-107
29	186	49.2	1071	1	N81654	LVIJ regions of human	1.20e-106
30	185	48.9	354	33	T72129	CEA-specific antibody	5.87e-106
31	185	48.9	357	5	Q38670	MAB GAH variable regi	5.87e-106
32	185	48.9	1431	29	T62513	Primitised anti-human	5.87e-106
33	184	48.7	413	33	T73434	Human immunoglobulin	2.84e-105
34	182	48.1	524	33	T73444	Human immunoglobulin	6.73e-104
35	178	47.1	1404	32	T62870	Human gamma-4PE heavy	3.76e-101
36	178	47.1	1404	32	T62868	Human gamma-4 heavy c	3.76e-101
37	178	47.1	1404	32	T62869	Human gamma-4E heavy	3.76e-101
38	176	46.6	321	2	Q11949	Anti-human RHD MAD-2	8.87e-100
39	176	46.6	402	33	T85840	Monoclonal antibody 2	8.87e-100
40	176	46.6	402	24	T45132	Monoclonal antibody 2	8.87e-100
41	176	46.6	402	10	O64052	Sequence of the VH re	8.87e-100
42	176	46.6	420	32	T62865	Monkey anti-CD4 heavy	8.87e-100
43	176	46.6	423	6	Q35903	Anti-CD4 VH coding se	8.87e-100
44	170	45.0	381	2	Q11947	Anti-human RHD FOG-B	1.15e-95
45	164	43.4	372	2	Q11950	Anti-human RHD FOG-1	1.14e-91

ALIGNMENTS

RESULT 1
 ID T45035 standard; cDNA; 372 BP.
 AC T45035;
 DT 23-MAY-1997 (first entry)
 DE Human lung cancer specific antibody heavy chain variable region cDNA.
 KW Heavy chain; light chain; variable region; human; monoclonal antibody;
 OS lung cancer tissue; diagnosis; purification; cancer-specific antigen; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_PNA 91..108
 FT /tag= a
 FT /product= CDR1
 FT /note= "Fig 5, Claim 7"
 FT /misc_difference 139..141
 FT /tag= b
 FT /codon= seq:gag, aa:Gln
 FT misc_RNA 151..198
 FT /tag= c
 FT /product= CDR2
 FT /note= "Fig 6, Claim 7"
 FT misc_RNA 295..339
 FT /tag= d
 FT /product= CDR3
 FT /note= "Fig 7, Claim 7"
 PN J08280386-A.
 PD 29-OCT-1996.
 PR 14-APR-1995; 112671.
 PR 14-APR-1995; JP-112671.
 PA (MORI) MORINAGA & CO LTD
 WP1: 97-014849/02.
 P-PSDR: W06474
 FT Antibody specifically reactive to human lung cancer cells - also
 corresponding cDNA, used to diagnose cancer, or for purification of
 cancer-specific antigen
 Claim 1: Fig 1: 9pp: Japanese.
 CC The sequences given in T45035-36 encode the heavy chain and light
 chain variable regions from a human monoclonal antibody which is
 specific for human lung cancer tissue. The monoclonal antibody may
 be used for clinical diagnosis of cancers, for immunological therapy

CC or for purification of a cancer-specific antigen.
SQ Sequence 372 BP; 77 A; 102 C; 117 G; 76 T;

Query Match 59.5%; Score 225; DB 28; Length 372;
Best Local Similarity 88.4%; Pred. No. 1.41e-133;
Matches 259; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 2 aggtgcagctgcagagctcggggcccgagcactggtgaagccttcggggaccctgtccctca 61
|||||
Qy 2 AGTGTGACAGTGTCTGAGTCTGGGCGCCAGGACTGGTGAAGCTTCGGGGAGCCCTGTCTCTCA 61
|||||
Db 62 ctgcgctgtctctgtggttcacatcagcagtagtaactcgttgagcctgggtccgcacg 121
|||||
Qy 62 CTTGCATCTGTCTCTGCTGGCTCCATCAGGAGCAGTCTCTGCTGGAGTCTGGTCCGCCAGC 121
|||||
Db 122 cccagggaaagggtgagtgatgggaaatctatcatagtgaggagcaccacactata 181
|||||
Qy 122 CCCCAGGGAAGGAGTGGAGTGGATTGGAGAGTCTTTTATTAGTGGAGGACCATCTACA 181
|||||
Db 182 accgctccctcaagagctcgagtcaccatcaccatcagcgagacacgctcccaagacagttctccc 241
|||||
Qy 182 ACCATCCCTCAAGATCGAGTCTTTCATGTCTGTAGACACAAGTCCAAAGGACCAAGGTCTCTCC 241
|||||
Db 242 tgaaggtgaactctgtcaccgcgcgagacacgcccgtgtattactgtgcgaga 294
|||||
Qy 242 TGAAGGTGAGCTGTGTGACCCGCGGACACAGCGCCGTGTATTACTGTGGGAGA 294
|||||

RESULT 2
ID Q78966 standard; DNA; 624 BP.
AC Q78966;
DT 03-AUG-1995 (first entry)
DE Human immunoglobulin Vh gene #28.
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 151..583
FT /tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 197..278
FT /tag= b
FT /tag= c
FT /tag= c
FT /note= "miscellaneous signal, does not conform to
terminator or splice site sequence"
FN WO9426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-PSDB: R66320.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
production of human immunoglobulin in mammalian hosts
PS Disclosure; Page 67-68; 130pp; Japanese.
CC A series of genes (078939-79002) encoding human immunoglobulin variable
heavy chains. The genes were isolated and cloned from a series of cosmid
constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M18 and M131, by PCR
amplification using primers 078917-38. The genes are subdivided into 5
families of Vh genes. The fragments cover a region of 800 kb. The DNA
placenta. The DNA was partially digested with TagI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
were collected. The fragments were ligated with ClaI-digested cosmid
vector pJB81. The ligation products were in vitro packed and infected
CC - into E.coli 490A. The fragments were then subcloned by colony
hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 624 BP; 141 A; 179 C; 168 G; 136 T;

Query Match 59.08; Score 223; DB 13; Length 624;

Best Local Similarity 88.1%; Pred. No. 3.42e-132;
Matches 258; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Db 291 aggtgcagctgcagagctcggggcccgagcactggtgaagccttcggggaccctgtccctca 350
|||||
Qy 2 AGTGTGACAGTGTCTGAGTCTGGGCGCCAGGACTGGTGAAGCTTCGGGGAGCCCTGTCTCTCA 61
|||||
Db 351 ctgcgctgtctctgtggttcacatcagcagtagtaactcgttgagcctgggtccgcacg 410
|||||
Qy 62 CTTGCATCTGTCTCTGCTGGCTCCATCAGGAGCAGTCTCTGCTGGAGTCTGGTCCGCCAGC 121
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Db 411 cccagggaaagggtcagtgagtgattgggttacatctattatagtgaggagcactactaca 470
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Qy 122 CCCCAGGGAAGGAGTGGAGTGGATTGGAGAGTCTTTTATTAGTGGAGGACCATCTACA 181
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Db 471 accgctccctcaagagctcgagtcaccatcagtcagtagacacgctcccaagacagttctccc 530
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Qy 182 ACCATCCCTCAAGATCGAGTCTTTCATGTCTGTAGACACAAGTCCAAAGGACCAAGGTCTCTCC 241
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Db 531 tgaaggtgaactctgtcaccgcgcgagacacgcccgtgtattactgtgcgaga 583
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Qy 242 TGAAGGTGAGCTGTGTGACCCGCGGACACAGCGCCGTGTATTACTGTGGGAGA 294
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RESULT 3
ID Q78993 standard; DNA; 800 BP
AC Q78993;
DT 04-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #55.
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 230..675
FT /tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 276..358
FT /tag= b
FT /tag= c
FT /tag= c
FT /tag= d
FT /note= "miscellaneous signal, does not conform to
terminator or splice site sequence"
FN WO9426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-PSDB: R66343.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
production of human immunoglobulin in mammalian hosts
PS Claim 62; Page 102-103; 130pp; Japanese.
CC A series of genes (078939-79002) encoding human immunoglobulin variable
heavy chains. The genes were isolated and cloned from a series of cosmid
constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M18 and M131, by PCR
amplification using primers 078917-38. The genes are subdivided into 5
families of Vh genes. The fragments cover a region of 800 kb. The DNA
placenta. The DNA was partially digested with TagI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
were collected. The fragments were ligated with ClaI-digested cosmid
vector pJB81. The ligation products were in vitro packed and infected
CC - into E.coli 490A. The fragments were then subcloned by colony
hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 800 BP; 184 A; 235 C; 219 G; 154 T;

Query Match 58.7%; Score 222; DB 13; Length 800;
Best Local Similarity 87.6%; Pred. No. 1.09e-131;

[illegible]

REFERENCE 2 (bases 1 to 366)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 TITLE Direct Submission
 JOURNAL Submitted (29-Nov-1996) Immunology, Virginia Mason Research Center,
 1000 Seneca Street, Seattle, WA 98101, USA

FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /note="CD19+ peripheral blood B cells obtained from a bone marrow transplant recipient 1 year post transplant; clone 66 in reference 1"
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 /tissue_type="peripheral blood"
 /clone_3fidll"
 /chromosome="14"
 /map="14q32-q33"
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 /db_xref="PID:g1791125"
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 BASE COUNT 74 a 109 c 110 g 73 t
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Query Match 64.8%; Score 245; DB 95; Length 366;
 Best Local Similarity 91.0%; Pred. No. 4,12e-180;
 Matches 272; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 2 aggtgcagctgcaggagtcggccaggagctggtgaagccttcggggaccctgtccctca 61
 QY 2 AGGTGCAGCTGCTCAGTCGGSCCCAGGACTGGTGAAGCTTCGGGGACCTGCTCCCTCA 61

Db 62 cctgcctgtctctgtgctccatcagcagtagtaactggtgagttggttcgcgcagc 121
 QY 62 CCTGCCTGTCTCTGTGCTCCATCAGGAGCAGTCTGTTGAGTGGGTGGCGCCGAGC 121

Db 122 ccccagggaagggtggtgagtgattggggaatctatcatagtgaggagcaccactaca 181
 QY 122 CCCAGGGAAGGACTGGATGGAGAGTCTTTTATTAGTGAAGCACCATCTACA 181

Db 182 accgtccctcaagatcgagtcaccatcatcagtagaacaagtcacaagaccagttctccc 241
 QY 182 ACCCATCCCTCAAGATCGAGTCACCTTCTATCTGTAGAACCAAGTCCCAAGGACTCTCCC 241

Db 242 tgaagctgagctgtgacccgcgggacacgcccgtgtattactgtgcgagagtcctccc 300
 QY 242 TGAGGCTGAGCTGTGAGCTGTGAGTCTGATCTGTAGAACCAAGTCCCAAGGACTCTCCC 300

RESULT 2
 LOCUS HSIGHXX26 432 bp PNA PPT 07-DEC-1993
 DEFINITION H sapiens mRNA for XIA IG heavy chain VDJ region (LE 4-56)
 ACCESSION X65908 S58699
 MID g395106
 KEYWORDS diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 432)
 AUTHORS Schiff C.
 TITLE Direct Submission
 JOURNAL Submitted (08-APP-1992) C. Schiff, Centre d'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
 REFERENCE 2 (bases 1 to 432)
 AUTHORS Milili,M., Le Veist,F., de Saint-Basile,G., Fischer,A.,

Fougerau,M. and Schiff,C.
 Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
 JOURNAL J.Clin Invest. 91 (4), 1616-1629 (1993)
 MEDLINE 93232287
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /tissue_type="bone marrow"
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 /clone_lib="LE library"
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 BASE COUNT 88 a 126 c 123 g 95 t
 ORIGIN

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 Best Local Similarity 91.2%; Pred. No. 3.03e-179;
 Matches 270; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 59 aggtgcagctgcaggagtcggccaggagctggtgaagccttcggggaccctgtccctca 118
 QY 2 AGGTGCAGCTGCTCAGTCGGSCCCAGGACTGGTGAAGCTTCGGGGACCTGCTCCCTCA 61

Db 119 cctgcctgtctctgtgctccatcagcagtagtaactggtgagttggttcgcgcagc 178
 QY 62 CCTGCCTGTCTCTGTGCTCCATCAGGAGCAGTCTGTTGAGTGGGTGGCGCCGAGC 121

Db 179 ccccagggaagggtggtgagtgattggggaatctatcatagtgaggagcaccactaca 238
 QY 122 CCCAGGGAAGGACTGGATGGAGAGTCTTTTATTAGTGAAGCACCATCTACA 181

Db 239 accgtccctcaagatcgagtcaccatcatcagtagaacaagtcacaagaccagttctccc 298
 QY 182 ACCCATCCCTCAAGATCGAGTCTTCTATCTGTAGAACCAAGTCCCAAGGACTCTCCC 241

Db 299 tgaagctgagctgtgacccgcgggacacgcccgtgtattactgtgcgagagtc 354
 QY 242 TGAGGCTGAGCTGTGAGCTGTGAGTCTGATCTGTAGAACCAAGTCCCAAGGACTCTCCC 297

RESULT 3
 ID HSIGHXX26 standard; RNA; HUM; 432 BP.
 AC X65908; S58699;
 NI g395106
 DT 13-JUL-1993 (Rel. 36, Created)
 DT 26-JUL-1997 (Rel. 52, Last updated, Version 8)
 DE H sapiens mRNA for XIA IG heavy chain VDJ region (LE 4-56)
 KW diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.
 OS Homo sapiens (human)
 OC Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP 1-432
 RA Schiff C.;
 RT ;
 PL Submitted (08-APP-1992) to the EMBL/GenBank/DBI databases.
 PL C. Schiff, Centre d'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
 RN [2]
 RP 1-432
 MEDLINE; 93232287.


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Best Local Similarity 91.5%; Pred. No. 2,24e-178;
Matches 268; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 62 CCTGCACCTCTCTGCTGCTCCATCAGGAGCAGTCTGCTGGAGTGGGTCCGCGAGC 121

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Qy 122 CCCACAGGGAAGGAGCTGAGAGTGGATGGAGAGTCTTTTGTAGTGAAGCACCATCTACA 181

Db 182 accgctccctcaagatcagtcacccatcatcagtagacaaatcacaagaacagttctccc 241
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Qy 182 ACCCATCCCTCAAGCATCGAGTCTTCATCTCTGTAGACAAGTCCAAAGGACAGGTCTCCC 241

Db 242 tgaagctgagctctgacccgcgggacagccgctgtattactatgtgcgaga 294
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Qy 242 TSAGCTGAGCTCTGACGCGGCGGAGCAAGTCCGCGCTGATTATCTGCGGAGA 294

RESULT 6 HUMIGHCAD 308 bp DNA PRI 09-NOV-1994
LOCUS Human Ig germline H-chain gene V4-region, partial cds.
DEFINITION
ACCESSION L10091
NID g185221
KEYWORDS V-region; germline; immunoglobulin heavy chain.
SOURCE Homo sapiens (tissue library: 3116 EMBL3) Male Adult blood DNA.
ORGANISM Homo sapiens
Eukaryote; mitochondria eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 308)
AUTHORS Bull, A. and Milner, E.C.
TITLE Chromosomal organization of the human VH4 gene family. Location of
individual gene segments
JOURNAL J. Immunol. 150 (7), 2858-2868 (1993)
MEDLINE 93203606
FEATURES
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            /map="14q32.33"
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Matches 268; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 10 aggtgcagctgcagagtcggccagagctgggtgaagccttcgggaacccctgcctca 69
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Qy 2 AGGTGCAGCTGTCGAGTTCGGGCGCCAGGACTGGTGAAGCCTTCGGGGAGCCCTGTCCTCA 61

Db 70 cctgcagctctctctggtggtccatcagcagctagtaactggtgagttgggtccgcagc 129
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Qy 62 CCTGCACCTCTCTGCTGCTCCATCAGGAGCAGTCTGCTGGAGTGGGTCCGCGAGC 121

Db 130 ccccaaggaaagggctgaagtagattgggaaattcatcatagtgaggagcacaactaca 189
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Qy 132 CCCACAGGGAAGGAGCTGAGAGTGGATGGAGAGTCTTTTGTAGTGAAGCACCATCTACA 181

Db 190 accgctccctcaagatcagtcacccatcatcagtagacaaatcacaagaacagttctccc 249
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Qy 182 ACCCATCCCTCAAGCATCGAGTCTTCATCTCTGTAGACAAGTCCAAAGGACAGGTCTCCC 241

Db 250 tgaagctgagctctgacccgcgggacagccgctgtattactatgtgcgaga 302
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Qy 242 TSAGCTGAGCTCTGACGCGGCGGAGCAAGTCCGCGCTGATTATCTGCGGAGA 294

RESULT 7 HSU96389 317 bp mRNA PRI 12-MAY-1997
LOCUS Human anti-streptococcal/anti-mysin immunoglobulin heavy chain
DEFINITION variable region mRNA, partial cds.
ACCESSION U96389
NID g2078357
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondria eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 317)
AUTHORS Adderson, E. F., Shinkman, A. P., Ward, K. E. and Cunningham, M. W.
TITLE Molecular analysis of human anti-streptococcal/anti mysin antibody
V region genes from rheumatic carditis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 317)
AUTHORS Adderson, E. F.
TITLE Direct Submission
JOURNAL Submitted (04-APR-1997) Pediatrics, University of Utah, 50 N
Medical Drive, Salt Lake City, UT 84132, USA
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Best Local Similarity 91.5%; Pred. No. 2,24e-178;
Matches 268; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 2 aggtgcagctgcagagtcggccagagctgggtgaagccttcgggaacccctgcctca 61
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Qy 2 AGGTGCAGCTGTCGAGTTCGGGCGCCAGGACTGGTGAAGCCTTCGGGGAGCCCTGTCCTCA 61
    
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WATERBURY

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:57:36 1998; Maspar time 116.03 Seconds
Tabular output not generated. 789.302 Million cell updates/sec

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Description: (1-363) from US08944215 seq
Perfect Score: 363
N A Sequence: 1 CTCGAGTGGGGGAGGGG
Comp: GAGTTCAGCCCGCTCCGCA GGGACCACTGGACAGACGT

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0: Query 0
Searched: 333433 seqs, 126143548 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
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9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
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Statistics: Mean 9.854; Variance 1.966; scale 5.012
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

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	6	35	6.6	238 35	AA505044	aa63q01.r1	NCL-CCAP_G	4.12e-24	
	7	35	9.6	238 69	AA505044	aa63q01.r1	NCL-CCAP_G	4.12e-24	
	8	33	9.1	230 57	HS1227079	z47h07.r1	Soares ova	5.52e-31	
	9	27	7.4	511 63	HS1258634	z47h07.r1	Soares ova	4.23e-12	
	10	27	7.4	511 17	AA464794	z47h07.r1	Soares ova	4.23e-12	
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	12	23	6.3	259 30	AA488043	ab12f07.r1	Stratagene	1.01e-06	
	13	23	6.3	259 66	HS1281117	ab12f07.r1	Stratagene	1.01e-06	
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C	17	20	5.5	470 60	HS1244837	z47h07.r1	Soares ova	4.43e-03	
C	18	20	5.5	475 84	MM1277242	z47h07.r1	Soares ova	4.43e-03	
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C	22	20	5.5	545 89	MM129079	vi32c07.r1	Barstead m	4.43e-03	
C	23	20	5.5	563 57	HS1228508	z47h07.r1	Soares tot	4.43e-03	
C	24	19	5.2	141 19	AA466346	z47h07.r1	Barstead m	5.83e-02	
C	25	19	5.2	141 82	MM1260127	z47h07.r1	Barstead m	5.83e-02	
C	26	19	5.2	169 12	HMMSW574	human chromosome 7	ST	5.93e-02	
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C	28	19	5.2	302 10	HMMSW693	human chromosome X	ST	5.93e-02	
C	29	19	5.2	302 10	HS339X31	Human chromosome	DNA segment	5.93e-02	
C	30	19	5.2	314 10	HS2202H2	H sapiens	DNA segment	5.93e-02	
C	31	19	5.2	322 90	CSG75CA	H sapiens (D4S2972)	D	5.83e-02	
C	32	19	5.2	364 5	G11722	Human cDNA, partial	sc	5.83e-02	
C	33	19	5.2	387 86	MM1295527	vi84a02.r1	Stratagene	5.83e-02	
C	34	19	5.2	387 34	AA499045	vi84a02.r1	Stratagene	5.83e-02	
C	35	19	5.2	400 6	G17929	human STS	SHG-8253	C	5.83e-02
C	36	19	5.2	410 81	MM1250713	z47h07.r1	Soares mou	5.83e-02	
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C	42	19	5.2	435 22	AA283169	z47h07.r1	Soares ova	5.83e-02	
C	43	19	5.2	435 52	HS1187712	z47h07.r1	Soares ova	5.83e-02	
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ALIGNMENTS

RESULT 1 AA472093 597 bp mRNA EST 18-JUN-1997
LOCUS vhl0a05.r1 Soares mouse mammary gland NEMMG Mus musculus cDNA clone
DEFINITION 875024 5' similar to gb:S55761 IG GAMMA-2 CHAIN C REGION (HUMAN);
gb:L36938 Mus musculus germline immunoglobulin gamma constant
region (MOUSE);..
ACCESSION AA472093
NID G2100084
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryote; mitochondrial eukaryotes. Metazoa. Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 597)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dibucque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, R.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.

1 (bases 1 to 511)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 414.
Location/Qualifiers
1..511
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCGAAGTGGAGCGCCGCGGTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Patricia Bonaldo."
/clone="810397"
/lab_host="DH10B (ampicillin resistant)"
/sex="Female"
/tissue.type="ovarian tumor"
/db_xref="GDB:6040750"
106 a 169 c 154 g 112 t

BASE COUNT
ORIGIN

Query Match 7.4%; Score 27; DB 17; Length 511;
Best Local Similarity 90.9%; Pred. No. 4.23e-12;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 388 tggggccaggagacactggtcacccgtctctca 420
||||||| || |||||||||||||||||
QY 331 TGGGGCCAGGAGACCTGGTCCCGTCTCTCA 363

REFERENCE
11
ID HS1214338 standard; RNA; EST; 551 BP.
AC AA418907;
NI 92080726
DT 14-MAY-1997 (Rel. 51, Last updated, Version 2)
DE zw01q09.s1 Soares NhMPu S1 Homo sapiens cDNA clone 768064 3'
DE similar to gb:K03191 CYTOCHROME P450 1A1 (HUMAN);.
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
White Y., Wylie T., Waterston R., Wilson R.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
RC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -41ml3 fwd. ET from Amersham High
CC quality sequence stop: 261.
FH Key Location/Qualifiers
FH 1..551
FT source
FT /organism="Homo sapiens"
FT /note="Organ: mixed (see below); Vector: pT73D-Pac
FT (Pharmacia) with a modified polylinker; Site_1: Not I;
FT Site_2: Eco RI; Equal amounts of plasmid DNA from three
FT normalized libraries (melanocyte 2NBHM, pregnant uterus
FT NDHP0, and fetal heart NDH19W) were mixed, and ss circles
FT were made in vitro. Following HAP purification, this DNA
FT was used as tracer in a subtractive hybridization reaction

FT The driver was PCR-amplified cDNAs from pools of 5,000
FT clones made from the same 3 libraries. The pools consisted
FT of I.M.A.G.E. clones 250232-255223, 340488-345479, and
FT 484488-489479."
FT /clone="768064"
FT /tissue.type="Pooled human melanocyte, fetal heart, and
FT pregnant uterus"
FT /lab_host="DH10B"
FT complement(<1..>551)
FT mRNA
SQ Sequence 551 BP; 147 A; 127 C; 123 G; 154 T; 0 other;
Query Match 6.6%; Score 24; DB 56; Length 551;
Best Local Similarity 78.6%; Pred. No. 5.15e-08;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 224 gaaataccccccctcactccagccctagtctgtgctgtg 265
||||||| || ||||||||||| ||||| |||||
Cp 143 GAAATACCTGCCACCCACTCCAGCCCTTGGCTGGAGCGCTGG 102

RESULT 12
LOCUS AA488043 259 bp mRNA EST 24-JUN-1997
DEFINITION ab12f07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840613
5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);.
ACCESSION AA488043
NID g2215474
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 259)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
TITLE
JOURNAL
COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham.
Location/Qualifiers
1..259
/organism="Homo sapiens"
/note="Organ: lung; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XbaI; Cloned into: pGEM-11; Primer:

Oligo dT, normal lung. Average insert size: 1.0 kb;
 Uni-ZAP XP Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG
 3' -3' adaptor sequence: 5' CTCGAGATTTTITTTTTTTT 3'.

/clone="840613"
 /clone_lib="Stratagene lung (#937210)"
 /sex="male"

/dev_stage="72 years"
 /lab_host="SOLR cells (kanamycin resistant)"

<1..>259
 51 a 99 c 71 g 38 t

mrna
 BASE COUNT
 ORIGIN

Query Match 6.3%; Score 23; DB 30; Length 259;
 Best Local Similarity 96.0%; Pred No. 1.01e-06;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gggaacgtgtgcacgtctctca 25
 ||||| ||||| ||||| ||||| |||||
 QY 339 GGAACCGCTGTCACCGTCTCTCA 363

RESULT 13
 ID HSI281117 standard; RNA; EST: 259 BP.

AC AA488043;

NI 92215474

DT 27-JUN-1997 (Rel. 52, Created)

DE 27-JUN-1997 (Rel. 52, Last updated, Version 1)

DE ab12f07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840613

DE 5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);

KW EST.

OS Homo sapiens (human)

OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;

OC Homo.

RN [1]

RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,

RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,

RA Martin J., Moore P., Schellenberg K., Steptoe M., Tan F.,

RA Theising B., White Y., Wylie T., Waterston P., Wilson P.;

RT "WashU-NCI human EST Project";

RL Unpublished.

CC Contact: Wilson RK Washington University School of Medicine 4444

CC Forest Park Parkway, Box 9501, St. Louis, MO 63108 Tel: 314 286

CC 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is

CC available royalty-free through LBNL; contact the IMAGE Consortium

CC (info@image.lbnl.gov) for further information Seq primer: -28m13

CC rev1 ET from Amersham.

CC Location/Qualifiers

FT source

FT 1..259

FT /organism="Homo sapiens"

FT /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI

FT Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.

FT normal lung. Average insert size: 1.0 kb; Uni-ZAP XR

FT Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'

FT adaptor sequence: 5' CTCGAGTITTTTTTTTTTTT 3'

FT /clone="840613"

FT /clone_lib="Stratagene lung (#937210)"

FT /sex="male"

FT /dev_stage="72 years"

FT /lab_host="SOLR cells (kanamycin resistant)"

FT <1..>259

FT mrna

FT Sequence 259 BP; 51 A; 99 C; 71 G; 38 T; 0 other;

FT Query Match 6.3%; Score 23; DB 66; Length 259;

FT Best Local Similarity 96.0%; Pred No. 1.01e-06;

FT Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

Db 1 gggaacgtgtgcacgtctctca 25

||||| ||||| ||||| ||||| |||||

QY 339 GGAACCGCTGTCACCGTCTCTCA 363

RESULT 14

LOCUS

DEFINITION

P melanogaster STS determined from European Mapping Project

Cosmid.

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

STB

STB

STB

STB

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STB

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```

FH source
FT 1..189
FT /organism="Homo sapiens"
FT /note="vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT was prepared from human tonsillar cells enriched for
FT germinal center B cells by flow sorting (CD20+, IgD-),
FT provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
FT primed with a Not I - oligo(dT) primer
FT [5'-TCTTACCAATCTCAAGTGGAGCGCGCCGCTCATTTTTTTTTTTTTT-
FT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (
FT Pharmacia), digested with Not I and cloned into the Not I
FT and Eco RI sites of the modified pT7T3 vector. Library wen
FT t
FT through one round of normalization, and was constructed by
FT Bento Soares and M. Fatima Bonaldo."
FT /clone="814100"
FT /clone_lib="NCI_CGAP_GCB1"
FT /tissue_type="germinal center B cell"
FT /lab_host="DH10B"
FT complement(<1..>189)
FT mrna
FT SQ Sequence 189 BP; 32 A; 68 C; 59 G; 30 T; 0 other;

```

```

Query Match 5.8%; Score 21; DB 63; Length 189;
Best Local Similarity 73.3%; Pred. No. 3.00e-04;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

Db 119 gcacgcgagcgtctcggggacacccaagcaagaccacgcgctccc 163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Cp 56 GCACAGGAGAGTCTCAGGAGACCTCCCAAGGCTGGACACGCGCTCCC 12

```

Search completed: Tue Feb 24 12:05:08 1998
Job time : 452 secs.

Release 2 ID John F. Collins, Biocomputing Research Unit
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Distribution rights by IntelliGenetics, Inc.

```

mpsrch_nn a - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:48:27 1998. Maspar time 112.83 Seconds
907.284 Million cell updates/sec
Tabular output not generated

```

```
>US-08-844-215-25
Description:      (1-363) from US08944115.seq
Perfect Score:   363
N.A. Sequence:  GAGCTTCACCGGCGTGGCAGGT
Comp:            CGATCCACTGCAGACAGCAGCT
```

```

Scoring table:  TABLE default
                gap %
Nmatch      STD :  Dbase 0:  Query 0
Searched:    397346 seqs, 141010104 bases x 2
Post-processing: Minimum Match 0%
                  Listing first 45 summaries

```

Database: EST-C

1. EST197	2. EST198	3. EST199	4. EST200	5. EST201	6. EST202
7. EST203	8. EST204	9. EST205	10. EST206	11. EST207	12. EST208
13. EST209	14. EST210	15. EST211	16. EST212	17. EST213	18. EST214
19. EST215	20. EST216	21. EST217	22. EST218	23. EST219	24. EST220
25. EST221	26. EST222	27. EST223	28. EST224	29. EST225	30. EST226
31. EST227	32. EST228	33. EST229	34. EST230	35. EST231	36. EST232
37. EST233	38. EST234	39. EST235	40. EST236	41. EST237	42. EST238
43. EST239	44. EST240	45. EST241	46. EST242	47. EST243	48. EST244
49. EST245	50. EST246	51. EST247	52. EST248	53. EST249	54. EST250
55. EST251	56. EST252	57. EST253	58. EST254	59. EST255	60. EST256
61. EST257	62. EST258	63. EST259	64. EST260	65. EST261	66. EST262
67. EST263	68. EST264	69. EST265	70. EST266	71. EST267	72. EST268
73. EST269	74. EST270	75. EST271	76. EST272	77. EST273	78. EST274
79. EST275	80. EST276	81. EST277	82. EST278	83. EST279	84. EST280
85. EST281	86. EST282	87. EST283	88. EST284	89. EST285	90. EST286
91. EST287	92. EST288	93. EST289	94. EST290	95. EST291	96. EST292
97. EST293	98. EST294				

90: EST295 100: EST296 101: EST297 102: EST298 103: EST299
104: EST300 105: EST301 106: EST302 107: EST303 108: EST304
109: EST305 110: EST306 111: EST307 112: EST308 113: EST309
114: EST310 115: EST311 116: EST312 117: EST313 118: EST314
119: EST315

Statistics: Mean 9.837; Variance 1.898; scale 5.183

SUMMARIES

Result No.	Query			ID	Description	Pred. No.	
	Score	Match	Length				
1	14	34.2	341	25	AA325703	EST10902 Pancreas tis	5.22e-168
2	99	27.3	240	52	AA356289	EST63410 Lymph node	1.30e-146
3	98	27.0	280	37	AA325955	EST32457 Colon 1 Homo	1.39e-144
4	97	26.7	273	26	AA303682	EST13889 Testis tumor	1.47e-142
5	85	23.7	294	31	AA314630	EST18648 Lung Homo sa	2.11e-120
6	68	18.7	379	99	AA291381	EST44702 rl Soares ova	5.77e-85
7	55	15.2	219	58	AA3377061	EST89641 Small intest	2.72e-60
8	48	13.2	366	59	AA378312	EST19107 Synovial sar	1.78e-47
9	47	12.9	267	76	AA4025647	EST47597 rl Soares ova	1.11e-45
10	47	12.9	267	76	AA352777	EST62616 Activated T-	1.11e-45
11	47	12.9	279	26	AA300571	EST13661 Testis tumor	1.11e-45
12	44	12.1	265	58	AA377128	EST89660 Small intest	2.37e-40
13	41	11.3	268	52	AA360195	EST63374 Lymph node 1	4.01e-35
14	39	10.7	291	58	AA3377074	EST89603 Small intest	1.06e-31
15	35	9.6	187	37	AA327672	EST30322 Colon 1 Homo	4.98e-25
16	35	9.6	204	26	AA303045	EST13823 Testis tumor	4.98e-25
17	34	9.4	256	26	AA300605	EST13453 Testis tumor	2.11e-23
18	33	9.1	230	85	AA428970	EST49822 rl Soares ova	8.55e-22
19	33	9.1	266	24	AA295648	EST103185 Pancreas tis	8.55e-22
20	32	8.8	326	37	AA327241	EST30532 Colon 1 Homo	3.31e-20
21	29	8.0	278	60	AA381085	EST94138 Activated T-	1.43e-15
22	26	8.0	306	100	AA429249	EST47609 rl Soares ova	1.43e-15
23	29	7.7	371	37	AA337565	EST30921 Colon 1 Homo	4.49e-14
24	27	7.4	198	62	AA383972	EST97425 Rhyom 1 Ho	1.32e-12
25	26	7.2	348	62	AA385989	EST97408 Pancreas tum	3.65e-11
26	25	6.9	170	26	AA309999	EST13949 Testis tumor	9.38e-10
27	25	6.9	307	58	AA377311	EST89659 Small intest	9.38e-10
28	24	6.6	427	52	AA360197	EST19376 Lymph node 1	2.23e-08
29	24	6.5	260	1	AA175689	MS94502 rl Soares mon	2.23e-09
30	24	6.5	551	22	AA419907	EST14091 rl Soares NIH	2.23e-08
31	23	6.3	199	26	AA301099	EST14127 Testis tumor	4.87e-07
32	22	6.1	656	18	AA116663	MS23967 rl Barstead M	9.71e-06
33	21	5.8	329	52	AA360196	EST63375 Lymph node 1	1.75e-04
34	21	5.8	249	90	C04273	Human Heart cDNA, c10	1.75e-04
35	21	5.8	455	22	AA116478	MS95307 rl Soares mon	1.75e-04
36	20	5.5	221	33	AA312223	EST12553 Adipose tiss	2.84e-03
37	20	5.5	252	14	AA2448782	EST923304 F Human fet	2.84e-03
38	20	5.5	255	90	C05523	Human Heart cDNA, c10	2.84e-03
39	20	5.5	344	90	C05176	Human Heart cDNA, c10	2.84e-03
40	20	5.5	264	16	AA3028196	MS83266 rl Striobasal	2.84e-03
41	20	5.5	470	116	AA456765	EST27605 rl Soares ova	2.84e-03
42	20	5.5	475	63	AA3817670	EST57636 rl KO mouse c	2.84e-03
43	20	5.5	475	97	AA433631	EST93661 rl Soares mon	2.84e-03
44	20	5.5	552	115	AA4542318	EST484101 rl Soares tes	2.84e-03
45	20	5.5	552	85	AA427605	EST44907 sl Soares ova	2.84e-03

ALIGNMENTS

RESULT	
LOCUS	341 bp
DEFINITION	AAC95703 Homo sapiens EST 10 APR 1997 ES-10902 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to similar to EMBL:G06816 mu heavy chain, V region.
ACCSSION	AAC95703
NID	G1948048
KEYWORDS	EST
SOURCE	Human
ORGANISM	Homo sapiens
Eukaryotes:	mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata:	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo:	
	1 (bases 1 to 341)
REFERENCE	Adams M.D., Kerlavage A.R., Fleischmann P.D., Fuldner P.A., But.C.J., Lee N.H., Kirkness.E.F., Weinstock X.G., Gocayne J.D., White.O., Sutton.G., Blake.J.A., Brandon.P.C., Man-Wai.C., Clayton,P.A., Cline.T.P., Cotton M.D., Parle-Rughes I., Fine.L.D, Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
AUTHORS	

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 280)
AUTHORS Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A., Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brannon, P. C., Man-Wai, C., Clayton, R. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M., Moreno-Palancas, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Uitterlbeck, T. P., Weidman, J. F., Li, Y., Bednarek, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Fertie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P. S., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, I., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other ESTs: THC167575
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
Source 1..280
/organism="Homo sapiens"
/note="Organ: colon; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
/clone_lib="Colon 1"
/dev_stage="adult"
<1..>280
mRNA 53 a 56 c 83 q 72 t 6 others
BASE COUNT 53 a 56 c 83 q 72 t 6 others
ORIGIN
Query Match 27.0%; Score 98; DB 37; Length 280;
Best Local Similarity 88.1%; Pred. No. 1.39e-144;
Matches 118; Conservative 0; Mismatches 15; Indels 1; Gaps 1.
Db 134 gattctggggaggagcgtgtccagcctggaggagtcctcctgagactctctgtacagcctct 193
|||||
QY 4 GAGTCGGGGGAGGGTGTGTCTGAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 63
Db 194 ggattcaccttccgtatattatctacacacttggtccgcagactccaggaagggggctg 253
|||||
QY 64 GGATTACCTTTAAAGCTGTATGSCATGCACTGGGTCTGCGCAGGGTCCAGGTAAGGGGCTG 123
Db 254 gnaataggtgacag 267
|||||
QY 124 G-AGTGGGTGGCAG 136

RESULT 4
LOCUS AA300982 273 bp mRNA EST 18-APR-1997
DEFINITION EST13889 Testis tumor Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain gene, VDJC regions (38:M34024).
ACCESSION AA300982
NID g1953335
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 273)
AUTHORS Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A., Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brannon, P. C., Man-Wai, C., Clayton, R. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M., Moreno-Palancas, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Uitterlbeck, T. P., Weidman, J. F., Li, Y., Bednarek, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Fertie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P. S., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, I., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other ESTs: THC179200
Contact: Kerlavage, AR
Bioinformatics
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Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers 1..273
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/note="Organ: testis; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
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/sex="male"
/dev_stage="adult"
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BASE COUNT 47 a 52 c 95 g 75 t 4 others
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Best Local Similarity 84.8%; Pred. No. 1.49e-142;
Matches 117; Conservative 0; Mismatches 21; Indels 0; Gaps 0.
Db 127 gattcgggggggggggtgtgttggtagcctgggggggtccctggagactctctgtgcaatctct 186
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QY 4 GAGTCGGGGGAGGGTGTGTCTGAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 63
Db 187 ggattcacctttagagactatgacatgagctgggtccgcagactccaggaagggggctg 246
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QY 64 GGAATCACCTTTCAAGACGTATGSCATGCACTGGGTCTGCGCAGGGTCCAGGTAAGGGGCTG 123
Db 247 gattgggtctcaggcatt 264
|||||
QY 124 GAGTGGGTGGCAGGTATT 141

RESULT 5
LOCUS AA314630 284 bp mRNA EST 19-APR-1997
DEFINITION EST18648 Lung Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, V region.
ACCESSION AA314630

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NID          gl966978
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
1 (bases 1 to 294)
Adams,M.D., Kerlavage,A.R., Fleischmann,P.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,C., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geodagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,P.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Springs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,T., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Paymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M., and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280

FEATURES
Source
Bioinformatics
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Tel: 3018699036
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1..294
/organism="Homo sapiens"
/clone_lib="XhoI"
/seq_id="XhoI"
/clone_lib="Lung"
/dev_stage="adult"
<1..>294

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ORIGIN
Query Match 23.7%; Score 86; DB 31; Length 294;
Best Local Similarity 85.2%; Pred. No. 2,128-120;
Matches 109; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Db 136 gaatctggggagcctgtcaagccggggggtccctnagactctctgtgagcctct 195
QY 4 GAGTCGGGGGGGGCGTGTGCTCAGCTGAGAGGTCCTCTGAGACTCTCTCTGTCAGCTCT 63

Db 196 ggaattcatttcaacagttacagatgaactggtccaccag-ctccagggaaggcgtg 254
QY 64 GGATTCACCTTCAAGACGATATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 123

Db 255 cagtgaggt 262
QY 124 GAGTGGGT 131

RESULT 6
LOCUS A:291381 379 bp mRNA EST 16-MAY-1997
DEFINITION t44q02.r1 Soares ovary tumor NbHCT Homo sapiens cDNA clone 725334
5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION

(HUMAN):
AA291381
g1939359
EST
human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
1 (bases 1 to 379)
Hillier,L., Allen,M., Rowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisinger,R.,
White,Y., Willie,T., Waterston,R., and Willson,R.
WashU-Merck EST Project 1997
Unpublished (1997)

Contact: Willson RK
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amerisham
High quality sequence stop: 361.
Location/Qualifiers
1..379
/organism="Homo sapiens"
/clone_lib="Soares ovary tumor NbHCT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>379

BASE COUNT 85 a 82 c 121 g 91 t
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Best Local Similarity 63.9%; Pred. No. 5,77e-85;
Matches 156; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Db 84 tgagggtctctgttaagacctctgtttacacctttggcacttttgatatacaactgggtac 143
QY 41 TGAGACTCTCTCTGTGTCAGCGCTCTGCTTCACTTCAAGACGCTATGCTGCTGCTGCTGCT 100

Db 144 ggcagggccctggcaaggccttgagtggtggatggatgcagcgtttacaatggttaaga 203
QY 101 GCCAGGCTCCAGGCTCAAGGAGGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 150

Db 204 caaactttgaggaggagttttcaggagcagagtcagcttgacctgaccactgacacatccacgaata 263
QY 161 AATATTAAGGAGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 270

Db 264 cagcctacatggagctgagaaacctgagatcttcacacacagcccatattattattgca 323
QY 221 GGGTGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 280

Db 324 gaga 327
QY 281 CAGA 284

```


AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Conway, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudok, D.M., Shirley, R., Small, K.V., Springs, T.A., Nterback, T.P., Weidman, J.F., Li, Y., Bednarik, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Dimke, D., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL MEDLINE COMMENT

Nature 377 (6547 Suppl), 3-174 (1995)

Other_ESTS: THCI66571

Contact: Kerlavage, AR

Bioinformatics

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Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)

FEATURES

source

Location/Qualifiers

1..279

/organism="Homo sapiens"

/note="Organ: testis; Vector: pBluescript SK-; Site:1:

ECORI; Site:2: XhoI"

/clone_lib="Testis tumor"

/sex="male"

/dev_stage="adult"

<1..279

63 a 74 c 85 q 56 t 1 others

BASE COUNT

ORIGIN

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Best Local Similarity 66.9%; Pred. No. 111e-45;

Matches 91; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 105 agtctgggctgaggtgaagaagcctgggctcagtggaaggtctctgcgaaggtcttg 164

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QY 5 AGTCGGGGGAGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 64

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Db 165 gatacaccctcaccgctactatctacactgggtgcagacagccctggacaagagcttn 224

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QY 65 GATTACCTTCACAGAGTATGGCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 124

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 225 agtggatgggatgat 240

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 125 AGTGGGTGGCAGGTAT 140

RESULT 12

LOCUS AA377128 265 bp mRNA EST 21-APR-1997

DEFINITION EST09660 Small intestine I Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, VDJ region.

AA377128

ACCESSION

NID 92029456

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryotae; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

REFERENCE AUTHORS

1 (bases 1 to 265)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Conway, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudok, D.M., Shirley, R., Small, K.V., Springs, T.A., Nterback, T.P., Weidman, J.F., Li, Y., Bednarik, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Dimke, D., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL MEDLINE COMMENT

Nature 377 (6547 Suppl), 3-174 (1995)

Other_ESTS: THCI67579

Contact: Kerlavage, AR

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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..265

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/note="Organ: small intestine; Vector: pBluescript SK-;

Site:1: EORI; Site:2: XhoI"

/clone_lib="Small intestine I"

/dev_stage="adult"

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BASE COUNT

ORIGIN

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Best Local Similarity 65.4%; Pred. No. 2.37e-40;

Matches 89; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Db 111 agtctggaggtgaggtgaagaagcctgggctcagtggaaggtctctgcgaaggtcttg 170

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 171 gttacacctttaccac 230

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||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 231 agtggatgggatgat 246

||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 125 AGTGGGTGGCAGGTAT 140

RESULT 13

LOCUS AA360195 258 bp mRNA EST

DEFINITION EST59374 Lymph node I Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, VDJ regions (GB:X67906).

AA360195

ACCESSION

NID 92012573

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 258)
AUTHORS
Adams, M. D., Kerlavage, A. P., Fleischmann, R. D., Fuldner, R. A., Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Goran, J. D., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Wai, C., Clayton, R. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M., Moreno-Palauques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. P., Weidman, J. F., Wiley, B., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Weissner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Puhon, S. M., Dillion, P. J., Fannon, M. P., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL
Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE
96026280

COMMENT
Other ESTs: THCL69164
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Fax: 3018699423

Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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/note="organ: lymph node; Vector: pBluescript SK-; Site_1: EcoRI, Site_2: XhoI"
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/dev_stage="adult"
BASE COUNT
56 a 74 c 68 g 55 t 5 others

Query Match 11.3%; Score 41; DB 52; Length 258;
Best Local Similarity 65.9%; Prd No. 4 01e-35;
Matches 83; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Db 99 ggtgtctccgtcagtaattactactgagctgtggtatccagatcccccagggaaggactn 158
QY 64 GGATTCACCTTCAAGACGTATGTCATGCACCTGCGCTCCGCTCCGCTCCAGGCAAGGGGCTG 123

Db 159 gactgg 164
QY 124 GAGTGG 129

RESULT 14
LOCUS AA3277074 291 bp mRNA EST 21-APP-1997
DEFINITION EST89603 Small intestine I Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, V region. (GR:214165)
ACCESSION AA3277074
NID g2029413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 291)
AUTHORS
Adams, M. D., Kerlavage, A. P., Fleischmann, R. D., Fuldner, R. A., Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Goran, J. D., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Wai, C., Clayton, R. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M., Moreno-Palauques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. P., Weidman, J. F., Wiley, B., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Weissner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Puhon, S. M., Dillion, P. J., Fannon, M. P., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.

TITLE
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JOURNAL
Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE
96026280

COMMENT
Contact: Kerlavage, AR
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Fax: 3018699423

Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
source
1..291
/organism="Homo sapiens"
/note="organ: small intestine; Vector: pBluescript SK-; Site_1: EcoRI, Site_2: XhoI"
/clone_lib="Small intestine I"
/dev_stage="adult"
BASE COUNT
67 a 73 c 89 g 61 t 1 others

Query Match 10.7%; Score 39; DB 58; Length 291;
Best Local Similarity 64.2%; Prd No. 1.06e-31;
Matches 86; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Db 90 tctggggtgaggtgaagagcctgggtctctctgtgaaagtntcgtgcaaggtattgga 149
QY 7 TCGGGGGAGGCGTGTGTCACCGCTGGAGGTCCTGAGACTCTCTGTGTCAGGCTGGA 66

Db 150 tacaccttcactgattactactcaactcaactgggtgcgagagggcctggagagggactgag 200
QY 67 TTCACCTTCAGAGCGTATGGATGATGATGATGATGATGATGATGATGATGATGATGAT 126

Db 210 tggatggatggat 223
QY 127 TGGGTGGCAGGTAT 140

RESULT 15
LOCUS AA327072 187 bp mRNA EST 20-APP-1997
DEFINITION EST83022 Colon I Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, V region.
ACCESSION AA327072
NID g1979319
KEYWORDS EST.
SOURCE human.



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Db	215	aaatcagtcacccatgtcactcgcagcagctccacggacgaattctccctgaatgaact	274
Qy	182	AGGGTGGATTCATGCTGCTCCACACAAATTCAGGAGCAGGCTTTCTGCACATACGA	241
Db	275	ctgcgacacactgcggacacagcgcctctattactatg	310
Qy	242	ACCTCAGCTCGGAGCAGCAGCGTGTCTATTACTGTG	277

RESULT	13		
LOCUS	T27609	287 bp	mPNA EST
DEFINITION	EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, VJJC regions (GR-M19512) (HT-3056)		
ACCESSION	T27609		
NID	9609707		
KEYWORDS	EST.		
SOURCE	human primer-M13 Reverse library-Human pancreas.		
ORGANISM	Homo sapiens		
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 287)		
REFERENCE			

White, O., Sutton, G., Blake, J. A., Brandon, R. C., Chig, M. W., Clayton, P. A., Cline, P. T., Cotton, M. D., Earle-Hughes, J., Fine, L., Fitzgerald, D. M., FitzHugh, W. M., Fritchman, I. L., Geobadian, N. S., Glodde, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle Jr, P. S., Kelley, J. M., Kline, K. M., Kelley, J. C., Liu, L. I., Marmaro, S. M., Merrick, J. M., Moreno-Palancas, R. F., McDonald, L. A., Nguyen, D. T., Pellegrino, S. M., Phillips, C. A., Pyder, S. E., Scott, J. I., Saudou, D. M., Shirley, P., Snail, K. V., Springs, T. A., Utterback, J. A., Weidman, J. F., Li, Y., Bednarek, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dinke, D., Feng, P., Ferris, A., Fischer, C., Hastings, J. A., He, W.-W., Hu, J.-S., Greene, J. M., Li, Gruber, J., Hudson, P., Kim, A., Korzak, D. L., Kunsch, C., Li, H., Li, Messner, P. S., Olsen, H., Raymond, I., Wei, Y.-F., Weng, J., Xu, C., Yu, G.-L., Ruben, S. M., Dillon, P. J., Fannon, M. P., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence

Unpublished (1995)

JOURNAL

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL Unpublished (1995)

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

mrna
BASE COUNT 52 a 77 c 85 g 50 t 3 others

CYPIN

Query Match 10.5% Score 38; DB 58; Length 287;
Best Local Similarity 64.0%; Pred. No. 9 92e-30;
Matches 87; Conservative 0; Mis-matches 49; Indels (- gaps)

[illegible]

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Db 207 aatggatggatgat 222
LOCUS EST 06-SEP-1995
DEFINITION EST89669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy
chain V region (GB:X61012) (HT:3230).
QY 125 AGTGGGTGGCAGTAT 140

RESULT 14
LOCUS mRNA EST 06-SEP-1995
DEFINITION EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu
(gamma) heavy chain, V(IV)DJC regions (HT:3057).
QY 125 AGTGGGTGGCAGTAT 140

ACCESSION T27727
NID q609825
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human Testis.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,R.D., Fuldner,P.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,P.C., Chiu,M.-W.,
Clayton,R.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,J.M., FitzHugh,W.M., Fritchman,J.L., Georhagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,Jr,P.S.,
Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.P.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.P., Rosen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

FEATURES
source 1..299
Location/Qualifiers
/organism="Homo sapiens"
mRNA <1..>299
BASE COUNT 61 a 84 c 82 g 68 t 4 others
ORIGIN
Query Match 10.5%; Score 38; DB 58; Length 299;
Best Local Similarity 65.1%; Pred No 8 92e-30;
Matches 82; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Db 94 gactggggccagactgtagctactgagacttcggagaccctgtccctcaactgactgtctct 153
QY 4 GAGTCGGGGGAGGGCGTGGTCCAGCTGAGAGTGGCTCCCTGAGACTCTCTGTCAGCGCTCT 63

Db 154 ggtgggtccatcagtagtactgactgagactgagactgattccggcagcccccaggaagagctg 213
QY 64 GGATTACCTTCAAGACGATATGCCATGCTACTGGCTCCGCGCAGGCTCCAGGAGGCGTG 123

Db 214 cagtgg 219
QY 124 GAGTGG 129

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Search completed: Tue Feb 24 11:48:05 1998
Job time : 789 secs.

WIRE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 15:39:10 1998: Maspar time 23.60 Seconds
707.450 Million cell updates/sec

Tabular output not generated

Title: >US-08-844-215-25
Description: (1-363) from US0844215.seq
Perfect Score: 363
N.A. Sequence: 1 CTCGAGTGGGGGAGGGGTCCCTGGTCACGGTCTCTCA 363
Comp: GAGTCACGCCCTCCGCA.....GGGACAGTGGCAGAGGT

Scoring table: TABLE default
Gap 5

Nmatch STD: Dbase 0: Query 0

Searched: 87531 seqs, 22996021 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1-back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PT90 9:PT91
10:PT92 11:PT93 12:PT94 13:PT95 14:PT96

Statistics: Mean 7.667; Variance 4.010; scale 1.912

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	219	60.3	433	6	US-08-259- Sequence 1, Applicatio	4,876-152
2	219	60.3	433	7	US-08-458- Sequence 1, Applicatio	4,876-152
3	210	57.9	436	7	US-08-305- Sequence 1, Applicatio	8,166-145
4	205	56.5	339	11	PCT-US93-1 Sequence 45, Applicati	8,336-141
5	190	52.3	372	11	PCT-US93-1 Sequence 43, Applicati	8,426-129
6	187	51.5	294	11	PCT-US93-1 Sequence 47, Applicati	2,106-126
7	185	51.0	345	11	PCT-US93-1 Sequence 41, Applicati	8,306-125
8	184	50.7	432	5	US-08-326- Sequence 1, Applicatio	5,226-124
9	183	50.4	364	11	PCT-US93-1 Sequence 3, Applicati	3,286-123
10	179	49.3	360	11	PCT-US93-1 Sequence 19, Applicati	5,086-120
11	179	49.3	360	11	PCT-US93-1 Sequence 21, Applicati	5,086-120
12	179	49.3	360	11	US-08-264- Sequence 13, Applicati	5,086-120
13	177	48.8	360	11	PCT-US93-1 Sequence 2, Applicati	2,006-118
14	177	48.8	360	11	PCT-US93-1 Sequence 23, Applicati	2,006-118
15	177	48.8	360	11	PCT-US93-1 Sequence 33, Applicati	2,006-118
16	177	48.8	360	11	PCT-US93-1 Sequence 31, Applicati	4,906-116
17	174	47.9	360	11	PCT-US93-1 Sequence 29, Applicati	4,906-116
18	174	47.9	360	11	PCT-US93-1 Sequence 35, Applicati	3,066-115
19	173	47.7	351	11	PCT-US93-1	

20 173 47.7 360 11 PCT-US93-1 Sequence 39, Applicati 3,066-115
21 168 46.3 366 11 PCT-US93-0 Sequence 42, Applicati 2,916-111
22 168 46.3 376 11 PCT-US93-0 Sequence 2, Applicatio 2,916-111
23 156 45.7 389 11 PCT-US93-0 Sequence 11, Applicati 1,136-109
24 154 45.2 389 11 PCT-US93-0 Sequence 13, Applicati 4,406-108
25 154 42.4 393 7 US-08-468- Sequence 3, Applicatio 3,756-100
26 154 42.4 393 6 US-08-259- Sequence 3, Applicatio 3,756-100
27 153 42.1 369 5 US-08-199- Sequence 3, Applicatio 2,326-99
28 148 40.8 354 11 PCT-US93-0 Sequence 9, Applicatio 2,066-95
29 147 40.5 405 13 PCT-US95-0 Sequence 7, Applicatio 1,296-94
30 147 40.5 444 5 US-07-826- Sequence 38, Applicati 1,296-94
31 145 39.9 405 13 PCT-US95-0 Sequence 3, Applicatio 4,916-93
32 143 39.4 1347 1 5455030-2 Patent No. 5455030
33 142 39.1 417 7 US-08-398- Sequence 21, Applicati 1,146-90
34 142 39.1 417 7 US-08-398- Sequence 21, Applicati 1,146-90
35 142 39.1 756 7 US-08-398- Sequence 29, Applicati 1,146-90
36 142 39.1 756 7 US-08-398- Sequence 29, Applicati 1,146-90
37 141 38.8 752 1 5455030-12 Patent No. 5455030
38 140 38.6 339 4 US-07-789- Sequence 9, Applicatio 4,326-89
39 139 38.3 3343 1 F53363-2 Patent No. 545363
40 138 38.0 357 7 US-08-207- Sequence 26, Applicati 1,626-87
41 138 38.0 711 1 5455030-8 Patent No. 5455030
42 138 38.0 923 12 PCT-US94-0 Sequence 1, Applicatio 1,626-87
43 137 37.7 357 7 US-08-331- Sequence 21, Applicati 9,956-87
44 137 37.7 375 7 US-08-331- Sequence 59, Applicati 9,956-87
45 137 37.7 717 12 PCT-US94-1 Sequence 58, Applicati 9,956-87

ALIGNMENTS

RESULT 1
ID US-08-259-372A-1 STANDARD; DNA; UNC; 423 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08259372A.
CC Sequence 1, Application US/08259372A
CC Patent No. 5565354
CC GENERAL INFORMATION:
CC APPLICANT: Ostberg, Lars G.
CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
N
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.50
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/38/259,372A
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196

RESULT 14
 ID PCT-US93-10555-25 STANDARD: DNA: UNC: 360 BP
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 25, Application PC/TUS9310555
 CC Sequence 25, Application PC/TUS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 THROUGH
 CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
 TES
 CC TITLE OF INVENTION: THEREOF
 CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1 0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: PD-2530
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 25:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 360 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC IMMEDIATE SOURCE:
 CC CLONE: SpA3-15
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1 360
 SQ Sequence 360 BP: 75 A: 97 C: 111 G: 77 T: 0 other:

Query Match 48.8% Score 177: DB 11: Length 360:
 Best Local Similarity 81.7% Pred. No. 2 Gaps-118:
 Matches 228: Conservative 0: Mismatches 51: Indels 0: Gaps 0:
 Db 13 CTCGAGTCTGGGAGGATTGGTACAGTCGCGGGGGTCTGTGAGACTCTCTGTGTGAGGC 72
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 Db 133 CTGAGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 192
 QY 121 CTGAGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
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Db 253 AGCTGAGAGCTGGAAACACAGCGGCTTATATATATATATATATATATATATATATAT 291
 QY 241 AGCTGAGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 279
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 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 23, Application PC/TUS9310555.
 CC Sequence 23, Application PC/TUS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 THROUGH
 CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
 TES
 CC TITLE OF INVENTION: THEREOF
 CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: PD-2630
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 23:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 360 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC IMMEDIATE SOURCE:
 CC CLONE: SpA3-13
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1 360
 SQ Sequence 360 BP: 75 A: 97 C: 111 G: 77 T: 0 other:

Query Match 48.8% Score 177: DB 11: Length 360:
 Best Local Similarity 81.7% Pred. No. 2 Gaps-118:
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 Db 13 CTCGAGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 72
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QY 241 AGCCTGAGACTCGAGGACACGCGCTGTCTATTACTGTGCG 279
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Search completed: Tue Feb 24 15:41:13 1998
Job time : 123 secs.

MUSE (TM)

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Copyright (C) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.
MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:49 1998: Maspar time 53.66 Seconds
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Comp: GAGCTCAAGCCGCCCTCCGCA GGGACCAATGGCAAGAGGT
Scoring table: TABLE default
Gap 6

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Post-processing: Minimum Match 0%
Listing first 45 summaries
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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
Statistics: Mean 8.049; Variance 4.621; scale 1.742
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
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2	231	63.6	583 13	Q78971	Human immunoglobulin
3	228	62.8	336 2	Q11957	Anti-human Rhd HAM-B
4	227	62.5	512 13	Q78968	Human immunoglobulin
5	226	62.3	339 2	Q11956	Anti-human Rhd HAM-B
6	225	62.0	369 33	T60380	Anti-TGF beta-1 scFv
7	224	61.7	732 25	T44089	Ulcerative colitis-as
8	222	61.2	345 33	T50369	Anti-TGF beta-2 scFv
9	221	60.9	369 33	T50381	Anti-TGF beta-1 scFv
10	221	60.9	1521 2	Q11880	Encodes heavy chain v
11	219	60.3	337 28	T60122	Coding sequence for h
12	219	60.3	423 24	T46128	Monoclonal antibody p
13	219	60.3	423 33	T85838	Monoclonal antibody p
14	219	60.3	429 10	Q64050	Sequence of the VH re
15	215	59.5	350 33	T60370	Anti-TGF beta-2 scFv

15 216 59.5 357 28 T60116 Coding sequence for h
17 216 59.5 699 25 T44088 Ulcerative colitis-as
18 216 59.2 342 2 Q11953 Anti-human Rhd HAM-B
19 214 59.0 369 33 T60382 Anti-TGF beta-1 scFv
20 212 58.4 342 2 Q11955 Anti-human Rhd HAM-B
21 211 58.1 657 6 Q36133 MH47 Mab heavy chain
22 210 57.9 426 32 T80758 54-863 antibody H5Vef
23 209 57.6 925 2 Q12839 Variable region of u
24 203 55.9 339 10 Q64855 SPA-reactive VH regio
25 202 55.6 423 14 Q87336 Anti-interleukin-1-a
26 201 55.4 357 28 T60118 Coding sequence for h
27 197 54.3 357 28 T60120 Coding sequence for h
28 194 53.4 375 1 Q03608 Sequence encoding 461
29 194 53.4 456 1 Q03610 Sequence encoding 461
30 193 53.2 514 13 Q78961 Human immunoglobulin
31 192 52.9 459 29 T42619 Heavy chain transcrip
32 191 52.6 402 30 T43529 DNA encoding anti-lym
33 191 52.6 1576 8 Q49944 Human anti-HBs heavy
34 190 52.3 354 33 T72129 CEA-specific antibody
35 189 52.1 705 1 N81639 Sequence of genomic D
36 189 52.1 743 13 Q78986 Human immunoglobulin
37 188 51.8 372 10 Q64854 SPA-reactive VH regio
38 187 51.5 294 10 Q64856 SPA-reactive VH regio
39 185 51.0 519 13 Q78959 Human immunoglobulin
40 185 51.0 345 10 Q64953 SPA-reactive VH regio
41 185 51.0 649 13 Q79002 Human immunoglobulin
42 185 51.0 877 13 Q78945 Human immunoglobulin
43 183 50.4 264 14 Q89332 DP54 VH gene
44 183 50.4 369 10 Q64851 SPA-reactive VH regio
45 182 50.1 432 12 Q71717 Monoclonal antibody L

ALIGNMENTS

RESULT 1
ID Q43772 standard: CDNA: 909 BP.
AC Q43772:
DT 01-OCT-1993 (first entry)
DE Sequence encoding the heavy chain variable region (VH) of human
DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line
DE 88BV59, ATCC CRL 10634
KW B-cell; immunoglobulin g; cancer; tumour; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
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FT /tag= a 58..432
FT /tag= b
FT /product= VAR
FT /note= "1st AA of VAR is denoted AA#1"
FT CDS 148..204
FT /tag= c
FT /product= CDR 1 205..351
FT /tag= d
FT /product= CDR 2 352..426
FT CDS
FT /tag= e
FT /product= CDR 3 427..726
FT CDS
FT /tag= f
FT /product= CH 1 727..771
FT CDS
FT /tag= g
FT /product= Hinge 772..990
FT /tag= h
FT /product= FAB'
PN EP-546634-A.
PD 16-JUN-1993.
PF 09-DEC-1991: 203827.
PR 13-DEC-1991: US-807300.
PA (ALKU) AKZO NV.

```

RESULT      2
ID          Q78971 standard; DNA; 583 BP.
AC          Q78971;
DE          03-AUG-1995 (first entry)
DT          Human immunoglobulin Vh gene #33.
PR          primer: PCR: amplify; human; immunoglobulin; variable; heavy chain;
KW          cosmid; placenta; vector; pJB81; E.coli; mammalian; ds..
OS          Homo sapiens.
FH          Key
FH          Location/qualifiers
FT          CDS
FT          /*tag= a
FT          /*product= human immunoglobulin variable heavy chain
FT          intron
FT          66..167
FT          /*tag= b
FT          misc_signal
FT          473..475
FT          /*tag= c
FT          /*note= "miscellaneous signal, does not conform to
FT          terminator or splice site sequence"
FT          W09426895-A.
FT          24-NOV-1994.
FT          PD
FT          10-MAY-1993; J00603.
FT          10-MAY-1993; W0-J00603
FT          (NIBS) JAPAN TOBACCO INC.
FT          Panjo T, Matsuda F;
FT          WPI: 95-C06791/01.
FT          P-PSDB; R66323.
FT          DA

```

```

Query Match      63.6%; Score 231, DB 13, Length 583.
Best Local Similarity 91.1%; Pred No 7,54e-146;
Matches 256; Conservative 0; Mismatches 25; Indels 0; Gaps 0.

Db 194  gadtctgggggaggggtgtccagcgtggaggtccctcgacactctctctgtcgacgtct 253
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4   GAGTCGGGAGAGAGGCTGAGCTAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 63

Db 254  gattcaccttcagtagctatggcctgcactcgtgtccgcaggctccaggcaagggtctg 313
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64  GATTTACCTTTAAAGACGATGCAATGACATGCTGGTGGGCTAGCTTCAGTAAAGGACATG 123

Db 314  gdtgggtggcagttatgggtatgtaagagtaataaatactatcgagactccgcdaag 373
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124  GAGTGGGTGGTAAAGTATTGTTTGTATGAGCTAACTAAATATTAACTGAGACTCGGTGAAG 183

Db 374  ggcgaattcaccatctccagaagaactccagcaacacgtctgttcgcaataaacagc 433
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184  GSCCGAATTCATGCTCTCCAGAGACAAATTCAGGAGCACTGGTGTTTCTACATAGTAGGC 243

Db 434  ctgaagccgaggaacacggctgtgtattactotgcgaaga 474

QY 244  CTGAGACTCTGAGGACACGGCTGTCTATTACTCTGTCGACAGA 284

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RESULT	3	
ID	Q11957 standard; DNA; 336 BP.	
AC	Q11957;	
DE	15-AUG-1991 (first entry)	
DI	Anti-human RHD HAM-B MAb (VH chain).	
DE	Monoclonal antibody; rhesus D; blood-typing; CDR;	
KW	haemolytic disease of the newborn; HDN; ss.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	misc_feature	68..82
FT	/*tag= a	
FT	/label= CDR1	
FT	misc_feature	125..175
FT	/*tag= b	
FT	/label= CDR2	
FT	misc_feature	272..319
FT	/*tag= c	
FT	/label= CDR3	
PN	WO9107492-A.	
PD	30-MAY-1991.	
PE	13-NOV-1990; E01964.	
PR	13-NOV-1989; GB-025590.	
PA	(BLOO-) CENT BLOOD LAB AUTH.	
PI	Hughes- Jones N;	
PI	WPI: 91-178104/24.	
DR	P-PSDB: R12275.	
PT	DNA encoding complementary determining regions - of human	
PT	anti-rhesus D antibodies, useful in prodn. of monoclonal	
PT	antibodies and for passive immunisation	
PS	Disclosure: Fig 14: 32pp; English.	

Query Match 62.3%; Score 226; DB 2; Length 339;
 Best Local Similarity 90.4%; Pred. No. 3,446-142;
 Matches 253; Conservative 0; Mismatches 27; Indels 0; Gaps 0.

Db 1 gggagcgggtccagcctggagctccctgagactccctgagctccctgagcgtctgagctcag 60
 QY 12 GGGAGCGGTGGCCAGCCCTGGGAGGTGCTGAGACTTCCTGTGCGAGGTCTGGATTCA 71

Db 61 ctccaataattatggcatgacactgggtccgagcagctccagcaggaagggtggagtggt 120
 QY 72 CTTCAAGAGCTATGGCATGCACTGGTCCGCGCAGGCTCCAGGCAAGGGCTGGAGTGG 131

Db 121 ggcagttatggtatgagtggaagtaataaaactatcagactccctggaaggccgatt 180
 QY 132 GGCAGGTATTTGTTTATGSAAGTAACCAATATTACAGACACCCGCTGAAGGGCCGATT 191

Db 181 caccatctccagagacaaatccaaagaaacagctgtatctgcaaatgaacacccctgagagc 240
 QY 192 CATCGCTCTCCAGAGACAATTCAGGGGACACGGGTGTTCTGCAGATGAGCACTTSA 251

Db 241 cgaggacagcgtgtgtattactgtcagagagaacagctact 280
 QY 252 CGAGGACAGCGGTGTCTATTACTGTCCGACAGAGGGTCT 291

RESULT 6
 ID T60380 standard; DNA; 369 BP.
 AC T60380;
 DE Anti-TGF beta-1 scfv antibody 1-B2 VH gene.
 KW Transforming growth factor beta-1; TGF-beta-1; human;
 KW antibody engineering; scFv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy; ss.
 OS Homo sapiens.
 PN GB2305921-A.
 PD 23-APR-1997.
 PF 07-OCT-1996; 020920.
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L., Green JA., Jackson RH., Johnson KS., Pope AR;
 PI Tempest PR., Thompson JE., Vaughan TJ., Williams AJ;
 PI Wilton AJ;
 DR WPI; 97-215360/20.
 DR P-PSDB; W15534.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT immune and inflammatory disease
 PS Example 1; Fig 1a(i); 184pp: English.
 CC This DNA sequence comprises the gene encoding the VH domain
 CC (W15534) of human scfv antibody 1B2 (also known as 7A3), which
 CC is specific for transforming growth factor (TGF) beta-1. It was
 CC isolated by panning a phage antibody library produced from a
 CC peripheral blood lymphocyte library. The antigen-binding domains
 CC of human antibodies (see W15532-40) to TGF beta-1 and/or beta-2 can
 CC be used to counter the adverse effects of TGF beta, such as (i)
 CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
 CC fibrosis, arterial injury, proliferative retinopathy, retinal
 CC detachment, adult respiratory distress syndrome, liver cirrhosis,
 CC post-myocardial infarction, post-angioplasty restenosis,
 CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
 CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
 CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
 CC arthritis, macrophage deficiency diseases or macrophage pathogen
 CC infection). Nucleic acids encoding human antibody VH and VL can be
 CC used for prodn. of recombinant antigen-binding domains. These are

CC highly specific, have low dissociation constants (pref. less than 5
 CC nM) and low IC50s for neutralisation.
 SQ Sequence 369 BP, 87 A, 86 C, 115 G, 81 T;

Query Match 62.0%; Score 225; DB 33; Length 369;
 Best Local Similarity 90.6%; Pred. No. 1,856-141;
 Matches 251; Conservative 0; Mismatches 26; Indels 0; Gaps 0.

Db 16 gagtcctggggagcgtggtccagcctgggaggtccctgagactccctgacacccctct 75
 QY 4 GAGTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 63

Db 76 ggattcacctcagtagctatggcatgacactgggtcggcaggtcggcaggtcggcaggtc 135
 QY 64 GGATTTCACCTTTCAAGAGAGGTATGGCATGCTGCTGGGTGGGTGGGTGGGTGGGTGG 123

Db 136 gagtggtggcagtgatcatatcatatgagtggaagttaataataactatgcagactccgtgaag 195
 QY 124 GAGTGGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 183

Db 196 ggcattccaccatctccagagacaattccaaagaaacacgctgtatctgcaaatgaaacac 255
 QY 184 GGCATTTCATCGTCTCCAGAGACAATTCAGGGGACACAGGCTGTTCTTCTGAGATGA 243

Db 256 ctgagagcgtgagacacggtctgtattactgtgctga 292
 QY 244 CTGAGACTCGAGGACACGGTGTGTTACTTGTGCGA 280

RESULT 7
 ID T44089 standard; CDNA; 732 BP.
 AC T44089;
 DE 27-FEB-1997 (first entry)
 DE ulcerative colitis-associated PANCA Fab 5-4 heavy chain cDNA.
 KW ulcerative colitis; anti-neutrophil cytoplasmic antibody; ANCA;
 KW PANCA; UCPANCA; antibody engineering; phage display; diagnosis;
 KW cyclic; ds.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT /tag= a
 FT /product= UC-associated ANCA IgG heavy chain
 FT misc_RNA 1..15
 FT /tag= b
 FT /product= N-terminal tag
 FT misc_RNA 16..93
 FT /tag= c
 FT /label= FR1
 FT /note= "framework region 1"
 FT misc_RNA 94..108
 FT /tag= d
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT misc_RNA 109..150
 FT /tag= e
 FT /label= FR2
 FT /note= "framework region 2"
 FT misc_RNA 151..201
 FT /tag= f
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT misc_RNA 202..297
 FT /tag= g
 FT /label= FR3
 FT /note= "framework region 3"
 FT misc_RNA 298..360
 FT /tag= h
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT misc_RNA 361..393
 FT /tag= i
 FT /label= FR4
 FT /note= "framework region 4"

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FT misc_RNA 394...684
FT /tag- j
FT /label- CH1
FT /note- "heavy chain constant region"
FT misc_RNA 685...711
FT /tag- k
FT /label- Hinge
FT /note- "partial hinge segment of the heavy chain"
FT misc_RNA 712...732
FT /tag- l
FT /label- Hex-HTAG
FT /note- "hexahistidine tag"
FT misc_RNA 16...684
FT /tag- m
FT /label- Fd
FT /note- "heavy chain Fd"
FT misc_RNA 16...297
FT /tag- n
FT /label- VHSEGMENT
FT /note- "heavy chain variable segment"
FT misc_RNA 298...363
FT /tag- o
FT /label- D
FT /note- "diversity segment"
FT misc_RNA 364...408
FT /tag- p
FT /label- JH
FT /note- "heavy chain joining segment"
FT misc_RNA 16...408
FT /tag- q
FT /label- VHDOMAIN
FT /note- "heavy chain variable domain"
PN W09639186-AL.
PD 12-DEC-1996.
PF 05-JUN-1996: 008756.
PP 06-JUN-1995: US-472688.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PA (PFGC ) UNIV CALIFORNIA.
PI Braun J., Eggena MT., Targan SR.
DR WPI: 97-042866/04.
DR P-PSDB: W07614.
PT Antibody material associated with ulcerative colitis - comprising
PT anti-neutrophil cytoplasmic antibody, characterised by perinuclear
PT neutrophil staining pattern.
PS Disclosure: Page 113-114: 145pp; English.
CC A cDNA clone (T44089) derived from human gut-associated lymphoid
CC tissue codes for the heavy chain (W07614) of recombinant UcpANCA
CC Fab clone 5-4. Anti-neutrophil cytoplasmic antibody characterised
CC by perinuclear neutrophil staining pattern (pANCA) associated with
CC ulcerative colitis (UC) was recombinantly produced and
CC characterised using a phase display technique. Libraries of VH-
CC and VL-encoding DNA homologues having the immunoreactivity of
CC UcpANCA antigen were created. Recombinant UcpANCA Fab clones 5-3
CC and 5-4 were generated (see also W07613-16). These can be used in
CC methods for screening for UcpANCA and for isolating UcpANCA
CC antirens.
SQ Sequence 732 BP. 169 A. 227 G. 124 C. 142 T.

Query Match 61.7%; Score 224; DB 25; Length 732;
Best Local Similarity 89.4%; Pred No. 9,976-141;
Matches 254; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 1 ctgagctcggggagggcgtggccagcctgggaagctccctcagactctcctgtacagcc 60
    |||||
QY 1 CTCGAGTCGGGGGAGGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 60
    |||||

Db 61 tctgattcacccttcagcaactatgcacatgcactggctcggccagctccagggcaagg 120
    |||||
QY 61 TCTGGATTCACTTCGAAGAGTATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 120
    |||||

Db 121 ctgagtgaggtgacaggtattcctcctgatacaaaaaaataatgtgactccgtg 180
    |||||
QY 121 CTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
    |||||

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Db 181 aagggccgagttcttcattctccagagacacattccagagacacaccttatctgcaatgaac 240
    |||||
QY 181 AAGGGCCGATTCTTCATTCTCCAGAGACAAATTCAGAGACACACCTTATCTGCAATGAGC 240
    |||||

Db 241 accctgagagctcagagacacagctctctattactctcccaaaa 284
    |||||
QY 241 ACCCTGAGACTCGAGAGACAGCTCTCTATTACTCTCCCAAGA 284
    |||||

RESULT 8
ID T60369 standard; DNA; 345 BP.
AC T60369.
DT 27-Nov-1997 (first entry)
DE Anti-TGF beta-2 scFv antibody 2A-H11 VH gene.
KW Transforming growth factor beta-2; TGF-beta-2; human;
KW antibody engineering; scFv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy; ss.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
PN GB2305921-A.
PD 23-APR-1997.
PF 07-OCT-1996: 020920.
PR 19-JAN-1996: GB-001081.
PP 06-OCT-1995: GB-020486
PA (CAME-) CAMERIDGE ANTIBODY TECHNOLOGY.
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
DR WPI: 97-215360/20.
DR P-PSDB: W15522.
PT Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
PS Example 1; Fig 2a(i); 184pp; English.
CC This DNA sequence comprises the gene encoding the VH domain
CC (W15522) of human scFv antibody 2A-H11 (also known as 6H1), which
CC is specific for transforming growth factor (TGF) beta-2. It was
CC isolated by panning a phage antibody library produced from cloned
CC germline V genes and synthetic CDRs. The antigen-binding domains
CC of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can
CC be used to counter the adverse effects of TGF beta, such as (i)
CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
CC fibrosis, arterial injury, proliferative retinopathy, retinal
CC detachment, adult respiratory distress syndrome, liver cirrhosis,
CC post myocardial infarction, post-angioplasty restenosis,
CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
CC arthritis, macrophage deficiency diseases or macrophage pathogen
CC infection). Nucleic acids encoding human antibody VH and VL can be
CC used for prodn. of recombinant antigen-binding domains. These are
CC highly specific, have low dissociation constants (pref. less than 5
CC nM) and low IC50s for neutralisation.
SQ Sequence 345 BP. 76 A; 83 C; 112 G; 74 T;

Query Match 61.2%; Score 223; DB 33; Length 345;
Best Local Similarity 90.5%; Pred No. 4,496-139;
Matches 248; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 16 gagctcggggagggcgtggctcagcctgggaggtccctggaactctcctgtacacatct 75
    |||||
QY 4 GAGTCGGGGGAGGGAGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 63
    |||||

Db 76 gaattcacccttcagtagtgcacatgcactggctccgagggctccagggcaaaagctct 135
    |||||

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QY 64 GGATTCACCTTCAGACGATATGACATGAGTGGTCCGCTCCAGGCTCCAGGCAAGGGGCTG 123
Db 136 gattgagtgacattatggtatgataagaaataataactatgcagactccggtgaag 195
QY 124 GAGTGGGTGCGCAGGATATTCGTTTGATGAGNAGTAACCAATATACGACACTCCGTGAAG 183
Db 196 ggcgattaccattccagagacaaattccaaagaacacgctgtatctgcataatggacacg 255
QY 184 GGCGGATTATCTCTCCAGAGACAAATCCAGGGACACGGTGTCTTCGTCAGATGAGCAGC 243
Db 256 ctgagagccagagacagcgccgtgtattactgtg 289
QY 244 CTGAGACTCGAGGACACGGCTGTCTATTACTGTG 277

RESULT 9
ID T60381 standard; DNA; 369 BP.
AC T60381;
DE Anti-TGF beta-1 scfv antibody 31G9 VH gene.
KW Transforming growth factor beta-1; TGF-beta-1; human;
KW antibody engineering; scfv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy; ss.
OS Homo sapiens.
PN GR230521-A.
PD 23-APR-1997.
PF 07-OCT-1996; 020920.
PR 19-JAN-1996; GB-001081.
PR 06-OCT-1995; GB-020486.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
DR WPI: 97-215360/20.
DR P-PSDB; W15535.
PT Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
PS Example 1: Fig 1a(ii); 194pp; English.
CC This DNA sequence comprises the gene encoding the VH domain
CC (W1535) of human scfv antibody 31G9, which is specific for
CC transforming growth factor (TGF) beta-1. It was isolated from
CC a large single chain Fv library. The antigen-binding domains
CC of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can
CC be used to counter the adverse effects of TGF beta, such as (i)
CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
CC fibrosis, arterial injury, proliferative retinopathy, retinal
CC detachment, adult respiratory distress syndrome, liver cirrhosis,
CC post myocardial infarction, post-angioplasty restenosis,
CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
CC arthritis, macrophage deficiency diseases or macrophage pathogen
CC infection). Nucleic acids encoding human antibody VH and VL can be
CC used for prodn. of recombinant antigen-binding domains. These are
CC highly specific, have low dissociation constants (pref. less than 5
CC nM) and low IC50s for neutralisation.
SQ Sequence 369 BP; 83 A; 88 C; 117 G; 81 T;

Query Match 60.9%; Score 221; DB 33; Length 369;
Best Local Similarity 90.2%; Pred. No. 1.56e-138;
Matches 248; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 17 agtctggggagcggtggtccacccctggaggtccctcctgagactcctctgagcctctg 76
QY 5 AGTCGGGGGAGCGGTGTCAGGCTGGGAGGTCCCTGAGACTCTCTCTGTCAGGCTCTG 64

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Db 77 gattcacttcagtagctatggcatgctcagctgggtccgccaggctccagacaaaggactgg 136
QY 65 GATTACACTTCAAGACGTATGGCATGCACTGCGTCCGCTAGGCTTCAGGTAAGGGGCTG 124
Db 137 agtgggtggcagttatcatatgatggaagtattaaatactatgcagactccgttaagg 196
QY 125 AGTGGGTGGTAGGTATTTCTGTTTGGTATGATGSAASTAACCAATATTACGGAGACATCGCTGAAG 184
Db 197 ggcattccacatctccagagacaaattccaaagaacacgctgtatctgcaaatgaacagcc 256
QY 185 GCCGATTATCTGCTCCAGAGACAAITCCAGGACACGGTGTCTTCGTCAGATGAGCAGCC 244
Db 257 tgagagctgagggacacgctgtgtattactgtg 291
QY 245 TGAGACTCGAGGACACGGTGTCTATTACTGTGCG 279

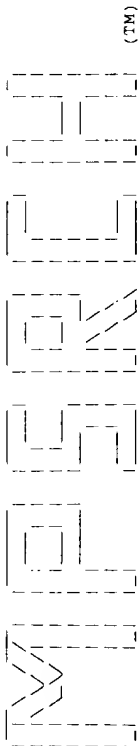
RESULT 10
ID Q11880 standard; DNA; 1521 BP.
AC Q11880;
DE 01-AUG-1991 (first entry)
DE Encodes heavy chain variable region for 4B9 human monoclonal Ab.
KW immunoglobulin G; heavy chain; variable region; duplication;
KW passive immunity; group B streptococci; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_RNA 450..57
FT /*tag= a
FT /*note= "octamer"
FT sig_peptide 583..628
FT /*tag= b
FT /*note= "leader"
FT misc_RNA 732..1107
FT /*tag= c
FT /*product= heavy chain variable region
FN W09106305-A.
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WP: 91-153947/22.
DE P-PSDB: P12132, P12133, P12134.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Claim 44; Fig 18; 104pp; English.
CC The leader peptide and the L/V region are encoded in different
CC reading frames. The L/V region corresponds to the last three amino
CC acids of the leader peptide and the variable region gene.
CC See also Q11878 and Q11879.
SQ Sequence 1521 BP; 349 A; 376 C; 425 G; 371 T;

Query Match 60.9%; Score 221; DB 2; Length 1521;
Best Local Similarity 89.3%; Pred. No. 1.56e-138;
Matches 251; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 756 gattctgggggagcggtgtccagcctggaggtccctgagactcctctatgcagctct 815
QY 4 GAGTCGGGGGAGGCGTGTGCTCCAGCTGGAGGTGCTGAGACTCTCTCTGTCAGGCTCT 63
Db 816 ggaattcccttcagagagctatggcagctcctgggtccgcagagctccagcaaggagctg 875
QY 64 GGATTCACCTTCAGACGATATGGCATGCTGGTCCGCTCCAGGCTCCAGGAGGGCTG 123
Db 876 gattgggtggcagttatcatctatgcagagtggaagtgttgactactatgcagactccgtgaag 935
QY 124 GAGTGGGTGCGCAGGATATTCGTTTGATGAGNAGTAACCAATATACGACACTCCGTGAAG 183
Db 936 ggcgattccacattccagagacaaattccagagatctgctgtatgtgcaaatgaacagc 995
QY 184 GGGGATTTCATCTCTCTAGAGACAAITCCAGGAGACACGGTGTCTTCGTCAGGCTCTG 243

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(TM)

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MPsearch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:59:04 1998: MasPar time 459.90 seconds
Tabular output not generated. 1121.143 Million cell updates/sec

Title: >US-08-844-215-25
Description: (1-363) from US08844215 seq
Perfect Score: 363
N.A. Sequence: 1 CTCGAGTGGGGGAGGGGTT.....CCCTGGTCACTGCTCTCA 363
Comp: GAGCTCAGCCGCTCTCTCA

Scoring table: TABLE default
Gap 6
Nmatch STD: Dbase 0; Query 0
Searched: 430261 seqs. 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new
1: BCT 2: FUN 3: GEN 4: HTG1 5: HTG2 6: HTG3 7: HTG4 8: HUM1
9: HUM2 10: HUM3 11: INV1 12: INV2 13: ORG 14: MAM 15: VRT
16: PLN 17: PLO1 18: PLO2 19: ROD 20: SYN 21: UNC 22: VIF
Database: genbank101
23: BCT1 24: BCT2 25: BCT3 26: BCT4 27: BCT5 28: BCT6 29: BCT7
30: BCT8 31: BCT9 32: BCT10 33: BCT11 34: BCT12 35: BCT13
36: GEN1 37: GEN2 38: GEN3 39: GEN4 40: GEN5 41: GEN6 42: HTG1
43: HTG2 44: HTG3 45: HTG4 46: HTG5 47: INV1 48: INV2 49: INV3
50: INV4 51: INV5 52: INV6 53: INV7 54: INV8 55: INV9 56: INV10
57: INV11 58: INV12 59: MAM1 60: MAM2 61: MAM3 62: VRT1
63: VRT2 64: VRT3 65: VRT4 66: PAT1 67: PAT2 68: PAT3 69: PAT4
70: PAT5 71: PAT6 72: PAT7 73: PHG 74: PLN1 75: PLN2 76: PLN3
77: PLN4 78: PLN5 79: PLN6 80: PLN7 81: PLN8 82: PLN9 83: PLN10
84: PLN11 85: PLN12 86: PPL1 87: PPL2 88: PPL3 89: PPL4
90: PPL5 91: PPL6 92: PPL7 93: PPL8 94: PPL9 95: PPL10
96: PPL11 97: PPL12 98: PPL13 99: PPL14 100: PPL15 101: PPL16
102: PPL17 103: ROD1 104: ROD2 105: ROD3 106: ROD4 107: ROD5
108: ROD6 109: ROD7 110: ROD8 111: ROD9 112: STE 113: SYN
114: UNA

Database: genbankb101
115: VRL1 116: VRL2 117: VRL3 118: VRL4 119: VRL5 120: VRL6
121: VRL7 122: VRL8 123: VRL9 124: VRL10 125: VRL11
Database: genbank-new7
126: BCT 127: GEN 128: HTG1 129: HTG2 130: INV 131: MAM
132: VRT 133: PHG 134: PLN1 135: PLN2 136: PPL1 137: PPL2
138: ROD 139: SYN 140: UNA 141: VRL
Database: u-emb151.101
142: part1 143: part2

Statistics: Mean 9.942; Variance 4.310; scale 2.305
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Prod. No.
1	246	67.8	375	9	HSHAMRH	H sapiens mRNA for H3
2	246	67.8	375	91	HSHAMRH	H sapiens mRNA for H3
3	245	67.5	375	92	HSLD140	H sapiens mRNA for H3
4	243	66.9	378	9	HSPEGAH	H sapiens mRNA for H3
5	243	66.9	378	93	HSPEGAH	H sapiens mRNA for H3
6	242	66.7	377	95	HSU0162	Human immunoglobulin
7	239	65.8	375	92	HSLD1110	H sapiens mRNA for H3
8	238	65.6	373	101	HUMVH3J	Human mRNA for immunoglobulin
9	238	65.6	373	95	HSU0104	Human immunoglobulin
10	236	65.0	378	95	HUMIGVDJ2	Human immunoglobulin
11	235	64.7	454	99	HUMIGVDJ2	Human immunoglobulin
12	234	64.5	375	95	HSU0105	Human immunoglobulin
13	234	64.5	375	95	HSU0102	Human immunoglobulin
14	231	63.6	341	99	HUMIGHYABK	Human Ig germline H-c
15	231	63.6	341	99	HUMIGHYABN	Human Ig germline H-c
16	231	63.6	341	99	HUMIGHYABL	Human Ig germline H-c
17	231	63.6	342	91	HSIHCVDI1	H sapiens mRNA for H3
18	231	63.6	359	96	HSVH3132	H sapiens rearranged
19	231	63.6	360	99	HUMIGHYAA5	Human Ig germline H-c
20	231	63.6	365	96	HSVH31348	H sapiens rearranged
21	231	63.6	384	90	HSEUP94H	Homo sapiens mRNA for H3
22	231	63.6	399	91	HSIGVHC28	H sapiens rearranged
23	231	63.6	412	99	HUMIGHYAA2	Homo sapiens germline
24	231	63.6	412	91	HSIGVH28	H sapiens germline im
25	231	63.6	412	99	HUMIGHYAAE	Homo sapiens germline
26	231	63.6	583	98	HUMIGH333X	Human immunoglobulin
27	230	63.4	333	91	HSIHCVDA	H sapiens mRNA for H3
28	230	63.4	355	99	HUMIGHYAAW	Human Ig germline H-c
29	230	63.4	355	99	HUMIGHYAAZ	Human Ig germline H-c
30	230	63.4	355	99	HUMIGHYAAI	Human Ig germline H-c
31	230	63.4	355	99	HUMIGHYAAU	Human Ig germline H-c
32	230	63.4	257	102	S70739	Ig VH-anti-DNA mAb WR
33	230	63.4	363	95	HSU0108	Human immunoglobulin
34	230	63.4	366	91	HSIG040VH	H sapiens mRNA for H3
35	230	63.4	378	94	HSU00519	Human immunoglobulin
36	230	63.4	411	90	HSACVPC	H sapiens mRNA for H3
37	229	63.1	294	91	HSIGDP50	H sapiens germline Ig
38	229	63.1	294	91	HSIGVH277	H sapiens germline im
39	229	63.1	341	99	HUMIGHYABP	Human Ig germline H-c
40	229	63.1	341	99	HUMIGHYABQ	Human Ig germline H-c
41	229	63.1	360	99	HUMIGHYAAZ	Human Ig germline H-c
42	229	63.1	363	95	HSU0161	Human immunoglobulin
43	229	63.1	412	99	HUMIGHYAAD	Homo sapiens germline
44	229	63.1	450	90	HSBEL29	H sapiens rearranged
45	229	63.1	523	99	HUMIGH2CCM	Human Ig chain VDJC

ALIGNMENTS

RESULT 1
ID HSHAMRH standard: RNA: HUM: 375 BP.
AC X64154;
NI 938353
DT 06-MAP-1993 (rel. 35, Created)
TT 26-JUL-1997 (rel. 52, Last updated, Version 6)
DE H.sapiens mRNA for HAMBH heavy chain variable Ig domain
KW heavy chain, Ig heavy chain;
KW immunoglobulin heavy chain variable region, variable region.
OS Homo sapiens (human)
OC Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
OC Homo.
RN [1]
RP 1-375
RA Hughes-Jones N.C.;
RT ;

RL Submitted (08-JAN-1992) to the EMBL/GenBank/DBJ databases.
 PL N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research,
 RN Babraham Hall, Cambridge CB2 4AT, UK
 RP [2]

RX MEDLINE: 93107334.
 RA Bve J.M., Carter C., Cui Y., Gorick B.D., Songsivilai S.,
 PA Winter G., Hughes-Jones N.C., Marks J.D.;
 RT "Germline variable region gene segment derivation of human
 RT monoclonal anti-Rh(D) antibodies. Evidence for affinity maturation
 RT by somatic hypermutation and repertoire shift";
 RL J. Clin. Invest. 90:2481-2490(1992).
 DR IMGT/HLIM: X64154; Release 97.06.
 CC See also X64148-69

FH Key Location/Qualifiers

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 FT /note="PCR primer"
 FT misc_feature 1..375
 FT /note="VDJ region"
 FT misc_feature 1..294
 FT /note="Vh region"
 FT misc_feature 91..106
 FT /note="CDR1 region"
 FT misc_feature 148..198
 FT /note="CDR2 region"
 FT misc_feature 295..324
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 FT misc_feature 295..342
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 FT misc_feature 360..375
 FT /note="PCR primer"
 FT SQ Sequence 375 bp; 81 A; 88 C; 122 G; 81 T; 3 other;

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 Best Local Similarity 83.5%; Pred. No. 1.30e-201;
 Matches 299; Conservative 3; Mismatches 56; Indels 0; Gaps 0;

Db 16 sagctcgggggggctggtccagcctggaggctccctgagactctctgtgcagctct 75
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 Db 76 ggattcaccttcagtagctatggcagctgggtccgagcagctccaggggctg 135
 QY 64 GGATTCACCTTCAAGACGATGGCATGCATGGTCCGCCAGGCTCCAGGCAAGGGCTG 123
 Db 136 gactgggtggcagctatttgggtatgaggaatgaataataactatgcagactccctgaag 195
 QY 124 GAGTGGGTGGCAGGTATTTTCGTTTGATGGAAGTAACCAATATTACGACACTCCGCTGAAG 183
 Db 196 ggcggttaccatctccagagacaattcccaagaacagcgtgtatctgcaaatgaacagc 255
 QY 184 GCGCGATTTCATCTCTCCAGACAAATCCAGGGACACAGCTGTTTCTGCAGATGACACG 243
 Db 256 ctgagagcagagacagcgtgtgtattactgtgcagagagaagttactatggttcgggga 315
 QY 244 CTGAGACTCGAGACACAGCGGTGTCTATTACTGTGCGACAGGGGTTCCTTTTGGCTCG 303
 Db 316 gttaggcgttactacggtatgacgtctgtggccagggagacacaggtcacggtctcct 373
 QY 304 AITTAGGGCGGTTCATACCTTGAAATTTGGGGCCAGGGAAATCTTGTACCGTCTCTCT 361

RESULT 2 HSHAMBH 375 bp RNA PRI 10-MAR-1993
 LOCUS

DEFINITION H. sapiens mRNA for HAMBH heavy chain variable Ig domain.
 ACCESSION X64154
 NID g38353
 KEYWORDS heavy chain; Ig heavy chain; immunoglobulin heavy chain variable region; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; mitochondria; eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 375)
 AUTHORS Hughes-Jones, N.C.
 TITLE Direct Submission
 JOURNAL Submitted (08-JAN-1992) N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research, Babraham Hall, Cambridge CB2 4AT, UK

REFERENCE 2 (bases 1 to 375)
 AUTHORS Winter, J.M., Carter, C., Cui, Y., Gorick, B.D., Songsivilai, S., Bve, J.M., Hughes-Jones, N.C., and Marks, J.D.
 TITLE Germline variable region gene segment derivation of human monoclonal anti-Rh(D) antibodies. Evidence for affinity maturation by somatic hypermutation and repertoire shift
 JOURNAL J. Clin. Invest. 90 (6), 2481-2490 (1992)

MEDLINE 93107334
 COMMENT See also X64148-69.

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 misc_feature 1..375
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 /note="CDR1 region"
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 misc_feature 295..324
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 misc_feature 325..375
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 misc_feature 360..375
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BASE COUNT 81 a 88 c 122 g 81 t 3 others
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 Best Local Similarity 83.5%; Pred. No. 1.30e-201;
 Matches 299; Conservative 3; Mismatches 56; Indels 0; Gaps 0;

Db 16 sagctcgggggggctggtccagcctggaggctccctgagactctctgtgcagctct 75
 QY 4 GAGTCGGGGGAGGCGGTGGTCCAGCCTGGGAGGTCCTTGAGACTCTCTGTGCAGCGTCT 63
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 QY 64 GGATTCACCTTCAAGACGATGGCATGCATGGTCCGCCAGGCTCCAGGCAAGGGCTG 123
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 QY 124 GAGTGGGTGGCAGGTATTTTCGTTTGATGGAAGTAACCAATATTACGACACTCCGCTGAAG 183
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QY 244 CTGAGACTCGAGGACAGCGGTGCTATTACTGTGGACAGAGGGTCTCTCTTTGGCTCG 303
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QY 304 ATTAAGGGGGGTTTACTACCTTGAATAATGGGCGCAGGGAACCCCTGGTCACCGCTCTCCT 361

RESULT 3
LOCUS HSLD140 375 bp RNA PRI 11-SEP-1996
DEFINITION H. sapiens mRNA for immunoglobulin heavy chain, clone LD1-40.
ACCESSION Y07816
NID g1536906
KEYWORDS heavy chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 375)
AUTHORS Miescher, S.M.
JOURNAL Unpublished
AUTHORS Miescher, S.M.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1996) S M Miescher, Institute of Immunology And
Allergology, University Of Bern, Sahli Haus 2, Inselspital, CH-3010
Bern, SWITZERLAND

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BASE COUNT 89 a 91 c 114 g 81 t
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Query Match 67.5%, Score 245, DB 92, Length 375,
Best Local Similarity 83.7%, Pred. No. 1.19e-200;
Matches 304; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Db 133 ctgagtggtggtcaggtatattggttggatgaagtaacaaaactatgcagactccgtg 192
QY 121 CTGAGTGTGGTGGCAGGTATTTCTGTTGATGGAAGTAACCAATATACCGACACTCCGTG 180
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Db 313 attctaggttctattactacatgaacgtctgtgggcaaggggacacaggttcacgtctcc 372
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Db 373 cca 375
QY 361 TCA 363

RESULT 4
ID HSPGAGH standard: PNA: HUM; 378 BP.
AC X64157;
NI g38356
DI 06-MAR-1993 (Rel. 35, Created)
DT 26-JUL-1997 (Rel. 52, Last updated, Version 6)
DE H.sapiens mRNA for REGAH heavy chain variable Ig domain
KW heavy chain; Ig heavy chain;
KW immunoglobulin heavy chain variable region; variable region.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
OC Homo.
RN [1]
PP 1-378
RA Hughes-Jones N.C.;
RT Submitted (08-JAN-1992) to the EMBL/GenBank/DBJ databases.
RL N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research,
RL Babraham Hall, Cambridge CB2 4AT, UK
RP [2]
RX MEDLINE: 93107334.
RA Bye J.M., Carter C., Cui Y., Gorick R.D., Songasivilai S.,
Winter G., Hughes-Jones N.C., Marks J.D.;
RT "Germline variable region gene segment derivation of human
monoclonal anti-Rh(P) antibodies: Evidence for affinity maturation
by somatic hypermutation and repertoire shift";
PL J. Clin. Invest. 90:2481-2490(1992)
DR TMGT/LIGM: X64157; Release 97.06.
CC See also X64148-69
FH Key Location/Qualifiers
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FT /note="Vh region"
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FT misc_feature 148..198
FT /note="CDR2 region"
FT misc_feature 295..333
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FT misc_feature 334..378
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Best Local Similarity 85.1%; Pred. No. 1.00e-198;
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BASE COUNT 82 a 89 c 116 g 90 t

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Best Local Similarity 84.8%; Pred. No. 9,18e-198;
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QY 64 GGATTCACCTTCAGAGCTATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 123
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QY 124 GAGTGGGTGGAGGTATTCGTTTGAAGGTAACCAATATTAAGCAAGCTGCTGGAAG 183
Db 196 gqccgattcacctctccagagacattccagagacattccagagacattccagagacatt 255
QY 184 GGCCTGATTCATGCTCTCCAGAGCAATTCAGAGCAATTCAGAGCAATTCAGAGCAAT 243
Db 256 ctgaagccgagagacacgtctgtgtattactgtgcagatgacagatttttgagtggttaa 315
QY 244 CTAGAGTCTGAGGACACGCTGTATATCTATCTATCTATCTATCTATCTATCTATCT 303
Db 316 tcttttagcccgagctgagctgtgagctgtgagctgtgagctgtgagctgtgagctgt 375
QY 304 A-TTAAAGGGGGTACTACCTT-GAAATTTGGGGGCAAGCAACCTGCTGACCTGCTGCT 361
Db 376 ca 377
QY 362 CA 363

RESULT 7 HSLD1110 375 bp RNA PRI 19-SEP-1996
LOCUS H.sapiens mRNA for variable region of immunoglobulin G heavy chain,
clone-LDI-110.
DEFINITION Y08180
ACCESSION g1552279
NID heavy chain; IgG; immunoglobulin; variable region.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo
REFERENCE 1 (bases 1 to 375)
AUTHORS Miescher, S.M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 375)
AUTHORS Miescher, S.M.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1996) S.M. Miescher, Institute of Immunology and
Allergy, University of Bern, Sahlg Haus 2, Inselspital, CH-3010
Bern, SWITZERLAND
FEATURES
Location/Qualifiers
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BASE COUNT 94 a 92 c 114 g 75 t

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Best Local Similarity 82.9%; Pred. No. 7.03e-185;
Matches 301; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Db 73 tctgattcaccttcagtagctatgagctgagctgagctgagctgagctgagctgagctg 132
QY 61 TCTGAGTTCACCTTCAGAGCTATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 133 ctggagctgggtggcaggtatggtttgagagacattccagagacattccagagacatt 192
QY 121 CTCGAGTCTGCGAGCTATTCGCTTTCATGCAACTACCAATATTAAGCAATTCGCTG 180
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Db 313 atcagtagatataacttactgagctgtgagctgtgagctgtgagctgtgagctgtgagct 372
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QY 361 TCA 363

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LOCUS Human mRNA for immunoglobulin M (IgM), partial cds (VH1-N-D-N-1H4);
clone H2-27E.
DEFINITION D83684
ACCESSION g1213573
NID IgM; immunoglobulin M.
KEYWORDS Homo sapiens Blood B-cell rearranged cDNA to mRNA, clone H2-27E.
SOURCE Homo sapiens
ORGANISM Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 373)
AUTHORS Hakoda, M., Kametani, N., Hayashimoto-Kurumada, S., Silverman, G.,
Yamanaka, H., Terai, C. and Kashiwazaki, S.
TITLE Differential binding avidities of human IgM for staphylococcal
protein A derive from specific germline VH3 gene usage
JOURNAL Unpublished (1996)
REFERENCE 2 (bases 1 to 373)
AUTHORS Hakoda, M.
TITLE Direct Submission

DEFINITION Human immunoglobulin heavy chain variable region (V3-30) gene, partial cds.
 ACCESSION U00104
 NID q1791050
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 378)
 AUTHORS Glas A.M., Nottenburg, C. and Milner, E.C.
 TITLE Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient
 JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1992)
 MEDLINE 97182739
 REFERENCE 2 (bases 1 to 378)
 AUTHORS Glas A.M., Nottenburg, C. and Milner, E.C.
 TITLE Direct Submission
 JOURNAL Submitted (26-NOV-1995) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
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 BASE COUNT 85 a 97 c 114 g 82 t
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 Db 16 gaggctggggaggcgtggtccagcctggaggtccctgaactctctctgtgcagctct 75
 QY 4 GAGTCGGGGGAGGGCTGCTCCAGCTGGAGCTGGAGTCCCTGAGACTCTCTCTGTGCGCGTCT 63
 Db 76 qattcaacttcagtagctatgagctgagctgagctgagctgagctgagctgagctg 135
 QY 64 GGATTCACCTTTCAACAAGTATGGATGCTACTGGCTGCTGGCTGCTGGCTGCTGGCTG 123
 Db 136 gattggtggcgttatcatcatatgagagatgaataataactatgagactccgtgaag 195
 QY 124 GAGTCGGTGGAGGATATTCGTTTATGGAAATAGCAATATTAAGCAATCGSIGAAG 183
 Db 196 ggcuaattcaccatccagagacacaaattccagagacacgctgtatctgcacaaatgaacagc 255
 QY 184 GCGCGATTCATGCTCTCCAGAGACATTCATCCATGGACAGGCTGTTCTTCATCATGAGCAGC 243
 Db 256 ctgaagacttgagacacgctgtgattactgtggaagacgcaagcctgtagtagagt 315
 QY 244 CTGAGACATCGAGACACGGCTGCTATATATGATGAGACAGAGAGTGTCTCTTTTGGGCT 301
 Db 316 ggcgtgtagcctcctcctgactttgactactggggccagggaaacccctgacccgtctcc 375
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Db 376 tca 378
 QY 361 TCA 363
 RESULT 11 HUMIGVDJZ 454 bp mRNA PFI 21-DEC-1993
 LOCUS Homo sapiens IgH chain mRNA, VDJC region.
 DEFINITION L23571
 ACCESSION G388021
 NID
 KEYWORDS D-region; J-region; immunoglobulin heavy chain.
 SOURCE Homo sapiens adult peripheral blood cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 454)
 AUTHORS Chai, S.K., Kasalan, M.T., Ikematsu, H., Kim, M.Y., and Casali, P.
 TITLE VH-D-JH gene sequences of mAb produced by human B-1a, B-1b, and B-2 cells
 JOURNAL Unpublished (1993)
 FEATURES
 Location/Qualifiers
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 Best Local Similarity 84.7%; Pred. No. 4.90e-191;
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 Db 127 gattcaacttcagtagctatgagctgagctgagctgagctgagctgagctgagctg 186
 QY 64 GGATTCACCTTTCAACAAGTATGGATGCTACTGGCTGCTGGCTGCTGGCTGCTGGCTG 123
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Db 247 ggcgattcaccatctccagagacaattccaagaacacgcgtgtatctgcaaatgaacagc 306
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Db 307 ctgagacccagagacgcgtgtgtattactgtgcgagaccagtat-tactat-ggttc- 363
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QY 304 ATTAAGGGCGGTACTACCTTGAATATGGGCGCAGGGAACCTGGTCACCGTCTCCTCA 363

RESULT 12
LOCUS HSU80105 375 bp DNA PRI 19-FEB-1997
DEFINITION Human immunoglobulin heavy chain variable region (V3-30) gene,
partial cds.
ACCESSION U80105
NID 91791052
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 375)
JOURNAL Glas.A.M., Nottenburg,C. and Milner,E.C.
MEDLINE Analysis of rearranged immunoglobulin heavy chain variable region
AUTHORS genes obtained from a bone marrow transplant (BMT) recipient
REFERENCE Clin Exp Immunol 107 (2), 372-380 (1997)
JOURNAL 91782739
TITLE 2 (bases 1 to 375)
AUTHORS Glas.A.M., Nottenburg,C. and Milner,E.C.B.
JOURNAL Glas.A.M., Nottenburg,C. and Milner,E.C.B.
SUBMITTED (26-Nov-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
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marrow transplant recipient 90 days post transplant; clone
28 in reference 1"
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/gene="V3-30"
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BASE COUNT 89 a 97 c 113 g 76 t
ORIGIN
Query Match 64.5%; Score 234; DB 95; Length 375;
Best Local Similarity 82.5%; Pred. No. 4.47e-190;
Matches 297; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Db 76 ggattccacttcagtagctatgcacgtgggtccgcagagctccagggcagggcgctg 135
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QY .64 GGATTCACCTTCGAAGACGTATGGATGCTACTGGGTCGGCGCAGGCTCCAGGCAAGGGGCTG 123

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RESULT 13
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DEFINITION Human immunoglobulin heavy chain variable region (V3-30) gene,
partial cds
ACCESSION U80102
NID 91791046
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 375)
JOURNAL Glas.A.M., Nottenburg,C. and Milner,E.C.
MEDLINE Analysis of rearranged immunoglobulin heavy chain variable region
AUTHORS genes obtained from a bone marrow transplant (BMT) recipient
REFERENCE Clin Exp Immunol 107 (2), 372-380 (1997)
JOURNAL 91782739
TITLE 2 (bases 1 to 375)
AUTHORS Glas.A.M., Nottenburg,C. and Milner,E.C.B.
JOURNAL Glas.A.M., Nottenburg,C. and Milner,E.C.B.
SUBMITTED (29-Nov-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
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marrow transplant recipient 90 days post transplant; clone
25 in reference 1"
/cell_type="CD19+ B cells"
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BASE COUNT 83 a 92 c 117 g 83 t
ORIGIN
Query Match 64.5%; Score 234; DB 95; Length 375;
Best Local Similarity 82.5%; Pred. No. 4.47e-190;
Matches 297; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Db 16 gactctggggagcgctgctcagactggagagtccttgagactctctgtgcagcctct 75
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QY 4 GAGTCGGGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 63

Db 76 ggattccacttcagtagctatgcacgtgggtccgcagagctccagggcagggcgctg 135
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QY 64 GCATTCACCTTCACAGCATGATGGCATGCACCTGGGTCCGCCAGGCTCCAGCGCAAGGGGCTG 123

Db 136 gactggtgagcagttatcatatgatggaagtaataataactatgcagactccgtgaaag 195

QY 124 GAGTGGGTGGGAGGTATTTCTGTTTCATGGAAGTAACCAATATTACGCGAGACTCCGTGAAG 183

Db 196 acccattaccatctccagagacaattccaaagacacagctgtatctgcaaatgaaacacg 255

QY 184 GGCCTATTCATGCTCTCCAGAGCAATTCAGGACACGGTGTTCTTCGACATGACGACG 243

Db 256 ctgagagctgagacacagctgtgtattactgtgcagagagattccacaggggggttatg 315

QY 244 CTGACACTCGAGGACAGCGCTGTCTATTACTGTCCGACAGAGGGTTCCTTTTGGGTCTG 303

Db 316 attcagcttctactacatgagctctggagcaaaagggagaccacagctcacgctctctca 375

QY 304 ATTAAAGGGGGGTATACCTTTAAATTTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363

RESULT 14 HUMIGHYABK 341 bp DNA PRI 03-JAN-1995

LOCUS Human Ig germline H-chain gene V-region, Clones b9-12,33,35.

DEFINITION M77333

ACCESSION g185761

NID

KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain

SOURCE Homo sapiens (individual isolate Baji) adult DNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 341)

AUTHORS Glee.T., Yang.P.M., Simionovitch.K.A., Olsen.N.J., Hillson.J., Wu.J., Kozin.F., Carson.D.A. and Chen.P.P.

TITLE Molecular basis of an autoantibody-associated restriction fragment length polymorphism that confers susceptibility to autoimmune diseases

JOURNAL J. Clin. Invest. 88 (1), 193-203 (1991)

MEDLINE 91277280

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Best Local Similarity 91.1%; Pred. No. 3.39e-187; Mismatches 25; Indels 0; Gaps 0;

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Db 116 gattacccttcagtagctatgcatgacatgggtccgcagagctccacagcaaggagctg 175

QY 64 GATTCACCTTCACAAAGCAATGGCATGACATGGGTCCGCCAGGCTCCAGGCAAGGGGCTG 123

Db 176 gagtgggtggcagttatcatatgatggaagtaataataactatgcagactccgtgaaag 235

QY 124 GAGTGGGTGGGAGGTATTTCTGTTTCATGGAAGTAACCAATATTACGCGAGACTCCGTGAAG 183

Db 236 ggcctattaccatctccagagacaattccaaagacacagctgtatctgcaaatgaaacacg 295

QY 184 GGCCTATTCATGCTCTCCAGAGCAATTCAGGACACGGTGTTCTTCGACATGACGACG 243

Db 256 ctgagagcagacacagcgtgtgtattactgtccagagaga 336

QY 244 CTGAGACTCGAGGACAGCGCTGTCTATTACTGTCCGACAGA 284

RESULT 15 HUMIGHYABN 341 bp DNA PRI 03-JAN-1995

LOCUS Human Ig germline H-chain gene V-region, Clone b13,35.

DEFINITION M77336

ACCESSION g185767

NID

KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain.

SOURCE Homo sapiens (individual isolate Baji) adult DNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 341)

AUTHORS Glee.T., Yang.P.M., Simionovitch.K.A., Olsen.N.J., Hillson.J., Wu.J., Kozin.F., Carson.D.A. and Chen.P.P.

TITLE Molecular basis of an autoantibody-associated restriction fragment length polymorphism that confers susceptibility to autoimmune diseases

JOURNAL J. Clin. Invest. 88 (1), 193-203 (1991)

MEDLINE 91277280

FEATURES

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337..>341

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/note="7 mer recombination signal"

BASE COUNT 77 a 79 c 106 g 79 t

ORIGIN

Query Match 63.6%; Score 231; DB 99; Length 341.

Best Local Similarity 91.1%; Pred. No. 3.39e-187; Mismatches 25; Indels 0; Gaps 0;

Db 56 gactctggggagcagctggtccagcctggaggtccctgcagactctctgtgcagcgtct 115

QY 4 GAGTCGGGGGAGGCGGTGCTCCAGCTTGGAGGTCCTTGAGACTCTCTGTCGACGCTCT 63

Search completed: Tue Feb 24 11:31:27 1998
Job time : 1343 secs.

WASHU

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit
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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:00:51 1998; Maspar time 117.90 Seconds
Tabular output not generated. 795.384 Million cell updates/sec

Title: >US-08-844-215-24
Description: (1-372) from US08844215 seq
Perfect Score: 372
N.A. Sequence: 1 CTCGACGAGTCTCGGGCTGA
Comp: GAGCTCGTACAGCTTACAT

Scoring table: TABLE default
Gap 5

Nmatch STD: DBase 0; Query 0

Searched: 332433 seqs, 12614348 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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9:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19
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95:STS95 96:STS96

Statistics: Mean 9.902; Variance 1.949; scale 5.081

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES			
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4	35	9.4	230.57	HS1227073	zu49b02.r1 Soares ova	2.15e-24
5	30	8.1	597.83	MM1263658	vh10a05.r1 Soares mou	1.35e-16
6	30	8.1	597.24	AA472093	vh10a05.r1 Soares mou	1.35e-16
7	27	7.3	511.63	HS1258634	zx82h07.r1 Soares ova	3.29e-12
8	27	7.3	511.17	AA464794	zx83h07.r1 Soares ova	3.29e-12
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13	21	5.6	259.66	HS1281117	ab31f07.r1 StrataGene	2.80e-04
14	21	5.6	259.33	AA488043	ab31f07.r1 StrataGene	2.80e-04
15	21	5.6	259.33	HS124338	ab31g09.s1 Soares NIH	2.80e-04
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41	19	5.1	582.1	BTU95694	Bos taurus microsatel	5.70e-02
42	19	5.1	583.72	HS1315572	ng31h13.s1 NCI_CGAP_2	5.70e-02
43	19	5.1	605.98	MM1317661	vi37b03.r1 Barstead m	5.70e-02
44	19	5.1	605.41	AA524432	vi37b03.r1 Barstead m	5.70e-02
45	19	5.1	642.71	HS1312122	aa73g03.s1 NCI_CGAP_3	5.70e-02

ALIGNMENTS

RESULT 1
ID HS1202138 standard, RNA, EST, 266 BP.
AC AA02547:
NI 92056386

DT 01-MAY-1997 (Pel. 51, Created)
DT 22-MAY-1997 (Pel. 52, Last updated, Version 2)
DE zu47h07.r1 Soares ovary tumor N80T, Homo sapiens cDNA clone 741181
DE 5. similar to gb:U87899 IG GAMMA-1 CHAIN C REGION (HUMAN):
KW EST.

OS Homo sapiens (human)
OC Eukaryotes; mitochondria; euKaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-256

RA Hillier L., Allen M., Rowley L., Dubuque T., Geisels C., Post S.,
RA Kuraba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
PA Moore R., Scheinberg R., Steffen M., Tan F., Theising B.,
RA White Y., Wylie T., Waterston P., Wilson P.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63104 Tel.: 314 286 1800 Fax: 314 286 1810 Email:
CC estw@wustl.edu This clone is available royalty-free through
CC LNL, contact the IMAS Consortium (info@imacore.com) for
CC further information. Seq primer: 28m13 rev2 Et from AmerSham.

```

FH Key Location/Qualifiers
FH source
FT 1..266
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT modified polylinker; Site1: Not I; Site2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5',
FT TGTTACCAATCGAAGTGGAGGCGGCTTTTTTTTTTTTTTTT 3'],
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M. Fatima Bonaldo."
FT /clone="741181"
FT /sex="Female"
FT /tissue_type="Ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT <1..>266
FT mRNA
SQ Sequence 266 BP; 54 A; 90 C; 70 G; 52 T; 0 other;

Query Match 22.3%; Score 83; DB 54; Length 266;
Best Local Similarity 83.2%; Pred. No. 7 20p-112;
Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 17 caaggtacacagagtcacagcagcagtcacccctgaccaggacacgtccacagca 76
QY 164 CAAACTCCGACAGAGATTCAGGGGACAGTCTCGATTACCGCGGAGCA 223
Db 77 cactctacatggctgagcagcagtcagtcagcagcagcagcagcagcagcagc 136
QY 224 CAGCCTACATGAGCTGAGTACCTGAGATCGGAGGACACGCCATCTATTACTGTCGA 283
Db 137 gagac 141
QY 284 AAGAC 288

RESULT 2
LOCUS aa63g01.r1 NCI-CGAP_GCB1 Homo sapiens cDNA clone 825648 5' similar
DEFINITION to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
ACCESSION AA505044
NID 92241204
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Mammalia, Eutheria, Primates; Catarrhini; Homiidae,
Homo.
1. (bases 1 to 238)
REFERENCE NCI-CGAP.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel. (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 1.

```

```

FEATURES
source
Location/Qualifiers
1..238
/organism="Homo sapiens"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CREP). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCGAAGTGGAGGCGGCTTTTTTTTTTTTTT-
3']. Double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
/clone="825648"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
<1..>238
mRNA
BASE COUNT 57 a 66 g 46 t
ORIGIN
Query Match 10.2%; Score 38; DB 35; Length 238;
Best Local Similarity 65.8%; Pred. No. 3.16e-29;
Matches 79; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 8 gaqgttaaaagaccggggagtcctctgagatctctgtgagactcttgatcacgcttt 67
QY 19 GAGGTGAAGAAAGCTGGTCTCTCAGTGAAGTCTCTCTGCAAGGCTTCIGAGAGCACTTTC 78
Db 68 accagcgactggatccactgggtgcgcacatgcccggaagaaactctagctatagac 127
QY 79 AAGCGGCAATGTTATCAGCTGAGTGGGACAGGCGGCTTGGACAGGGGCTTATGTCATGGGG 138

RESULT 3
ID HS1300461 standard; RNA; EST; 238 BP.
AC AA505044;
NI 92241204
DT 04-JUL-1997 (Rel. 52, Created)
DE 04-JUL-1997 (Rel. 52, Last updated, Version 1)
DE aa63g01.r1 NCI-CGAP_GCB1 Homo sapiens cDNA clone 825648 5' similar
DE to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
KW EST.
OS Homo sapiens (human)
OC Eukaryotes, mitochondrial eukaryotes, Metazoa, Chordata;
OC Vertebrata, Mammalia, Eutheria, Primates; Catarrhini; Homiidae;
OC Homo.
RN [1]
RP 1-238
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP)".
RT Tumor Gene Index";
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel. (301) 496-1550 Email:
CC Robert_Strausberg@nih.gov Tissue Procurement: Louis M. Staudt,
CC M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library
CC Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA
CC Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by:
CC Washington University Genome Sequencing Center Clone distribution:
CC NCI-CGAP clone distribution information can be found through the
CC I.M.A.G.E. Consortium/LLNL at:
CC www-bio.llnl.gov/bbrp/image/image.html Trace considered overall
CC poor quality Possible reversed clone: similarity on wrong strand
CC Seq primer: -28ml3 revl ET from Amersham High quality sequence
CC stop: 1.
FH Key Location/Qualifiers
FH source
FT 1..238
FT /organism="Homo sapiens"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified

```



```

FT  mRNA
SQ  Sequence 597 BP; 155 A; 132 C; 153 G; 156 T; 1 other;

Query Match      8.1%; Score 30; DB 83; Length 597;
Best Local Similarity 61.4%; Pred. No. 1.35e-16;
Matches 81; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 120 cttgagagctcggaggagcttggtgcaacctggagagatccataaaactctcctgtgtt 179
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1 CTCGAGCAGCTCGGGCTGAGGTGAAGAAGCCTGGGTCTCTCAGTGAAGGTCTCTGCAAG 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 180 gtctctggattcaacttctcagtgacccctggatgagctgggtcccccagctctccagagaag 239
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GGTCTTGGAGGACCTTCAGCGGCCATCTTATCAGCTGGGTGGCAGCGGCCCTGGACAA 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 240 ggaactgagtg 251
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GGGCTTGAGTGG 132
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
LOCUS AA472093 597 bp mRNA EST 18-JUN-1997
DEFINITION vhl0a05.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone
875024 5' similar to gb:S65761 IG GAMMA-2 CHAIN C REGION (HUMAN);
gb:L36938 Mus musculus germline immunoglobulin gamma constant
region (MOUSE);.
ACCESSION AA472093
NID q2200084
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 597)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,P. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:514504
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 440.
Location/Qualifiers
1..597
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGCGCAATGTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p7T3 vector.
RNA provided by Dr. Minoru KO, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."
/clone="875024"
/clone_lib="Soares mouse mammary gland NbMMG"
/sex="male"
/dev_stage="4 weeks"

```

```

BASE COUNT 155 a 132 c 153 g 156 t 1 others
ORIGIN
Query Match      8.1%; Score 30; DB 24; Length 597;
Best Local Similarity 61.4%; Pred. No. 1.35e-16;
Matches 81; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 120 cttgagagctcggaggagcttggtgcaacctggagagatccataaaactctcctgtgtt 179
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1 CTCGAGCAGCTCGGGCTGAGGTGAAGAAGCCTGGGTCTCTCAGTGAAGGTCTCTGCAAG 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 180 gtctctggattcaacttctcagtgacccctggatgagctgggtcccccagctctccagagaag 239
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GGTCTTGGAGGACCTTCAGCGGCCATCTTATCAGCTGGGTGGCAGCGGCCCTGGACAA 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 240 ggaactgagtg 251
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GGGCTTGAGTGG 132
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
ID HS1258634 standard; RNA; EST: 511 BP.
AC AA464794;
NI q2189678;
DT 13-JUN-1997 (Rel. 52, Created)
DT 13-JUN-1997 (Rel. 52, Last updated, Version 1)
DE zx83h07.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810397
DE 5' similar to gb:L21964 IG HEAVY CHAIN V-II REGION (HUMAN);.
KW EST.
OS Homo sapiens (human)
OC Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP 1-511
RA Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,S.,
Kucaba,T., Lacy,M., Le,M., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,P., Wilson,P.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
est@watson.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 ET from Amersham High
CC quality sequence stop: 414.
FH Key
FH Location/Qualifiers
FT source 1..511
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: p7T3D (Pharmacia) with a
FT modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5',
FT TGTACCAATCTGAAGTGGGAGCGCGCGCAATGTTTTTTTTTTTTTTT
FT T 3']; double-stranded cDNA was size selected, ligated to Eco RI
FT adaptors (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified p7T3 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M. Fatima Bonaldo."
FT /clone="810397"
FT /clone_lib="Soares ovary tumor NbHOT"
FT /sex="Female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT mRNA <1..>511
SQ Sequence 511 BP; 106 A; 169 C; 124 G; 112 T; 0 other;

Query Match      7.3%; Score 27; DB 63; Length 511;
Best Local Similarity 90.9%; Pred. No. 3.29e-12;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```


b	breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T13 vector. Library is not normalized. (The normalized version of this library is NCI-CGAP.Br2.) Library was constructed by Bento Soares and M. Fatima Bonaudo."
c	/clone="964424"
d	/clone_lib="NCI_CGAP_Brl.l"
e	/sex="female, pooled"
f	/tissue_type="breast"
g	/lab_host="DH10B"
i	<1>->435
mRNA	
sQ	Sequence 435 BP; 94 A; 128 C; 112 G; 101 T; 0 other;
Query Match	5.9%; Score 22; DB 80; Length 435;
Best Local Similarity	70.4%; Pred.No.1.67e-05;
Matches	38; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Dn	ccactctagacccttcctgcaggcctgggaacccaatcatcgactcagtct 262 Cp 132 CCACCTCAAGCCGTTCGCAGCGGGTGATGCCAACCAGCATGAATAATGCGCGCT 79
RESULT	12
LOCUS	AA507475 435 bp mRNA EST 15-JUL-1997
DEFINITION	nh76c05.s1.NCI.CGAP.Brl.1.Homo sapiens cDNA clone 964424 similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V.III REGION (HUMAN)..
ACCESSION	AA507475
NID	32243914
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 435) National Cancer Institute, Cancer Genome Anatomy Project (CGAP). Tumor Gene Index Unpublished (1997)
REFERENCE	Contact: Robert Strausberg, Ph D Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Christopher Moskaiuk, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the IMA GE Consortium/LNL at: www-bio.llnl.gov/bbr/image/image.html
JOURNAL	
COMMENT	Insert Length: 558 Std Error: 0.00 Seq primer: -40ml3 fwd.EI from Amersham High quality sequence stop: 131. Location/Qualifiers 1 . 435 /organism="Homo sapiens" /note="vector: p7T13D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T13 vector. Library is not normalized. (The normalized version of this library is NCI-CGAP.Br2.) Library was constructed by Bento Soares and M. Fatima Bonaudo." /clone="964424" /clone_lib="NCI_CGAP_Brl.l" /sex="female, pooled" /tissue_type="breast"
FEATURES	
source	


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mRNA
BASE COUNT      94 a 128 c 112 g 101 t
ORIGIN
Query Match      5.9%; Score 22; DB 40; Length 435;
Best Local Similarity 70.4%; Pred. No. 1.67e-05;
Matches 38; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 209 caacttaaacacctccctgagctggggagcccaactcatgcctgctgt 262
      ||||| || || || || || || || || || || || || || || || ||
Cc 132 CCACCTCAAGCCCTTTCGAGGCGCTTCGACCCAGTGTATACATCGCGCT 79

RESULT 13
ID HS1281117 standard: RNA: EST: 259 BP.
AC AA488043;
NI 92215474
DT 27-JUN-1997 (Rel. 52, Created)
DE ab12f07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840613
DS 5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);..
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
OC Homo.
RN 1..259
RP 1..259
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
RA Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
RA Theising B., White Y., Wylie T., Waterston R., Wilson R.;
RA "WashU-NCI human EST Project";
RA Unpublished.
CC Contact: Wilson RK Washington University School of Medicine 4444
CC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
CC 1800 Fax: 314 286 1800 Email: est@watson.wustl.edu
CC This clone is available royalty-free through LNL; contact the
CC IMAGE Consortium (info@image.llnl.gov) for further information.
CC Seq primer: -28ml3 rev1 ET from Amersham.
CC revl ET from Amersham.
FH Key
FH Location/Qualifiers
FT source
FT 1..259
FT /organism="Homo sapiens"
FT /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
FT Site_2: XhoI; Cloned unidirectionally. Primer:
FT oligo dt: normal lung Average insert size: 1.0 kb;
FT Uni-ZAP XP Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -
FT 3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGTGT 3' -
FT /clone="840613"
FT /sex="male"
FT /dev_stage="72 years"
FT /lab_host="SOLP cells (kanamycin resistant)"
FT mpna
FT RASE COUNT 51 a 99 c 71 g 38 t
FT ORIGIN
Query Match 5.6%; Score 21; DB 30; Length 259;
Best Local Similarity 92.0%; Pred. No. 2.80e-04;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 gggaacgctgttcacccgtctctca 25
Cc 34a GAGCACCGTGTTCACCGTCTCTCA 372

RESULT 15
ID HS1214338 standard: RNA: EST: 551 BP.
AC AA418907;
NI 92080726
DT 14-MAY-1997 (Rel. 51, Created)
DT 24-MAY-1997 (Rel. 52, Last updated, Version 2)
DE zw101g09.s1 Soares NRMHPU S1 Homo sapiens cDNA clone 768064 3'
DE similar to gb:K03191 CYTOCHROME P450 1A1 (HUMAN);..
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN 1..551
RP 1..551
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White Y., Wylie T., Waterston R., Wilson R.;
RA "WashU-Merck EST Project 1997";
RA Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

```

Thu Feb 26 07:05:28 1998

rest@watson.wustl.edu This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. seq primer: ~4ml3 fwd. Et from Amersham High quality sequence stop: 261.

quality sequence stop: location/qualifiers

source

```
1. 551
/organism="Homo sapiens"
/notice=organ: mixed (see below); Vector: pT73D-Pac
(pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NDHPD, and fetal heart NDHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, the DNA
was used as tracer in a subtractive hybridization reaction
```

The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265233, 340488-345479, and 484488-489479."

```

/clone="768064"
/clone_lib="Soares NHMPu s1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
complement(<1..>551)
155 30 347.8 127 C 123 G: 154 T: 0 other;
mRNA

```

complement(<1..>551)	154	T: 0	other;
complement(<1..>551)	154	T: 0	other;

```

Query Match          5.6%; Score 21; DB 56; Length 551;
Best Local Similarity 80.0%; Pred. No. 2 80e-04;
Matches             28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

bb 230 cccccccctcactccagccctagtcctggtgcctg 264
 ||||| ||||| ||||| ||||| ||||| |||||
 cp 140 ccccccatccactcaagcccttgctccaggggcctg 106

Search completed: Tue Feb 24 11:08:37 1998
Job time : 466 secs.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 209)
REFERENCE
AUTHORS
Adams,M.D., Kerlavage,A.P., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brannon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.I., Geodhagen,N.S.M.,
Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,
Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palancas,P.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Fertie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.P., Posen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

CONTACT: Venter, J.C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

FEATURES
source
1..209
mRNA
BASE COUNT 43 a 62 c 48 g 55 t 1 others
ORIGIN
Query Match 32 5%, Score 121, DP 58, Length 209,
Best Local Similarity 79.4%, Pred. No. 3,96e-189;
Matches 162; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Db 1 cggatgtntccctgtaagtgaactctgcccctggaactctgtataattttgtgttac 60
Cp 217 CGGATTCGTCGGGTAATCGAGACTTCGCCCTGGAACTTCGTGCGGAGTTTGATGTGC 158
Db 61 cattgcagcgttgatccatccatccatccatccatccatccatccatccatccatcc 120
Cp 157 CAACAAGAGATACCTCCCGCCATCCACTCAGCCCTTGTCCAGGGGCTGTGCGACCC 98
Db 121 aatgcatacatagctagtagtagtagtagtagtagtagtagtagtagtagtagtag 180
Cp 97 AGCTGATCAATACATGCGGCTGAAGTGCTCCAGAAAGCCCTTCAGAGACCTTCACTGAGG 38
Db 181 cccagcgtcttcacatccatccatccatccatccatccatccatccatccatccatcc 204
Cp 37 ACCGAGGCTTCTTACCTCAGGCC 14

RESULT #2
LOCUS T27609 287 bp mRNA EST 06-SEP-1995
DEFINITION EST01034 Homo sapiens cDNA 5' end similar to immunoglobulin mu
heavy chain, VDJC regions (GB:M18512) (HT:3056).
ACCESSION T27609
NID g609707
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Pancreas.
ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 287)
REFERENCE
AUTHORS
Adams,M.D., Kerlavage,A.P., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brannon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.I., Geodhagen,N.S.M.,
Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,
Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palancas,P.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Fertie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.P., Posen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

CONTACT: Venter, J.C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

FEATURES
source
1..287
mRNA
BASE COUNT 62 a 77 c 85 g 60 t 3 others
ORIGIN
Query Match 29 3%, Score 109, DP 58, Length 287,
Best Local Similarity 79.7%, Pred. No. 1,23e-164,
Matches 145; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Db 80 ctggtgcagctcgggctgaggtgagagagcctggggtcagtgaggtgtctctggaag 139
Cp 1 CTCGAGCAGCTCTGGGGCTCAGGTGAAGAGCTTGGAGTCTAGTAAAGTCTTCTTAA 60
Db 140 actctgggtacgcttcacgctacactatatactggtggtggtggtggtggtggtg 194
Cp 61 GCTTCGGAGGACCTTCACGGCCATGTTATCAGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 200 ggcttgaatgaggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 259
Cp 121 GGGCTTCAGTGGATGGGGGGAGTATCTCTCTTTTGTGATCATCAAACTTGGCAGAG 180
Db 260 tt 261
Cp 181 TT 182

RESULT 3
LOCUS T29670 238 bp mRNA EST 06-SEP-1995
DEFINITION EST09669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy
chain V region (GB:X61012) (HT:3230).
ACCESSION T29670
NID g611768
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Small intestine.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Frederiksberg C, DENMARK
Location/Qualifiers
1..330

Source
/organism="Sus scrofa"
/tissue="small intestine"
/clone_lib="directionally cloned cDNA in Xli-blue MRF"
/clone="cld10"
1..>330

V_region

/note="expressed sequence tag"

/product="Ig heavy chain variable VDJ region"

BASE COUNT 71 a 77 c 104 g 76 t 2 others

ORIGIN

Query Match 16.4%; Score 61; DB 123; Length 330;

Best Local Similarity 61.5%; Pred. No. 3.47e-70;

Matches 158; Conservative 0; Mismatches 99; Indels 0; Gaps 0.

Db 74 agctgagagagcctggtgcaagctgagnggtctctgagactctctgtgtcgtctg 133
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QY 8 AGTCTGGGCTGAGTGAAGAGGCTGGTCTCAAGAGGCTCTCTGCAAGGCTTCTG 67
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Db 134 gattcaccctcagtgtaacctacattacgtggtccgcaggtccagggagggcttg 193
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QY 68 GAGGCACCTTCAGCGCCATGTTATCAGTGGCTGCGACAGCGCCCTGGACAGGGCTTG 127
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194 agtggctggcagctattagctactagctgtgtgttagtacctactacacagactctgtgagg 253
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 128 AGTGGATGGGGGAGATATCTTTCTTTTGGTAAATCAAAATCCGACAAAGTTCCAGG 187
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 254 gccgattccacctctccaaagacacccacagagagagcgtctctggaatnaacagcc 313
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QY 188 GCAGAGTCTCGATTACCGCGGACGAATCCGCGAGCACAGCTACATGGAGTGAATGACC 247
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Db 314 tgagacagagaagacagc 330
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QY 248 TGAGATCGGAGGACAGC 264

RESULT 6 H73816 419 bp mRNA EST 31-OCT-1995
LOCUS yslib01.rl Homo sapiens cDNA clone 214441 5' similar to gb:M62726
DEFINITION IG HEAVY CHAIN V-III REGION (HUMAN);.
ACCESSION H73816
NID g1046750
KEYWORDS EST.
SOURCE human clone-214441 primer-M13p1 library-Soares fetal liver spleen
INFLS vector-pT73D (Pharmacia) with a modified polylinker
host-DHI0B (ampicillin resistant) Psitel-Pac I Psitel-Eco RI Liver
and spleen from a 20 week-post conception male fetus. 1st strand
cDNA was primed with a Pac I - oligo(dT) primer [5',
AACTCGAAGATTAATTAAGATCTTTTITTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 419)

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 261

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers

1..419

/organism="Homo sapiens"

/clone="214441"

<1..>419

BASE COUNT 91 a 100 c 116 g 102 t 10 others

ORIGIN

Query Match 15.6%; Score 58; DB 90; Length 419;

Best Local Similarity 62.3%; Pred. No. 1.37e-64;

Matches 160; Conservative 0; Mismatches 96; Indels 1; Gaps 1;

Db 27 ctgggggctccctgagactctctgtgtcagcgtctgtgattccacttcagtagctagcca 86
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QY 32 CTGGGTCTCTCAAGTCTCTCTCAAGGCTCTCTGAGGCTCTCTGAGGCTCTCTGAGG 91
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Db 87 tgcactgggtctgcgcagagctccagcagggcgtgagtgagtgagtgagtgagtgag 146
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QY 92 TCAGCTGGGCTGCGACAGGCGCTGCGACAGGCGCTTACGTGATGCGGGGAGTATCICIT 151
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Db 147 atggaagtaataatattatgagagctccgtgagggcctattccacacatctctcagagaga 206
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QY 152 TCTTTGGTCAATCAATTCGACAGAGTTCGAGGCTTCGAGTCTCTGAGTCTCTGAGT 211
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Db 207 attccaaaacacacgtctgtctgcaaatgaacagcctgagagctgagacagagctgt 266
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QY 212 AATCGGAGGACAGCTTACATGGAGCTGAGTGGAGCTGAGTGGAGCTGAGTGGAGCT 271
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QY 272 ATTACTGTG-CGAAAGA 287

RESULT 7 H44771 97 bp mRNA EST 31-JUL-1995
LOCUS YP20e1.rl Homo sapiens cDNA clone 188012 5' similar to gb:U92325
DEFINITION IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);.
ACCESSION H44771
NID g920823
KEYWORDS EST.
SOURCE human clone-188012 library-Soares breast 3NEHst vector-pT73D
(Pharmacia) with a modified polylinker host-DHI0B (ampicillin
resistant) primer-M13p1 Psitel-Not I Psitel-Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTGGAGCGCGCCCTTTTITTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 97)

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

/note- record: p1130 fac (firmly made) which a "moulture"

U-Merck EST Project

TITLE	Wilson, R. The WashU-Merck EST Project
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TITLE	Wilson, R. The WashU-Merck EST Project
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 [REDACTED]

Release 2.0 John F. Collins, BioComputing Research Unit.
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 MParch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
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 Tabular output not generated.
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 Description: (1-372) from US08944215.seq
 Perfect Score: 372
 N A Sequence: 1 CTCGAGGAGTGTGGGGGTGA CCCTGGTCACGGTCTCTCA 372
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Scoring table: TABLE default
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 Nmatch STD: Dbase 0: Query 0
 Searched: 87531 seqs, 22996021 bases x 2
 Post-processing: Minimum Match 88
 Listing first 45 summaries
 Database: n-issued
 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PT90 9:PT91
 10:PT92 11:PT93 12:PT94 13:PT95 14:PT96
 Statistics: Mean 7.726; Variance 4.117; scale 1.877
 pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred No.
1	290	78.0	2207	14	PTC-US96-1	Sequence 8, Applicati
2	238	64.0	812	7	US-07-834-	Sequence 53, Applicati
3	238	64.0	812	10	PTC-US92-0	Sequence 53, Applicati
4	238	64.0	813	10	PTC-US92-1	Sequence 61, Applicati
5	238	64.0	813	7	US-08-053-	Sequence 61, Applicati
6	223	59.9	441	6	US-08-217-	Sequence 3, Applicati
7	218	58.6	687	13	PTC-US95-1	Sequence 1, Applicati
8	218	58.6	687	7	US-08-300-	Sequence 1, Applicati
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10	196	52.7	363	7	US-08-264-	Sequence 1, Applicati
11	156	41.9	360	11	PTC-US93-0	Sequence 7, Applicati
12	148	39.8	3282	13	PTC-US95-0	Sequence 154, Applicat
13	148	39.8	3282	13	PTC-US95-0	Sequence 154, Applicat
14	148	39.8	3282	13	PTC-US95-0	Sequence 154, Applicat
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17	148	39.8	13254	13	PTC-US95-0	Sequence 159, Applicat
18	148	39.8	13254	13	PTC-US95-0	Sequence 170, Applicat
19	148	39.8	13254	7	US-08-276-	Sequence 170, Applicat

20 139 37.4 451 11 PCT-US93-1 Sequence 11, Applicati 1.69e-86
 21 129 34.7 443 6 US-08-477- Sequence 9, Applicatio 8.77e-79
 22 129 34.7 443 7 US-08-487- Sequence 9, Applicatio 8.77e-79
 23 129 34.7 443 6 US-07-634- Sequence 9, Applicatio 8.77e-79
 24 129 34.7 443 7 US-08-474- Sequence 9, Applicatio 8.77e-79
 25 124 33.3 433 5 US-07-634- Sequence 18, Applicati 5.14e-75
 26 124 33.3 433 7 US-08-487- Sequence 18, Applicati 5.14e-75
 27 124 33.3 433 6 US-08-477- Sequence 18, Applicati 5.14e-75
 28 124 33.3 433 7 US-08-474- Sequence 18, Applicati 5.14e-75
 29 119 32.0 366 7 US-08-040- Sequence 5, Applicatio 4.20e-71
 30 119 32.0 366 6 US-08-236- Sequence 8, Applicatio 4.20e-71
 31 119 32.0 366 13 PCT-US95-0 Sequence 7, Applicatio 4.20e-71
 32 119 32.0 366 7 US-08-040- Sequence 7, Applicatio 4.20e-71
 33 118 31.7 357 7 US-08-467- Sequence 1, Applicatio 2.45e-70
 34 118 31.7 357 7 US-08-392- Sequence 1, Applicatio 2.45e-70
 35 117 31.5 351 6 US-08-236- Sequence 10, Applicati 1.43e-69
 36 117 31.5 351 13 PCT-US95-0 Sequence 10, Applicati 1.43e-69
 37 117 31.5 360 12 PCT-US94-0 Sequence 1, Applicatio 1.43e-69
 38 117 31.5 363 7 US-08-040- Sequence 4, Applicatio 1.43e-69
 39 117 31.5 363 7 US-08-040- Sequence 1, Applicatio 1.43e-69
 40 117 31.5 363 7 US-08-040- Sequence 2, Applicatio 1.43e-69
 41 117 31.5 366 7 US-08-040- Sequence 6, Applicatio 1.43e-69
 42 117 31.5 429 13 PCT-US95-0 Sequence 6, Applicatio 1.43e-69
 43 117 31.5 429 6 US-08-236- Sequence 5, Applicatio 1.43e-69
 44 117 31.5 1572 7 US-08-353- Sequence 23, Applicati 1.43e-69
 45 115 30.9 363 7 US-08-040- Sequence 3, Applicatio 4.83e-68

ALIGNMENTS

RESULT 1
 ID PCT-US96-10043-8 STANDARD; DNA; UNC; 2287 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 8, Application PCT/TUS9610043
 CC Sequence 8, Application PCT/TUS9610043
 CC GENERAL INFORMATION:
 CC APPLICANT: The General Hospital Corporation
 CC TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
 CC TITLE OF INVENTION: AND METHODS
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Fish & Richardson P.C.
 CC STREET: 225 Franklin Street
 CC CITY: Boston
 CC STATE: MA
 CC COUNTRY: USA
 CC ZIP: 02210-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1 0, Version #1 30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/TUS96/10043
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,213
 FILING DATE: 14-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lech, Karen F.
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 00786/244001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-5905
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2287 base pairs
 TYPE: nucleic acid


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CC SOFTWARE. PatentIn Release #1 0, Version #1 25
CC
CC CURRENT APPLICATION DATA:
CC CC
CC CC APPLICATION NUMBER: US 08/053,131
CC CC
CC CC FILING DATE: 26-APP-1993
CC CC
CC CC CLASSIFICATION: 800
CC CC
CC CC PRIOR APPLICATION DATA:
CC CC
CC CC APPLICATION NUMBER: US 07/990,860
CC CC
CC CC FILING DATE: 16-DEC-1992
CC CC
CC CC PRIOR APPLICATION DATA:
CC CC
CC CC APPLICATION NUMBER: US 07/810,279
CC CC
CC CC FILING DATE: 17-DEC-1991
CC CC
CC CC PRIOR APPLICATION DATA:
CC CC
CC CC APPLICATION NUMBER: US 07/853,408
CC CC
CC CC FILING DATE: 18-MAR-1992
CC CC
CC CC ATTORNEY/AGENT INFORMATION:
CC CC
CC CC NAME: Smith, William M.
CC CC
CC CC REGISTRATION NUMBER: 30,223
CC CC
CC CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC CC
CC CC TELECOMMUNICATION INFORMATION:
CC CC
CC CC TELEPHONE: 415-326-2400
CC CC
CC CC TELEFAX: 415-326-3422
CC CC
CC CC INFORMATION FOR SEQ ID NO: 61:
CC CC
CC CC SEQUENCE CHARACTERISTICS:
CC CC
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CC CC
CC CC TYPE: nucleic acid
CC CC
CC CC STRANDEDNESS: single
CC CC
CC CC TOPOLOGY: linear
CC CC
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CC CC
CC CC FEATURE:
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CC CC
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CC CC
CC CC FEATURE:
CC CC
CC CC NAME/KEY: CDS
CC CC
CC CC LOCATION: 373 678
CC CC
CC Sequence 813 BP: 204 A; 189 C; 223 G; 197 T; 0 other

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QY 61 GCTTCTGGAGGACCTTCACGGGCCATGTTATCAGCTGGGTGGGACAGGCCCCCTGGACAA 120
Db 121 GGGCTTGGAGTGGAGGAGGATCTTCCCTTTCCGTAATACAGAAAGTACGCAACAC 180
QY 121 GGGCTTGGAGTGGAGGAGGATCTTCTTCTTGGCACATCAAACTCCGACAGAG 180
Db 181 TTCAGGGCAGAGTACCATTCACGGGGAGGAATCCACGGGCACAGCCCTACATGGAGCTG 240
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Db 241 AGCAGCTGAGATCTGAGGACAGCGCATATATTATTGTGCGAGAG 286
QY 241 AGTACCTGAGATCGGAGGACAGCGCATCTATTACTGTGCGAAG 286

RESULT 9
ID PCT-US94-01258-1 STANDARD; DNA; UNC; 687 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9401258.
CC Sequence 1, Application PC/TUS9401258
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS.
CC NUMBER OF SEQUENCES: 61
CC COMPUTER READABLE FORM: 61
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01258
CC FILING DATE: 02-FEB-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 687 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ Sequence 687 BP; 155 A; 211 C; 195 G; 126 T; 0 other;

Query Match 58.6%; Score 218; DB 12; Length 687;
Best Local Similarity 88.1%; Pred. No. 2,93e-148;
Matches 252; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 1 CTCGAGCAGTCTGGGGCTGAGGTGAAGAGCCCTGGGTCTCGTGAAGGTCTCTCTGCAAG 60
QY 1 CTCGAGCAGTCTGGGGCTGAGGTGAAGAGCCCTGGGTCTCGTGAAGGTCTCTCTGCAAG 60
Db 61 GCCTTCTGGAGGACCTTCACAAATTAATGCAATAGTGGTGGAGAGGCCCCCTGGACAA 120
QY 61 GCCTTCTGGAGGACCTTCACAAATTAATGCAATAGTGGTGGAGAGGCCCCCTGGACAA 120
Db 121 GGGCTTGGAGTGGAGGAGGATCTTCCCTTTCCGTAATACAGAAAGTACGCAACAC 180
QY 121 GGGCTTGGAGTGGAGGAGGATCTTCTTCTTGGCACATCAAACTCCGACAGAG 180
Db 181 TTCAGGGCAGAGTACCATTCACGGGGAGGAATCCACGGGCACAGCCCTACATGGAGCTG 240
QY 181 TTCAGGGCAGAGTCTGATTCAGCGGGAGGAATCCGCGACACAGCCCTACATGGAGCTG 240
Db 241 AGCAGCTGAGATCTGAGGACAGCGCATATATTATTGTGCGAGAG 286

QY 241 AGTACCTGAGATCGGAGGACAGCGCATCTATTACTGTGCGAAG 286
RESULT 10
ID US-08-264-093-1 STANDARD; DNA; UNC; 363 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08264093.
CC Sequence 1, Application US/08264093
CC Patent No. 5639863
CC GENERAL INFORMATION:
CC APPLICANT: Michael D. Dan
CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CC TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
CC TITLE OF INVENTION: ANTIGEN
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ridout & Maybee
CC STREET: 2300 Richmond-Adelaide Centre
CC CITY: Toronto
CC STATE: Ontario
CC COUNTRY: Canada
CC ZIP: M5H 2J7
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: MS-DOS 6.00
CC SOFTWARE: ASCII Editor
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/264,093
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA: No. 5639863 applicable
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lake, James R.
CC REGISTRATION NUMBER: 31081
CC REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (416) 868-1482
CC TELEFAX: (416) 362-0823
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 363 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: linear
SQ Sequence 363 BP; 84 A; 97 C; 108 G; 74 T; 0 other;

Query Match 52.7%; Score 196; DB 7; Length 363;
Best Local Similarity 84.8%; Pred. No. 5.97e-131;
Matches 239; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Db 10 CTGCTGAGTCTGGAGCTGAGGTGAAGAGCCCTGGGGCCCTCAGTGAAGTCTCTCTGCAAG 69
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Db 70 GCTTCTGGTTACACCTTCACACCTATGCTCTCAGCTGGGTGGAGAGGCCCCCTGGACAA 129
QY 61 GCTTCTGGAGGACCTTCACGGGCCATGTTATCAGCTGGGTGGAGAGGCCCCCTGGACAA 120
Db 130 GGGCTTGGAGTGGAGTGGATGAGGAGTCAAGAGTCAATGCAATGCAATGCAATGCAATG 189
QY 121 GGGCTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 180
Db 190 TTCAGGGCAGAGTCTCCATGACACACAGACACATCCACAGAGACAGCCCTACATGGAGCTG 249
QY 181 TTCAGGGCAGAGTCTCCATGACACACAGACACATCCACAGAGACAGCCCTACATGGAGCTG 240
Db 250 AGGAGCTTCAGATCTGACGACAGCGCGCTGTTACTGTGCG 291
QY 241 AGTACCTGAGATCGGAGGACAGCGGCATCTATTACTGTGCG 282

CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10566 No. 5652138th Torrey Pines Road, Suite 220,
 CC STREET: Mail Drop TPC8
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCPI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 154:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 3282 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 15..452
 CC Sequence 3282 bp: 710 A: 1109 C: 864 G: 599 T: 0 other;
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 CC Query Match 39.8%; Score 148; DB 7; Length 3282;
 CC Best Local Similarity 76.4%; Pred. No. 1.81e-93;
 CC Matches 214; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
 CC
 Db 87 CAGTCCGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGGTTCCTTGTCAGGCTTCT 146
 QY 7 CAGTCTGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGGTTCCTTGTCAGGCTTCT 66
 Db 147 GGATACAGATTCACTTAATCTTTATTCATTTGGTGGCCGAGCCCGGAGAGAGTTT 206
 QY 67 GGAGGCACCTTCAGCGGCCATGTTATTCAGTGGGTGGGTCGACAGCGCCCTGGACAAGGGCTT 126
 Db 207 GAGTGGATGGATGATCAATCTTACACGCGAAACAAAGAAATTTACGCGAAGTTTCAG 266
 QY 127 GAGTGGATGGGCGGAGTATCTTCTTCTTGGACATCAAACTCCGACAGAGTTCCAG 186
 Db 267 GACAGATCACTTTATTCGCGGACATCCGCGAACAACAGCCTACATGAGTTGAGGAGC 326
 QY 187 GGCAGAGTCTGATTATCCGCGGAGGAATCCGCGAGCAGAGCCTACATGAGGTGAGTACG 246
 Db 327 CTCATCTCTAGATCAAGTGTGTATTTATTTATTTGTCAGAG 366
 QY ~ 247 CTGAGATGGAGGACAGGCGATCTATTACTGTGCGAAG 286

RESULT 14
 ID FCT-US95-08743-169 STANDARD; DNA: UNC; 3282 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 169, Application PC/TUS9508743.
 CC Sequence 169, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EP0)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
 CC INFORMATION FOR SEQ ID NO: 169:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 3282 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC Sequence 3282 bp: 599 A: 864 C: 1109 G: 710 T: 0 other;
 CC
 CC Query Match 39.8%; Score 148; DB 13; Length 3282;
 CC Best Local Similarity 76.4%; Pred. No. 1.81e-93;
 CC Matches 214; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
 CC
 Db 2917 CTCGCGCAATAATAACAAG 2076
 QY 286 CTTTCACAGAGTAAG 227
 Db 2977 CTGTSTTCGGGATGTGTCTGCGGTAAAGATGACTCTCTCTCTCTCTCTCTCTCTCT 3036
 QY 226 CTGTGTCGCGGATTCGTCGCGGTAAATCGAGATCTCGCTGCAACTCTCTCTCTCTCT 167
 Db 3037 CTTGTTTCGTTGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 3096
 QY 166 TTGATGTGTCGAG 107
 Db 3097 GCGCGACCAATGAATAACAAAGTACTGATGATGATGATGATGATGATGATGATGATG 3156
 QY 106 GTGCGACCCAGCTGATACATGCGCGGTGAAGTGTGATGATGATGATGATGATGATGAT 47
 Db 3157 TCAGTGAGGCCCGAGCTTCTTCACTCAGCCCGGAGCTG 3196
 QY 46 TCAGTGAGGCCCGAGCTTCTTCACTCAGCCCGGAGCTG 7
 RESULT 15
 ID US-08-276-852-169 STANDARD; DNA: UNC; 3282 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 169, Application US/08276852.
 CC Sequence 169, Application US/08276852
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:



WATERL

(TM)

Release 2.10 John F. Collins, BioComputing Research Unit
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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 10:09:25 1998: Maspar time 458.90 seconds
Tabular output not generated. 1151.231 Million cell updates/sec

Title: >US-08-844-215-24
Description: (-372) from US08844215.seq
Perfect Score: 372
N.A. Sequence: 1 CTCGAGGAGTCTGGCTGCA CCGTGTACCGCTCTCTCA 172
Comp: GAGCTCTGACACCCGACCT GGCACGAGTGGGAGAGCACT

Scoring table: TABLE default
Gap 6
Nmatch STD: Phase 0: Query 0
Searched: 430261 seqs, 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new7
1:ACT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7:HTG4 8:HUM1
9:HUM2 10:HUM3 11:INV1 12:INV2 13:PG3 14:MAM 15:VET
16:PLN 17:POL 18:POD 19:POD2 20:SYN 21:UNC 22:VIP
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23:BCR1 24:BCR2 25:BCR3 26:BCR4 27:BCR5 28:BCR6 29:BCR7
30:BCR8 31:BCR9 32:BCR10 33:BCR11 34:BCR12 35:BCR13
36:GEN1 37:GEN2 38:GEN3 39:GEN4 40:GEN5 41:GEN6 42:HTG1
43:HTG2 44:HTG3 45:HTG4 46:HTG5 47:INV1 48:INV2 49:INV3
50:INV4 51:INV5 52:INV6 53:INV7 54:INV8 55:INV9 56:INV10
57:INV11 58:INV12 59:MAM1 60:MAM2 61:MAM3 62:VET1
63:VET2 64:VET3 65:VET4 66:PAT1 67:PAT2 68:PAT3 69:PAT4
70:PAT5 71:PAT6 72:PAT7 73:PHG 74:PLN1 75:PLN2 76:PLN3
77:PLN4 78:PLN5 79:PLN6 80:PLN7 81:PLN8 82:PLN9 83:PLN10
84:PLN11 85:PLN12 86:PLN1 87:PLN2 88:PLN3 89:PLN4
90:PLN5 91:PLN6 92:PLN7 93:PLN8 94:PLN9 95:PLN10
96:PLN11 97:PLN12 98:PLN13 99:PLN14 100:PLN15 101:PLN16
102:PLN17 103:POD1 104:POD2 105:POD3 106:POD4 107:POD5
108:POD6 109:POD7 110:POD8 111:POD9 112:STP 113:SYN
114:UNA
genbankb101
115:VPL1 116:VPL2 117:VPL3 118:VPL4 119:VPL5 120:VPL6
121:VPL7 122:VPL8 123:VPL9 124:VPL10 125:VPL11
genbank-new7
126:POL 127:POL2 128:POL3 129:POL4 130:POL5 131:POL6
132:POL7 133:POL8 134:POL9 135:POL10 136:POL11 137:POL12
138:POL13 139:POL14 140:POL15 141:POL16 142:POL17
u-emb151_101
143:part1 143:part2
143:part3 143:part4

Database: genbankb101
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143:part1 143:part2
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Database: genbankb101
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126:POL 127:POL2 128:POL3 129:POL4 130:POL5 131:POL6
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u-emb151_101
143:part1 143:part2
143:part3 143:part4

Statistics: Mean 10.010: Variance 4.434: scale 2.260
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	257	69.1	528	99	HUMIGHDYN	Human Ig rearranged H	1.90e-207
2	254	68.3	534	99	HUMIGHDYN	Human Ig rearranged H	6.85e-207
3	253	68.0	507	97	HS201E5	H.sapiens mRNA for im	6.02e-204
4	253	68.0	507	97	HS201E4	H.sapiens mRNA for im	6.02e-204
5	253	68.0	507	97	HS201E2	H.sapiens mRNA for im	6.02e-204
6	253	68.0	507	97	HS201E3	H.sapiens mRNA for im	6.02e-204
7	252	67.7	524	93	HUM13HFN	Human Ig rearranged H	5.29e-203
8	251	67.5	522	97	HS201E8	H.sapiens mRNA for im	4.45e-203
9	249	66.9	480	97	HS201E4	H.sapiens mRNA for im	4.59e-200
10	249	66.9	483	87	HS201E5	H.sapiens mRNA for im	3.59e-200
11	249	66.9	510	87	HS201E9	H.sapiens mRNA for im	3.59e-200
12	249	66.9	510	87	HS201E6	H.sapiens mRNA for im	3.59e-200
13	249	66.9	510	87	HS201E7	H.sapiens mRNA for im	3.59e-200
14	249	66.9	510	87	HS201E2	H.sapiens mRNA for im	3.59e-200
15	249	66.9	522	97	HS201E3	H.sapiens mRNA for im	3.59e-200
16	249	66.9	525	87	HS201E1	H.sapiens mRNA for im	3.59e-200
17	249	66.9	525	87	HS201E4	H.sapiens mRNA for im	3.59e-200
18	248	66.7	360	96	HSVH3L18	H.sapiens germline + r	3.15e-199
19	247	66.4	510	87	HS201E1	H.sapiens mRNA for im	2.77e-198
20	247	66.4	525	87	HS201E2	H.sapiens mRNA for im	2.77e-198
21	247	66.4	525	87	HS201E3	H.sapiens mRNA for im	2.77e-198
22	246	66.1	421	99	HUMIGHVAN	Human (fetal) Ig for	2.43e-197
23	246	66.1	872	99	HUMIGHREVA	Homo sapiens (1951) c	2.43e-197
24	245	65.9	357	102	CC0502	Human immunoglobulin	2.13e-196
25	245	65.9	392	91	HS1GVH11M	H.sapiens germline im	2.13e-196
26	245	65.9	392	91	HS1GVH5M	H.sapiens germline im	2.13e-196
27	245	65.9	392	91	HS1GVH11	H.sapiens gene for im	2.13e-196
28	245	65.9	392	91	HS1GVH1G	H.sapiens gene for im	2.13e-196
29	245	65.9	392	91	HS1GVH1D	H.sapiens gene for im	2.13e-196
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33	245	65.9	392	91	HS1GVH2M	H.sapiens germline im	2.13e-196
34	245	65.9	483	87	HS201E7	H.sapiens mRNA for im	2.13e-196
35	245	65.9	513	99	HUMIGHDYN	Human Ig rearranged H	2.13e-196
36	245	65.9	525	99	HUMIGHDYN	Human Ig rearranged H	2.13e-196
37	245	65.9	527	95	HS1GVH82	Human clone HA immun	2.13e-196
38	245	65.9	527	95	HS1GVH82	Human clone HA immun	2.13e-196
39	244	65.6	448	99	HUMIGHBT	Human Ig rearranged H	1.87e-195
40	244	65.6	474	87	HS201E2	H.sapiens mRNA for im	1.87e-195
41	244	65.6	501	87	HS201E8	H.sapiens mRNA for im	1.87e-195
42	244	65.6	501	87	HS201E6	H.sapiens mRNA for im	1.87e-195
43	244	65.6	510	99	HUMIGHDYN	Human Ig rearranged H	1.87e-195
44	244	65.6	510	87	HS201E7	H.sapiens mRNA for im	1.87e-195
45	244	65.6	869	99	HUMIGHREVA	Human (1951K) germlin	1.87e-195

ALIGNMENTS

RESULT	1	HUMIGHDYN	528 bp	DNA	PRI	06-MAY-1996
LOCUS		Human Ig rearranged H chain gene V-region (V-D-J) hybridoma 14.				
DEFINITION		subgroup VH-1.				
ACCESSION		M65104				
NID		g185344				
KEYWORDS		V-region; immunoglobulin heavy chain subgroup VH-1; rearranged DNA.				
SOURCE		Homo sapiens				
ORGANISM		Homo sapiens				
REFERENCE		1 (bases 1 to 528)				
AUTHORS		Kipps, T.J., and Duffy, S.F.				
TITLE		Relationship of the CD5 B cell to human tonsillar lymphocytes that				
JOURNAL		express autoantibody-associated cross-reactive idiotypes				
MEMLINE		J Clin Invest 87 (5): 2087-2096 (1991)				
		91250563				

Db 463- actatgaactcttactgtactatactgaactgtatgaactcttggggcccaaggacacaggtc 522
 QY 301 TGTAGTGGTGAAGTCTGAGTGGGGTCTTCTTCAAGCAATGGGGTCAAGGCAAGTGGTC 360
 Db 523 accgtctctca 534
 QY 361 ACCGTCCTCTCA 372

RESULT 3
 LOCUS HS202E5 507 bp PNA PPI 03-AUG-1995
 DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 202-E5).
 ACCESSION Z47258
 NID g619469
 KEYWORDS immunoglobulin; variable region.
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
 REFERENCE 1 (bases 1 to 507)
 AUTHORS Lebecque, S.
 JOURNAL Direct Submission
 TITLE Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
 Schering-Plough, Laboratory for Immunological Research, 27, Chemin
 des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
 REFERENCE 2 (bases 1 to 507)
 AUTHORS Galibert, L., van Dooren, J., Durand, I., Pousset, F., Jefferis, R.,
 Bancheureau, J., and Lebecque, S.
 TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
 express unmutated immunoglobulin genes with intraclonal heavy chain
 isotype variability
 Eur. J. Immunol. 25 (3), 733-737 (1995)
 JOURNAL
 MEDLINE 95220422
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 /clone="202-E5"
 /tissue_type="blood"
 /cell_type="B-lymphocyte"
 BASE COUNT 106 a 139 c 158 g 104 t
 ORIGIN

Query Match 68.0%; Score 253; DB 87; Length 507;
 Best Local Similarity 86.0%; Pred. No. 6 02e-204;
 Matches 320; Conservative 0; Mismatches 49; Indels 3; Gaps 2;

Db 67 ctggtgcaactctggagctgaagtaagagcctgggtctctgggtgaaggtctctcaag 126
 QY 1 CTGAGCAAGTCTGGGGTCAAGGTGAAGAGGCTGGGTCTCAGTGAAGGTCTCTGCAAG 60
 Db 127 gctctgagggcaccttcagcagctatctatcagctgggtggcgacagggccctgggaca 186
 QY 61 GCTTCTGAGAGGCACTTCAGAGGCACTTCATCAAGTGGGTCATCAAGGTCCTGCAAG 120
 Db 187 gggcttgagtgatggaggagatcatcctctcttggatcacagcaaaactacgacagaag 246
 QY 121 GGGCTTGAGTGGATGGGGGGAGTATCTCTTTTGGCACATCAAACTCGGCACAGAAG 180
 Db 247 ttccaggcagagtcacagattaccgagcagaatccacgacacagcctacatggagctg 306
 QY 181 TTCCAGGCGCAGAGTCTCGATTACCGCGGAGCAATCCCGGAGACACAGGCTTACATGGAGCTG 240
 Db 307 agcaccttgagatctgagcagcagccgctgtattactgtgcgagtgagggatggagat 366
 QY 241 AGTACCTGAGATCGAGAGGAGGACACGCGGCACTATATCTGTGGGAAAGACCTGCCAAGATTT 300
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 QY 361 ACCGTCCTCTCA 372

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 ACCESSION Z47257

QY 361 ACCGTCCTCTCA 372

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 Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
 REFERENCE 1 (bases 1 to 507)
 AUTHORS Lebecque, S.
 JOURNAL Direct Submission
 TITLE Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
 Schering-Plough, Laboratory for Immunological Research, 27, Chemin
 des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
 REFERENCE 2 (bases 1 to 507)
 AUTHORS Galibert, L., van Dooren, J., Durand, I., Pousset, F., Jefferis, R.,
 Bancheureau, J., and Lebecque, S.
 TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
 express unmutated immunoglobulin genes with intraclonal heavy chain
 isotype variability
 Eur. J. Immunol. 25 (3), 733-737 (1995)
 JOURNAL
 MEDLINE 95220422
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NID	g619468	immunoglobulin; variable region.	
SOURCE	human.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata; Eutheria, Primates, Catarrhini, Hominoidea, Homo. (bases 1 to 507)		
AUTHORS	Lebecque, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology, Schering-Plough, Laboratory for Immunological Research, 27, Chemin des Peupliers, B.P. 11 CEDEX, Dardilly, France, 69572. FRANCE		
REFERENCE	2 (bases 1 to 522)		
AUTHORS	Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R., Banchemare, J., and Lebecque, S.		
TITLE	Anti-CD40 plus interleukin-4-activated human naive B cell lines express unmutated immunoglobulin genes with intracolon heavy chain isotype variability		
JOURNAL	Eur. J. Immunol. 25 (3), 733-737 (1995)		
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AUTHORS	Kipps, T.J. and Duff, S.F.		
TITLE	Relationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes		
JOURNAL	J. Clin. Invest. 87 (6), 2087-2096 (1991)		
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REFERENCE	Eukaryotae; mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata; Eutheria; Primates, Catarrhini, Hominoidea, Homo. (bases 1 to 534)		
AUTHORS	Kipps, T.J. and Duff, S.F.		
TITLE	Relationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes		
JOURNAL	J. Clin. Invest. 87 (6), 2087-2096 (1991)		
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REFERENCE 1 (bases 1 to 510)
AUTHORS Lebecque, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE 2 (bases 1 to 510)
AUTHORS Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
Bancheau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
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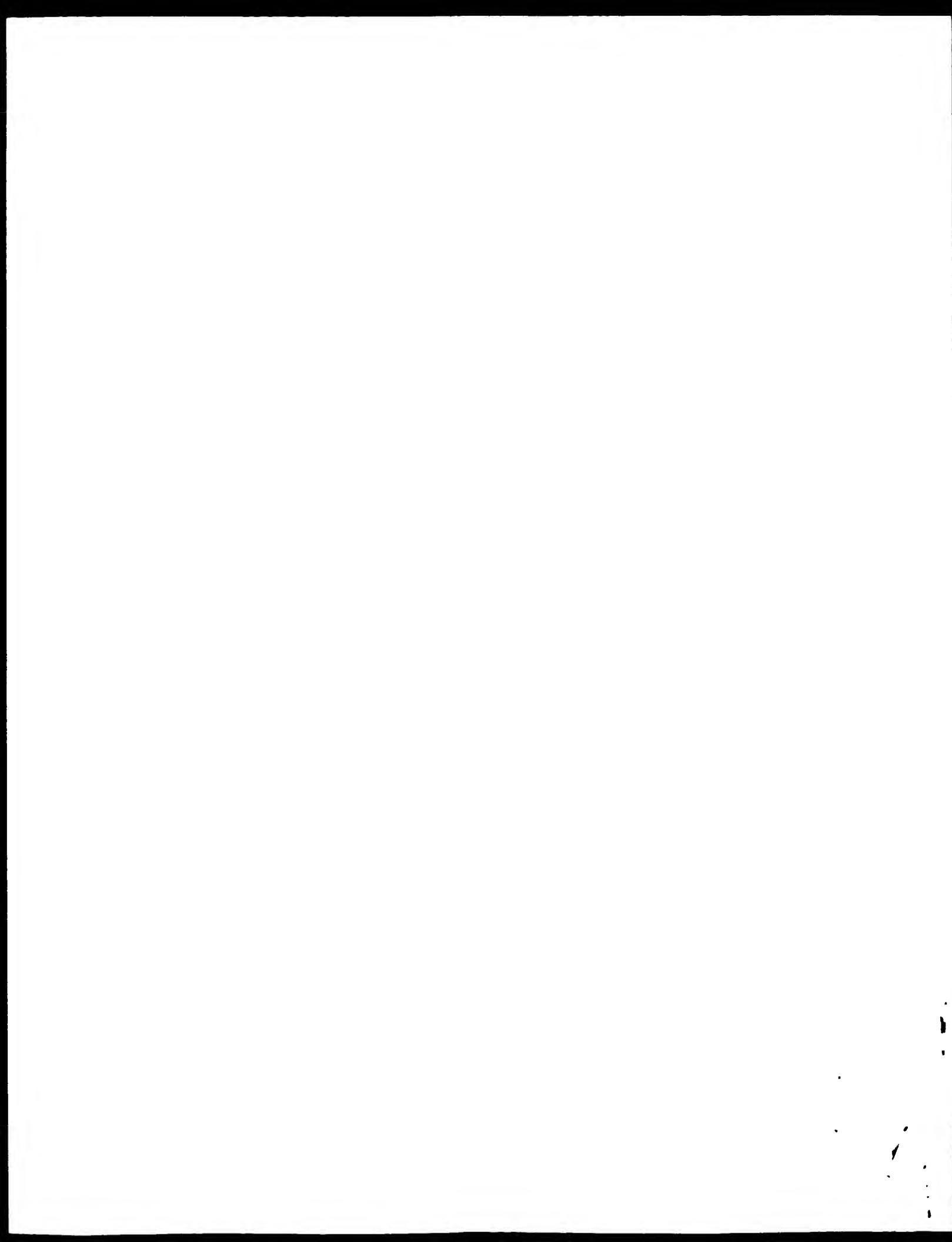
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REFERENCE 1 (bases 1 to 522)
AUTHORS Lebecque, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE 2 (bases 1 to 522)
AUTHORS Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
Bancheau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
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Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.
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AUTHORS Lebecque, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE 2 (bases 1 to 522)
AUTHORS Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
Bancheau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
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W E S R E L L (TM)

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MPSrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

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Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Statistics: Mean 8.112; Variance 4.715; scale 1.720

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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43	149	40.1	421	33	T73636	cDNA for humanised he	4 55e-85
44	148	39.8	3282	24	T40914	DNA encoding VH regio	2 33e-84
45	148	39.8	13254	24	T40915	Nucleotide sequence o	2 33e-84

ALIGNMENTS

RESULT 1
ID Q25443 standard; DNA: 2287 BP.
AC Q25443;
DI 02-JAN-1992 (first entry)
DE Sequence encoding antibody molecule IgG1.
KW Antibody; immunoglobulin G1; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT exon 1..453
FT /*tag= a 619..972
FT /*tag= b 1361..1405
FT /*tag= c 1524..1853
FT /*tag= d 1950..2273
FT /*tag= e
PN W09209293-A.
PD 11-JUN-1992; U08605.
PF 18-NOV-1991; US-618314.
PR 23-NOV-1991; GEN HOSPITAL CORP.
PA (GCHO) GEN HOSPITAL CORP.
PI Seed B, Walz G;
PF P-RSDB: R24442
PI - used in treating chronic inflammation, rheumatoid arthritis, psoriasis, etc.
CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The inventors designed a molecule including several such sites for attachment of sialyl-Lex side chains (see R24442). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Ig molecule.
CC Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins.
CC Disrupting this interaction has therapeutic applications, for

CC example, in minimising inflammation following tissue injury
SQ Sequence 2287 BP, 483 A, 753 C, 652 G, 399 T,

Query Match 78.0%; Score 290; DB 4; Length 2287;
Best Local Similarity 89.0%; Pred No 1 09e-186;
Matches 331; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Db 82 ctggtgagctctgggctgagtgaggaagcctgggtctcctgggtgaggtctctctcaag 141
QY 1 CTCGAGCAGTCTGGGCTCAGGTGAGGAAGCCTGGCTCCTCAGTGAAGGTCTCTCTGCAAG 60
Db 142 gcttctggagggacaccttcagagcctatgctatcagctgggtgagcagggccctctggacaa 201
QY 61 GCTTCTGGAAGAGATTTAAAGTGAAGTATATATAGCTGAGTACAGAGGCTGAGCAAA 120
Db 202 gggcttgagtgagggagggatcctcctctcttcttgtagcagcaaacctacgacagaaag 261
QY 121 GGGCTTGAAGTGAATGAGGAGATGATGCTTTCTTTGAGTATCAAAATGAGCAAGAG 180
Db 262 ttccagggcagagctacgattaccgagcagcaatccacagcagcagcagcagcagcagcag 321
QY 181 TTCAGGCGGAGAGTCTCGGATTACCGCGGACGGAATCCGCGAGACAGGCTATAGAGCTG 240
Db 322 agcagcctgaagctcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 381
QY 241 AGTAGGCTCAGATCGAGAGACAGCGGCTATCTATCTGTGCGAAGAGAGCTCCAGATTT 300
Db 382 ttagtggtgagtgagctgactcctgggtggtgagcagcagcagcagcagcagcagcagcagc 441
QY 301 TGTAGTGGTGGTAAGTCTACCGCGGAGTCTTCCAGCAGTGGGCGGAGGACCCCTGGTC 360
Db 442 accgtctcttca 453
QY 361 ACCGCTCTCTCA 372

RESULT 2

ID T60739 standard; DNA; 2287 BP.
AC T60739;
AT 22-APR-1997 (first entry)
DE IgG1 gene.
KW IgG1; P-selectin ligand; PSGL-1; counter-receptor; E-selectin;
KW sialyl-Lewis X; antiinflammatory; inflammation;
KW extravasation-dependent adverse reaction; organ damage; clotting;
KW adult respiratory distress syndrome; glomerular nephritis;
KW ischaemic myocardial injury; immune reaction; septic shock;
KW septicemia; therapy; diagnosis; ds.
OS Homo sapiens.
PN W09700079-A1.
PD 03-JAN-1997.
PF 11-JUN-1996; 010043.
PR 14-JUN-1995; US-000213.
PA (GENE) GEN HOSPITAL CORP
PI Pouyani T, Seed B;
DR P-PSDB; W10550
DP P-selectin and opt. E-selectin binding organic mol - having
PT sialyl-Le(x) and sulphated determinant, useful for protecting
PT against inflammatory or immune reactions
PS Disclosure: Page 40-41; 81pp; English.
CC The gene (T60739) encoding IgG1 (W10550) can be subjected to site-
CC directed mutagenesis in order to introduce one or more N-linked
CC glycan addition sites into the IgG1 molecule (see also W10551)
CC Eukaryotic host cells co-transfected with a vector carrying the
CC mutated IgG1 gene and with a vector that expresses an alpha-
CC (1,3)fucosyltransferase capable of attaching sialyl-Le(x) groups at
CC the glycosylation sites of the antibody molecule can be used in the
CC prodn. of sialyl-Le(x)-modified antibody. Such an antibody has
CC therapeutic applns., e.g. in minimising inflammation and
CC decreasing extravasation-dependent organ damage and/or clotting.
SQ Sequence 2287 BP, 483 A, 753 C, 648 G, 398 T,
Query Match 78.0%; Score 290; DB 28; Length 2287;

Best Local Similarity 89.0%; Pred No 1 09e-186;
Matches 331; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 82 ctggtgagctctgggctgagtgaggaagcctgggtctcctgggtgaggtctctctcaag 141
QY 1 CTCGAGCAGTCTGGGCTCAGGTGAGGAAGCCTGGCTCCTCAGTGAAGGTCTCTCTGCAAG 60
Db 142 gcttctggagggacaccttcagagcctatgctatcagctgggtgagcagggccctctggacaa 201
QY 61 GCTTCTGGAAGAGATTTAAAGTGAAGTATATATAGCTGAGTACAGAGGCTGAGCAAA 120
Db 202 gggcttgagtgagggagggatcctcctctcttcttgtagcagcaaacctacgacagaaag 261
QY 121 GGGCTTGAAGTGAATGAGGAGATGATGCTTTCTTTGAGTATCAAAATGAGCAAGAG 180
Db 262 ttccagggcagagctacgattaccgagcagcaatccacagcagcagcagcagcagcagcag 321
QY 181 TTCAGGCGGAGAGTCTCGGATTACCGCGGACGGAATCCGCGAGACAGGCTATAGAGCTG 240
Db 322 agcagcctgaagctcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 381
QY 241 AGTAGGCTCAGATCGAGAGACAGCGGCTATCTATCTGTGCGAAGAGAGCTCCAGATTT 300
Db 382 ttagtggtgagtgagctgactcctgggtggtgagcagcagcagcagcagcagcagcagcagc 441
QY 301 TGTAGTGGTGGTAAGTCTACCGCGGAGTCTTCCAGCAGTGGGCGGAGGACCCCTGGTC 360
Db 442 accgtctcttca 453
QY 361 ACCGCTCTCTCA 372

RESULT 3

ID Q89327 standard; DNA; 294 BP.
AC Q89327;
AT 26-SEP-1995 (first entry)
DE DP10 VH gene.
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen; monoclonal antibody; heavy chain; H chain;
KW variable region; autoimmunity; ss.
OS Homo sapiens.
PN W09508336-A.
PD 30-MAR-1995.
PF 22-SEP-1994; U10756.
PR 22-SEP-1993; US-124469.
PA (NICH) NICHOLS INST DIAGNOSTICS.
PI McLaughlin SM, Rapoport B;
DR WPI; 95-139383/18.
DR P-PSDB; R72068.
PT Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
PS Disclosure: Page 67; 94pp; English.
CC L- and H-chain RNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained. 13/15 clones of H chain (IgG1) genes
CC showed homology to the closest germline genes, Hg1G (H9937) and
CC Hg1263 (Q89328). The RNA (Q89329) and corresp. amino acid
CC (R72070) sequences of the VH region of a representative clone.
CC Q87H1.2, are provided.
SQ Sequence 294 BP; 67 A; 73 C; 97 G; 57 T;
Query Match 65.3%; Score 243; DB 14; Length 294;
Best Local Similarity 92.9%; Pred No 1 46e-152;
Matches 263; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Db 10 ctggtgagctctgggctgagtgaggaagcctgggtctcctgggtgaggtctctctcaag 69
QY 1 CTCGAGCAGTCTGGGCTCAGGTGAGGAAGCCTGGCTCCTCAGTGAAGGTCTCTCTGCAAG 60
Db 70 gcttctggagggacaccttcagagcctatgctatcagctgggtgagcagggccctctggacaa 129
QY 61 GCTTCTGGAAGAGATTTAAAGTGAAGTATATATAGTGAAGTGAAGGCTGAGCAAA 120

PF 19-OCT-1994: 211907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PA (Scri) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immunotherapy of
 PT HIV-induced disease
 PS Example 1: Page 185-188; 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
 CC the 406 residue minor phage coat protein, cpIII (cp3), which is expressed
 CC prior to extrusion in the phage assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector was designed for the cloning
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, FD/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a
 CC pEB leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a pEB leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the M4 Fab display phagemid expression vector, pM4-3 (see also
 CC Q92540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 SQ Sequence 4591 BP; 1170 A; 1171 C; 1232 G; 1118 T;

Query Match 58.5%; Score 218; DB 16; Length 4631.
 Best Local Similarity 88.1%; Pred. No. 1 720-134.
 Matches 252; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Db 3424 ctcaagcagctctgggctgaggtgaagaagcctgggctctcgtgaggtctcctcagc 3483
 QY 1 CTCGAGCAGCTCGGGGTGAGGTGACAGAGCTGGGTCCTCACTGAAGTCTCTCAAG 60
 Db 3484 gctctggagcagccttcaacaattatgccatcaagctgggtgcagcagccctcgaaca 3543
 QY 61 GCTTCTGGAGGACACTTTCAGTGGTCTATGATCAGCTGGGTGCTGACAGTGGACAA 120
 Db 3544 gggcttaagtgatgggagggatcttcccttcttongtaatacagcaagtagcagcaacac 3603
 QY 121 GGGTTGAGTGGATGGGGGGAGTATATCTTTCITTTGGTACATCAAAATCCGACACAG 180
 Db 3604 ttccaggcagcagctcaacattacccgggagcagaatccaggggagcagcagctgagcgtg 3663
 QY 181 TTCCAGGGGACACAGCTCTGATTACGGGGAGCAATCCGGAGGACACAGCTACATGGAGCTG 240
 Db 3664 aacagcctgaatctgaggaacacagccatattatttgcagag 3709
 QY 241 AATAAGCTTGATATGAGAGAGACAGGAGATCTATATATCTCTCAAG 286

RESULT 13
 ID Q92547 standard; DNA: 6166 BP.
 AC Q92547.
 DT 11-MAR-1996 (first entry)
 DE Expression vector, pPho-IT.
 KW Human; Fab; variable chain; heavy, light, region, VH, VL, HIV, gp120;
 KW 3b1; 3b3; 3b4; 3b9; M4; humanised; monoclonal antibody; MAb;
 KW immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;
 KW alkaline phosphatase; phoA; ss; cyclic.

OS Synthetic.
 PN W09511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994: 211907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PA (Scri) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immunotherapy of
 PT HIV-induced disease
 PS Example 2: Page 193-197; 249pp; English.
 CC This sequence represents the expression vector, pPho-IT which is a
 CC modified version of the phagemid expression vector, pComb3 given in
 CC Q92546. pPho-IT provides for the expression of soluble Fabs which are
 CC secreted into the periplasmic space which is regulated from the alkaline
 CC phosphatase (phoA) promoter. This plasmid was used within the scope of
 CC the invention to express various mutagenised human Fab's which comprise
 CC heavy and light variable regions which bind to HIV gp120. pPho-IT
 CC consists of a DNA molecule having two cassettes to express two soluble
 CC proteins a heavy chain and a light chain. The vector comprises,
 CC operatively linked 5' to 3', a first cassette consisting of the phoA
 CC promoter/operator sequences, an EcoRI restriction site, a ribosome
 CC binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer
 CC region, a cloning region bordered by 5' SacI and 3' XbaI restriction
 CC sites, an NcoI restriction site between the two cassettes, and a second
 CC cassette consisting of an expression control RBS, a pEB leader, a human
 CC consensus amino terminus spacer region comprising the sequence EVQLLE,
 CC a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
 CC followed by a SfiI site, expression control stop sequences and a NotI
 CC restriction site. The pPho-IT expression vector contains a light
 CC chain stuffer that is 1200 bp in length and a heavy chain stuffer that
 CC is 300 bp in length. The nucleotide sequences of the heavy and light
 CC chain stuffers encode the heavy and light chain variable domains of a
 CC tetanus toxin-specific Fab.
 SQ Sequence 6166 BP; 1416 A; 1706 C; 1629 G; 1415 T;

Query Match 58.5%; Score 218; DB 16; Length 6166.
 Best Local Similarity 88.1%; Pred. No. 1 720-134.
 Matches 252; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Db 5354 ctcaagcagctctgggctgaggtgaagaagcctgggctctcgtgaggtctcctcagc 5413
 QY 1 CTCGAGCAGCTCGGGGTGAGGTGACAGAGCTGGGTCCTCACTGAAGTCTCTCAAG 60
 Db 5414 gctctggagcagccttcaacaattatgccatcaagctgggtgcagcagccctcgaaca 5473
 QY 61 GCTTCTGGAGGACACTTTCAGTGGTCTATGATCAGCTGGGTGCTGACAGTGGACAA 120
 Db 5474 gggcttaagtgatgggagggatcttcccttcttongtaatacagcaagtagcagcaacac 5533
 QY 121 GGGTTGAGTGGATGGGGGGAGTATATCTTTCITTTGGTACATCAAAATCCGACACAG 180
 Db 5534 ttccaggcagcagctcaacattacccgggagcagaatccaggggagcagcagctgagcgtg 5593
 QY 181 TTCCAGGGGACACAGCTCTGATTACGGGGAGCAATCCGGAGGACACAGCTACATGGAGCTG 240
 Db 5594 aacagcctgaatctgaggaacacagccatattatttgcagag 5639
 QY 241 AATAAGCTTGATATGAGAGAGACAGGAGATCTATATATCTCTCAAG 286

RESULT 14
 ID Q92767 standard; CDNA: 325 BP.
 AC Q92767.
 DT 18-MAR-1993 (first entry)
 DE Gene for HV region of human rheumatoid factor antibody.
 KW Heavy chain; variable region; YES8C; arthritis; ss.
 KW Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 20..325

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FT /tag- a
FT misc_feature 7..19
FT /tag- b
FT /note- "leader sequence"
FT misc_feature 93..105
FT /tag- c
FT /note- "encodes CDR1"
FT misc_feature 150..198
FT /tag- d
FT /note- "encodes CDR2"
PN J04267889-A.
PD 24-SEP-1992.
PF 22-FEB-1991; 048704.
PP 22-FEB-1991; JP-048704
PA (EZAKI) EZAKI K.
PA (NISR) NISSUI PHARM CO LTD.
DR WPI: 92-368404/45.
DR P-PSDB: R25325.
PT Monoclonal human rheumatoid factor - obtd. by prodn. and
PT secretion of hybridoma obtd. from cell fusion of human bone
PT marrow derived lymphocyte and P3U1 mouse myeloma cell
PS Disclosure; Page 5; 7pp; Japanese.
CC The sequence shown encodes the variable region of the heavy chain of
CC a human monoclonal antibody rheumatoid factor VES8C. The gene may
CC be isolated from the bone marrow soln. of a rheumatoid arthritis
CC patient and used to produce hybridomas, allowing prodn. of the
CC rheumatoid arthritis factor at constant quality in large quantities.
CC See also Q29766.
SQ Sequence 325 BP; 67 A; 89 C; 104 G; 65 T.

Query Match 58.38; Score 217; DB 5; Length 325;
Best Local Similarity 88.38; Pred. No. 9,05e-134;
Matches 250; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Db 41 ctggtcagctcgggtgaggtgaaagacccctgggtcttcggtgaggtctccctgcaag 100
QY 1 CTCGAGCAGTCTGGGCTGAGGTGAGAGAGCCCTGGGTCTCAGTGAAGGTCTCTGCAAG 60

Db 101 gctctgagggacggcagcagctatcctatcagctgggtggcagagccctggacaa 160
QY 61 GCTTCTGGAGGACCTTCAGCGGCCATGTTATCAGTGGGTGGCAGAGCCCTGGACAA 120

Db 161 ggaactgagtggtggaggagatccctctcttcttggtacagcaactacgcacagagg 220
QY 121 GGGCTTAGTGATAGAGAGGAGATTCCTTTCTTTGGGACATCAAACTCCGACAGAG 180

Db 221 ttccagggcagagtcacgattaccggcagcaaatccacgcagcccgctacatgaggtg 280
QY 181 TTCCAGGGCAGAGTCTCSATTAGCGGGAGCAATCCGCGAGGACAGCCTACATGAGGTG 240

Db 281 aqacacttgagatctgaagacagcgccgtctattactgtgcca 323
QY 241 AGTAGCCTGAGATCGGAGGACAGGCCATCTATTACTGTGCGA 283

RESULT 15
ID Q78956 standard; DNA; 539 BP.
AC Q78956;
DT 02-AUG-1995 (first entry)
DE Human immunoglobulin Vh gene #18.
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 47..481
FT /tag- a
FT /product= human immunoglobulin variable heavy chain
FT intron 93..176
FT /tag- b
FT /tag- c
FT /tag- d
FT /note- "miscellaneous signal, does not conform to
FT terminator or splice site sequence"

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PN WO9426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NISR) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-PSDB: R66311.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS Claim 27; Page 54-55; 130pp; Japanese.
CC A series of genes (Q78939-79002) encoding human immunoglobulin variable
CC heavy chains. The genes were isolated and cloned from a series of cosmid
CC constructs. Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR
CC amplification using primers Q78917-38. The genes are subdivided into 5
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with TaqI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
CC were collected. The fragments were ligated with ClaI-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 539 BP; 135 A; 155 C; 148 G; 101 T;
Query Match 54.88; Score 204; DB 13; Length 539;
Best Local Similarity 85.48; Pred. No. 2.11e-124;
Matches 246; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Db 197 ctggtcagctcgggtgaggtgaaagacccctgggtcagtgaggtctctctgcaag 256
QY 1 CTCGAGCAGTCTGGGCTGAGGTGAGAGAGCCCTGGGTCTCAGTGAAGGTCTCTGCAAG 60

Db 257 gctctgaggtgaggtgaggtgaaagacccctgggtcagtgaggtctctctgcaag 316
QY 61 GCTTCTGGAGGACCTTCAGCGGCCATGTTATCAGTGGGTGGCAGAGCCCTGGACAA 120

Db 317 ggccttgagtgatgggtgaggtgaggtgaaagacccctgggtcagtgaggtctctctgcaag 376
QY 121 GGCCTTGAGTGGATGGGAGGAGATCTCTTTCTTTGGGACATCAAACTCCGACAGAG 180

Db 377 ctccagggcagagtcacccatgacccacagacacatccacgagcagcagcctacatgagctg 436
QY 181 TTCCAGGGCAGAGTCTCSATTAGCGGGAGCAATCCGCGAGGACAGCCTACATGAGGTG 240

Db 437 agagcctgagatctgacgacacagcccgctgtattactgtcgagagac 484
QY 241 AGTAGCCTGAGATCGGAGGACAGGCCATCTATTACTGTGCGAAGAG 288

Search completed: Tue Feb 24 10:36:25 1998
Job time : 193 secs.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
1	148	39.8	279	99	AA231281	at44c02.rl Soares ova	8.55e-147	
2	119	32.0	373	26	AA300571	EST13661 Testis tumor	1.65e-186	
3	109	29.3	291	58	AA337074	EST189603 Small intestine	5.44e-146	
4	100	26.9	265	58	AA4377129	EST184560 Small intestine	1.16e-147	
5	83	22.3	266	90	AA432547	u047h07.rl Soares ova	1.30e-113	
6	64	17.2	198	62	AA383972	EST197425 Testis tumor	1.18e-76	
7	42	11.3	273	26	AA393982	EST13889 Testis tumor	1.85e-36	
8	42	11.3	241	25	AA295703	EST100902 Pancreas	1.85e-36	
9	36	9.7	280	37	AA332695	EST130467 Colon I Homo	2.43e-26	
10	35	9.4	230	85	AA438970	u746f62.rl Soares ova	1.05e-24	
11	35	9.4	240	52	AA300289	EST169410 Lymph node	1.05e-24	
12	35	9.4	366	59	AA378312	EST191017 Synovial sar	1.06e-24	
13	30	8.1	256	26	AA306005	EST13453 Testis tumor	7.96e-17	
14	29	7.8	326	37	AA373241	EST139532 Colon I Homo	2.59e-15	
15	28	7.5	258	52	AA360195	EST163374 Lymph node	7.87e-14	
16	27	7.3	304	26	AA300945	EST13823 Testis tumor	2.27e-12	
17	26	7.0	364	16	AA098196	nm886h06.rl Stratagene	6.09e-11	
18	26	7.0	371	37	AA337565	EST130921 Colon I Homo	6.09e-11	
19	25	6.7	294	31	AA343630	EST18648 Lung Homo sa	1.52e-06	
20	23	6.2	420	1	AA175689	u944c02.rl Soares ova	7.48e-07	
21	22	5.9	278	60	AA381086	EST194138 Activated T	1.45e-06	
22	21	5.8	243	37	AA324972	EST130287 Colon I Homo	2.54e-04	
23	21	5.6	267	52	AA360197	EST169376 Lymph node	2.55e-04	
24	21	5.6	295	37	AA338574	EST132070 Embryo, 12 w	2.55e-04	
25	21	5.6	307	58	AA337311	EST189959 Small intestine	2.55e-04	
26	21	5.6	455	22	AA145478	mr05q07.rl Soares ova	2.55e-04	
27	21	5.6	551	82	AA418907	u012a09.sl Soares NHL	2.55e-04	C
28	20	5.4	170	79	AA400764	z717b05.sl Soares tes	4.01e-03	
29	20	5.4	255	76	AA332433	EST165427 Activated T	4.01e-03	
30	20	5.4	253	14	AA427551	ESG4510.seq.F Human	4.01e-03	
31	20	5.4	281	35	AA331921	EST124509 Cerebellum I	4.01e-03	
32	20	5.4	331	113	AA438458	zw83e11.sl Soares tes	4.01e-03	C
33	20	5.4	337	18	AA393400	EST11903 Hepatic tumor	4.01e-03	
34	20	5.4	334	26	AA290325	nm95h05.rl Stratagene	4.01e-03	C
35	20	5.4	371	16	AA089308	mx79437.rl Soares men	4.01e-03	
36	20	5.4	387	15	AA250114	zw94f12.sl Soares tes	4.01e-03	
37	20	5.4	400	112	AA447509	z717b09.sl Stratagene	4.01e-03	
38	20	5.4	425	114	AA443899	zw16d09.sl Soares ova	4.01e-03	
39	20	5.4	435	89	AA055774	u012a09.rl Soares men	4.01e-03	
40	20	5.4	469	12	AA055774	u012a09.rl Soares men	4.01e-03	
41	20	5.4	482	30	AA362281	EST161139 Jurkat cell	4.01e-03	
42	20	5.4	489	47	AA217616	u753a02.rl Soares men	4.01e-03	
43	20	5.4	500	14	AA245435	EST15332 Spine LB Bro	4.01e-03	
44	19	5.1	337	118	CEAK018AXP	C. elegans CGA CGA	5.60e-02	
45	19	5.1	431	11	AA336855	u012a09.sl Soares NHL	5.60e-02	

ALIGNMENTS

RESULT	1
LOCUS	AA291381
DEFINITION	Scars Ovary tumor NHEK Homo sapiens GINA C1060 745244 5' similar to 9b WIGGIC TO HEAVY GRAN PPTUPSE V I FESION (HUMAN)..
ACCESSION	AA291381
NID	G1939359
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 379) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,R., Post,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson.R. WashU-Merck EST Project 1997

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:51 11 November 2014


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RESULT 10
LOCUS      AA428970      230 bp      mRNA      EST      20-MAY-1997
DEFINITION zv49b2.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone Z56946
5' similar to gb:M97789 IG GAMMA-1 CHAIN C REGION (HUMAN) :
ACCESSION  AA428970
NID         q2110596
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 230)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,P. and Wilson,P.
WashU-Merck EST Project 1997
Unpublished (1997)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel : 314 286 1800
Fax : 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through INL : contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m31 rev2:Er from AmerSham.
              Location/Qualifiers
              1..230
FEATURES
    source

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/organism="Homo sapiens"
/notice="Organ: ovary; Vector: p7T3D (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTCGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo."
/clone="756939"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"

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/blast_host=Dhl0B (ampicillin resistant)"
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BASE COUNT
ORIGIN

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Best Local Similarity 71.7%;   Pred No 1,05e-24;
Matches          66; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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Db      67  ggctctggacacccgcctgtattactgtgcga 98
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Q2: 252  ATCGGAGGACACGGGCCATCTATTACTGTGGGA 283

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RESULT		11				EST	21-APR-1997
LOCUS	AA360289		240 bp	mRNA			
DEFINITION	ESF69410 Lymph node, subtracted Homo sapiens cDNA 5' end similar:					cDNA 5'	end Similar: 50
	similar to immunoglobulin gamma heavy chain, V(III) region					V(III)	region
	(GB:U03894).						
ACCESSION	AA360289						
NID	G2012607						
KEYWORDS	Est.						
SOURCE	human.						

Grigoriak, A., Gnanapavan, L., Hamada, M., Hattori, E., Hattori, P., J. J. Kelley, J. M., Kelley, J. C., Liu, L., Li, I., Marmaros, S. M., Marrison, J. M., Moreno-Palancas, P. F., McDonald, L. A., Nguyen, D. T., Pelliagino, S. M., Phillips, C. A., Pyder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Springs, T. A., Unterback, T. P., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, A., Collins, E. J., Dinked, D., Feng, D.-N., Fortie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, D. M., Gruber, J., Hudson, P., Kim, A. K., Korak, D. L., Kunsch, C., Hangjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, C. I., Pucsek, S. M., Dillion, P. J., Fauman, M. P., Rosen, C. A., Haseltine, W. A., Fields, C.

Thu Feb 26 07:05:27 1998

Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 94026280
COMMENT Other-ESTs: THCL69164
Contact: Kerlavage, AR

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse

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FEATURES             Seq Primer: MIS Reverse
                     Location/Qualifiers
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     /dev_stage="adult"
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11.238						

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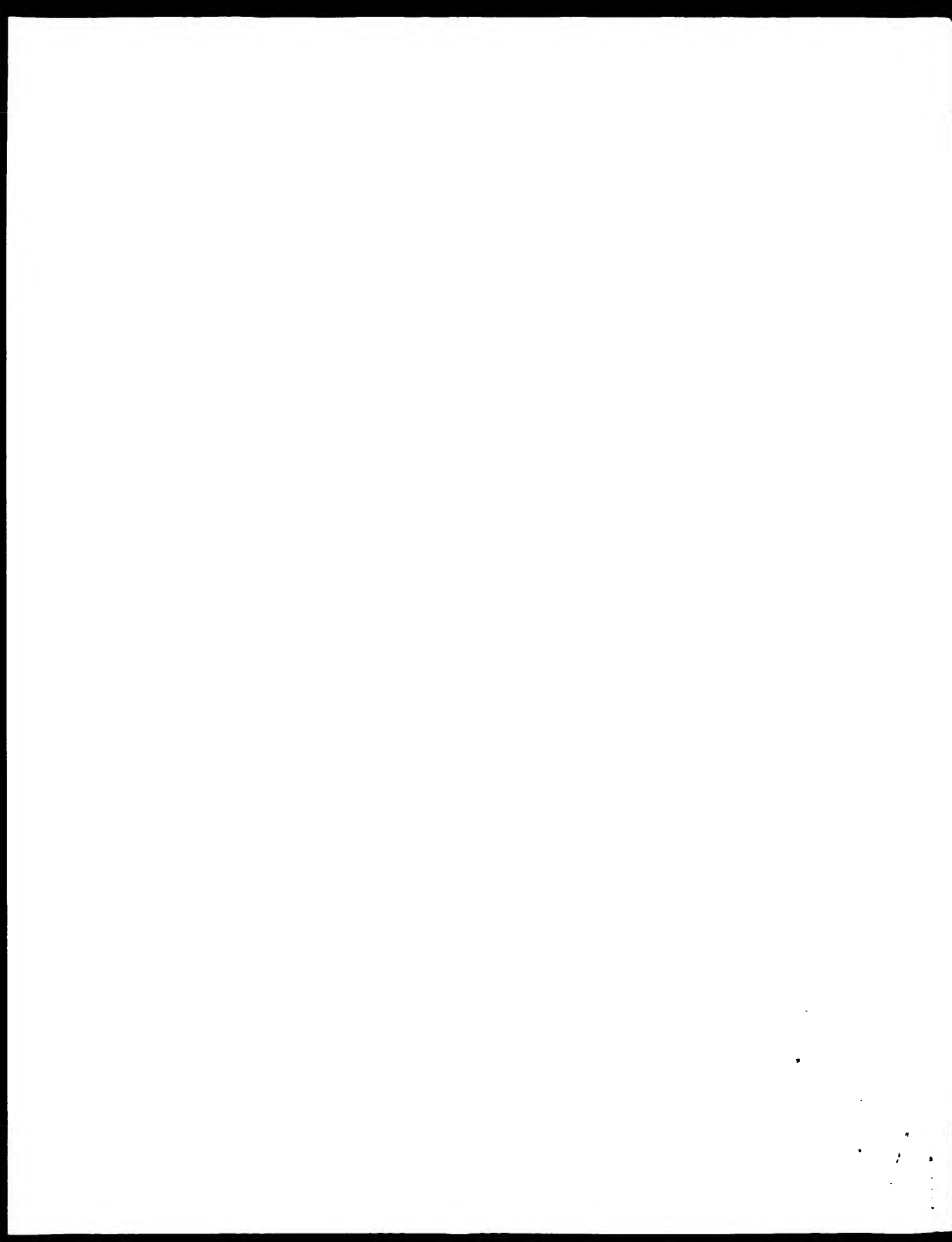
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5 ACCAGTCTGGGGCTGAGGTGAAGAAGATCTGGGTCTTCACGTAAAGGCTCTCTCGAAGGCCT 64

97 ctggtgtctcagtcacgaataattactactggagctggatccgacagtccccaggaaaggac 156
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65 CTGGAGGCACCTTCAGGCGCCATTTTATCAGCTGGGTGCCACAGGCGGCTGGACAGGGG 124

db 157 tngagtggattgg 169
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oy 125 TTGAGTCGATGGG 137

Search completed: Tue Feb 24 11:00:26 1998
Job time : 529 secs.

Job time : 529 secs.



and is derived by analysis of the total score distribution.

SUMMARIES

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1	224	60.7	528	99	HUMIGHDYN	Human Ig rearranged H	3,096-186
2	217	58.8	372	102	H00550	Human clone Amu39-3	2,540-179
3	217	58.8	534	99	HUMIGHKN	Human Ig rearranged H	2,540-179
4	216	58.5	421	99	HUMIGHVN	Human (fetal) Ig rear	2,476-178
5	215	58.3	448	99	HUMIGHBT	Human Ig rearranged H	2,396-177
6	215	58.3	483	97	HS203M5	H.sapiens mRNA for Im	2,396-177
7	215	58.3	510	97	HS203E9	H.sapiens mRNA for Im	2,396-177
8	215	58.3	510	97	HS203E6	H.sapiens mRNA for Im	2,396-177
9	215	58.3	510	97	HS203E7	H.sapiens mRNA for Im	2,396-177
10	215	58.3	510	97	HS203E2	H.sapiens mRNA for Im	2,396-177
11	215	58.3	525	87	HS203G4	H.sapiens mRNA for Im	2,396-177
12	215	58.3	525	87	HS203G1	H.sapiens mRNA for Im	2,396-177
13	214	58.0	365	102	H00562	Human immunoglobulin	2,326-176
14	214	58.0	366	96	HSVHP63	H.sapiens mRNA p53 fo	2,326-176
15	214	58.0	392	91	HSFVH13	H.sapiens gene for Im	2,326-176
16	214	58.0	392	91	HSFVH12	H.sapiens gene for Im	2,326-176
17	214	58.0	392	91	HSFVH14	H.sapiens germline Im	2,326-176
18	214	58.0	392	91	HSFVH11	H.sapiens gene for Im	2,326-176
19	214	58.0	392	91	HSFVH1	H.sapiens gene for Im	2,326-176
20	214	58.0	392	91	HSFVH1M	H.sapiens gene for Im	2,326-176
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22	214	58.0	392	91	HSFVH1M	H.sapiens gene for Im	2,326-176
23	214	58.0	392	91	HSFVH1B	H.sapiens gene for Im	2,326-176
24	214	58.0	392	91	HSFVH1B	H.sapiens gene for Im	2,326-176
25	214	58.0	392	91	HSFVH11	H.sapiens gene for Im	2,326-176
26	214	58.0	426	96	HSVH1B8	H.sapiens germline Im	2,326-176
27	214	58.0	426	96	HSVH1B2	H.sapiens mRNA for Im	2,326-176
28	214	58.0	474	86	HSVH1B2	H.sapiens mRNA for Im	2,326-176
29	214	58.0	474	87	HSVH1B2	H.sapiens mRNA for Im	2,326-176
30	214	58.0	501	87	HS201E7	H.sapiens mRNA for Im	2,326-176
31	214	58.0	501	87	HS201E6	H.sapiens mRNA for Im	2,326-176
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33	214	58.0	501	99	HUMIGHDQN	Human Ig rearranged H	2,326-176
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36	214	58.0	516	99	HUMIGH1N	Human Ig rearranged H	2,326-176
37	214	58.0	516	99	HUMIGHDWN	Human Ig rearranged H	2,326-176
38	214	58.0	516	87	HS201G3	H.sapiens mRNA for Im	2,326-176
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40	214	58.0	516	87	HS201G6	H.sapiens mRNA for Im	2,326-176
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43	214	58.0	972	99	HUMIGH1EAVA	Human sapiens (100%)	2,326-176
44	213	57.7	294	91	HS32D1C	H.sapiens germline Im	2,054-175
45	213	57.7	523	87	HS32D1C	H.sapiens mRNA for Im	2,054-175

ATTACHMENT C

RESULTS	1
LOCUS	HMICHCYN 528 bp DNA 06-MAY-1996
DEFINITION	Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L42.
ACCESSION	subgroup VH-1.
NID	M65104
KEYWORDS	g195344
SOURCE	V-region, immunoglobulin heavy chain subgroup VH-1; rearranged DNA
ORGANISM	Homo sapiens Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; vertebrata, Eutheria, Plimates, Catarrhini, Homidae, Homo.
REFERENCE	1 (bases 1 to 528)
AUTHORS	Kipps, T.J. and Boffy, S.F.
TITLE	Relationship of the CDS B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes
JOURNAL	J. Clin. Invest. 87 (5): 2087-2094 (1991)
MEDLINE	91250563

RESULT- 2

QY	301	GAATCCGGCACACGATG---GGATATTACTTTGACTACTGGGCGCAGGAAACCCCTGGGTC	357
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QY	358	ACCGTCTCCTCA 369 	
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DEFINITION	H.sapiens mRNA for immunoglobulin variable region (clone 203-E		03-AUG-1995
ACCESSION	247266		
NID	9619477		
KEYWORDS	immunoglobulin; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotae; mitochondrial eukaryotes. Metazoa, Chordata.		
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	1 (bases 1 to 510)		
JOURNAL	Lebecque,S.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,		
TITLE	Scherer-Plough, Laboratory for Immunological Research, 27, Ch		
JOURNAL	des Peupliers, B.P.11 CEDEX, Bardilly, Phone, 69572, FRANCE		
REFERENCE	2 (bases 1 to 510)		
AUTHORS	Galibert,L., van Dooren,J., Durand,I., Rousset,F., Jefferis,R.		
TITLE	Banchereau,J. and Lebecque,S.		
JOURNAL	Anti-CD40 plus interleukin-4-activated human naive B cell lines		
MEDLINE	express unmutated immunoglobulin genes with intracellular heavy		
FEATURES	isotype variability		
source	Eur. J. Immunol. 25 (3), 733-737 (1995)		
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QY	121	GGCCTGAGTGGATGGGAATATATCCCTGTCTTAATACACCAACTACGCGCAGAAG	180
Db	247	ttccagggcagaagtcacgattaccgcgggcaaatccacgacagcagcctacatggagctg	306
QY	181	TTTCAGGCGAGACTTCGATAATCGCGGACGATTTCAGGACACAGGCTATGAACTG	240
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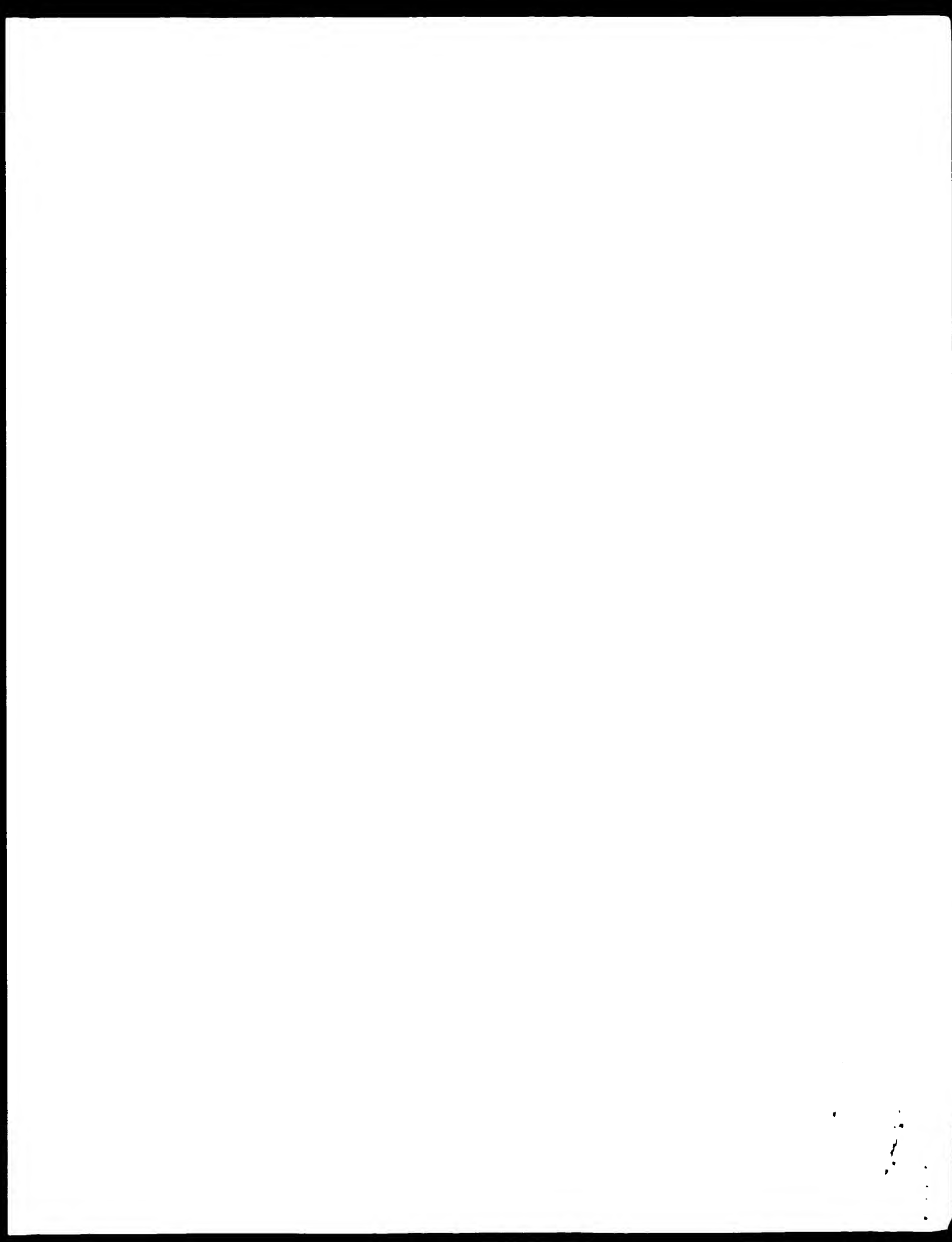
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Search completed: Tue Feb 24 09:57:27 1998
Job time : 492 secs.



W O R L D
***** (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsearch_n n.a. - n.a. database search, using Smith-Waterman algorithm
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10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					
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5	210	56.9	Sequence 61, Applicati	Sequence 61, Applicati	2 960-152
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7	194	52.6	Sequence 1, Applicatio	Sequence 1, Applicatio	8 570-139
8	194	52.6	Sequence 1, Applicatio	Sequence 1, Applicatio	8 570-139
9	192	52.0	Sequence 3, Applicatio	Sequence 3, Applicatio	4 100-137
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14	137	37.1	Sequence 169, Applicat	Sequence 169, Applicat	3 030-91
15	137	37.1	Sequence 169, Applicat	Sequence 169, Applicat	3 030-91
16	137	37.1	Sequence 156, Applicat	Sequence 156, Applicat	3 030-91
17	137	37.1	Sequence 156, Applicat	Sequence 156, Applicat	3 030-91
18	137	37.1	Sequence 170, Applicat	Sequence 170, Applicat	3 030-91
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20 132 35.8 451 11 PCT-US93-1 Sequence 11, Applicati 1 080-70
21 125 33.9 443 6 US-08-477 Sequence 9, Applicatio 2 380-81
22 125 33.9 443 7 US-08-477 Sequence 9, Applicatio 2 380-81
23 125 33.9 443 5 US-07-634 Sequence 9, Applicatio 2 380-81
24 125 33.9 443 7 US-08-474 Sequence 9, Applicatio 2 380-81
25 124 33.6 433 6 US-07-634 Sequence 18, Applicati 1 590-80
26 124 33.6 433 7 US-08-487 Sequence 18, Applicati 1 580-80
27 124 33.6 433 6 US-08-477 Sequence 18, Applicati 1 580-80
28 124 33.6 433 7 US-08-474 Sequence 18, Applicati 1 580-80
29 121 32.8 348 13 PCT-US95-0 Sequence 7, Applicatio 4 610-78
30 118 32.0 366 6 US-08-236 Sequence 8, Applicatio 1 330-75
31 118 32.0 366 13 PCT-US95-0 Sequence 8, Applicatio 1 330-75
32 117 31.7 351 6 US-08-236 Sequence 10, Applicati 8 770-75
33 117 31.7 351 13 PCT-US95-0 Sequence 10, Applicati 8 770-75
34 117 31.7 363 7 US-08-040 Sequence 1, Applicatio 8 770-75
35 117 31.7 363 7 US-08-236 Sequence 5, Applicatio 8 770-75
36 117 31.7 429 6 US-08-236 Sequence 5, Applicatio 8 770-75
37 117 31.7 429 13 PCT-US95-0 Sequence 5, Applicatio 8 770-75
38 116 31.4 357 7 US-08-467 Sequence 1, Applicatio 5 780-74
39 115 31.2 363 7 US-08-040 Sequence 3, Applicatio 3 810-73
40 115 31.2 366 7 US-08-040 Sequence 5, Applicatio 3 810-73
41 113 30.6 366 7 US-08-040 Sequence 2, Applicatio 1 640-71
42 113 30.6 366 7 US-08-040 Sequence 6, Applicatio 1 640-71
43 113 30.6 732 6 US-08-230 Sequence 1, Applicatio 1 640-71
44 112 30.4 660 7 US-08-392 Sequence 1, Applicatio 1 080-70
45 111 30.1 366 7 US-08-040 Sequence 7, Applicatio 7 060-70

ALIGNMENTS

RESULT 1
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DT 01-JAN-1900
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CC Sequence 8, Application PC/TUS9610043
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CC TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
CC TITLE OF INVENTION: AND METHODS
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02210-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US96/10043
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/009,213
CC FILING DATE: 14-JUN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lech, Karen F.
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 00785/244001
CC TELEPHONE: 617/542-8970
CC TELEFAX: 617/542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2287 base pairs
CC TYPE: nucleic acid

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
SQ Sequence 2287 BP, 483 A, 752 C, 554 G, 398 T, 0 other.

Query Match 58.8%; Score 217; DB 14; Length 2287;
Best Local Similarity 81.2%; Pred. No. 3,72e-158;
Matches 302; Conservative 0; Mismatches 67; Indels 3; Gaps 3;

Db 82 CTGGTCAGTCTGGGCTGAGTGAAGAGCTGGGTCCTGGTGAAGTCTCTGCAAG 141
QY 1 CTCGACGAGTCTGGGCTGAGTGAAGAGCTGGGTCCTGGTGAAGTCTCTGCAAG 60

Db 142 GTTCTTGAGGACCTTCAGGAGCTATCTATCAGTGGTGGGACAGGAGGAGGAG 201
QY 1 GTTCTTGAGGACCTTCAGGAGCTATCTATCAGTGGTGGGACAGGAGGAGGAG 120

Db 202 GGGCTTGAGTGGATGGGAGGAGTATCTCTATCTTTCTATAGGAGAACTAGGACAG 261
QY 1 GGGCTTGAGTGGATGGGAGGAGTATCTCTATCTTTCTATAGGAGAACTAGGACAG 180

Db 262 TTCCAGGGGAGAGTACGAGTATCCCGGACCAATCCAGGACAGGCTATGATGGAGCTG 321
QY 1 TTCCAGGGGAGAGTACGAGTATCCCGGACCAATCCAGGACAGGCTATGATGGAGCTG 240

Db 322 AGCAGCTGAGATCTGAGGACAGGAGGAGTATCTATCTGCGAGAGATATGGAGCGTAT 381
QY 1 AGCAGCTGAGATCTGAGGACAGGAGGAGTATCTATCTGCGAGAGATATGGAGCGTAT 299

Db 382 TGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 441
QY 1 TGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 357

Db 442 ACCGCTCTTCA 453
QY 1 ACCGCTCTTCA 369

RESULT 2
ID US-07-834-539A-53 STANDARD; DNA; UNC; 812 BP.
AC XXXXXX
DT 01-JAN-1900
DE Sequence 53, Application US/07834539A.
CC Sequence 53, Application US/07834539A
CC Patent No. 5633425
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 77
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/834,539A
CC FILING DATE: 19920205
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9500

CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 53:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 812 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 241..335
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 372..677
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
SQ Sequence 812 BP, 204 A, 188 C, 223 G, 197 T, 0 other;

Query Match 56.9%; Score 210; DB 7; Length 812;
Best Local Similarity 86.7%; Pred. No. 2.9e-152;
Matches 248; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Db 393 CTGGTGCAGTCTGGGCTGAGTGAAGAGCTGGGTCCTGGTGAAGTCTCTGCAAG 452
QY 1 CTCGAGCAGTCTGGGCTGAGTGAAGAGCTGGGTCCTGGTGAAGTCTCTGCAAG 60

Db 453 GTTCTTGAGGACCTTCAGGAGCTATCTATCAGTGGTGGGACAGGAGGAGGAG 512
QY 1 GTTCTTGAGGACCTTCAGGAGCTATCTATCAGTGGTGGGACAGGAGGAGGAG 120

Db 513 GGGCTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 572
QY 1 GGGCTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180

Db 573 TTCCAGGGGAGAGTACGAGTATCCCGGACCAATCCAGGACAGGCTATGATGGAGCTG 632
QY 1 TTCCAGGGGAGAGTACGAGTATCCCGGACCAATCCAGGACAGGCTATGATGGAGCTG 240

Db 633 AGCAGCTGAGATCTGAGGACAGGAGGAGTATCTATCTGCGAGAGATATGGAGCGTAT 678
QY 1 AGCAGCTGAGATCTGAGGACAGGAGGAGTATCTATCTGCGAGAGATATGGAGCGTAT 286

RESULT 3
ID FCT-US92-06185-53 STANDARD; DNA; UNC; 812 BP.
AC XXXXXX
DT 01-JAN-1900
DE Sequence 53, Application PC/TUS9206185.
CC Sequence 53, Application PC/TUS9206185
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 75
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PC/TUS92/06185
CC FILING DATE: 19910828
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.

```

CC REGISTRATION NUMBER: 87654
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 53:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 812 base pairs
 CC TYPE: NUCLEIC ACID
 CC STRANDEDNESS: double
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: Exon
 CC LOCATION: 241..335
 CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
 CC NAME/KEY: Exon
 CC LOCATION: 372..677
 CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
 CC sequence 812 BP: 204 A: 188 C: 223 G: 197 T: 0 other:

Query Match: 56.9%, Score 220, DB 10, Length 812
 Best Local Similarity: 86.7%, Pred. No. 2,96e-152,
 Matches 248: Conservative 0; Mismatches 38; Indels 0; Gaps 0;

DB 344 CTGCTGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 452
 QY 1 CTGAGAGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 60
 DB 453 GCTTCTGAGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 512
 QY 61 GTTCTGAGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 120
 DB 513 GGGCTTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 572
 QY 121 GGGCTTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 180
 DB 574 TCCAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 542
 QY 181 TTTAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 240
 DB 613 AGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 678
 QY 241 AGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 286

RESULT 4
 ID PCT-US92-10983-61 STANDARD: DNA; UNC: 813 BP.

AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 61, Application PC/TUS9210983.
 CC Sequence 61, Application PC/TUS9210983.
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic Non-Human Animals for
 CC PRODUCTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 152
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/10983

CC FILING DATE: 19921217
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-2
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 61:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 813 base pairs
 CC TYPE: NUCLEIC ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 241..285
 CC NAME/KEY: CDS
 CC LOCATION: 373..678
 CC sequence 813 BP: 204 A: 199 C: 223 G: 197 T: 0 other:

Query Match: 56.9%, Score 210, DB 10, Length 813
 Best Local Similarity: 86.7%, Pred. No. 2,96e-152,
 Matches 248: Conservative 0; Mismatches 38; Indels 0; Gaps 0;

DB 344 CTGCTGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 453
 QY 1 CTGAGAGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 60
 DB 454 GCTTCTGAGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 513
 QY 61 GTTCTGAGAGTGTGGGGTTCAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 120
 DB 514 GGGCTTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 573
 QY 121 GGGCTTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 180
 DB 574 TCCAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 542
 QY 181 TTTAGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 240
 DB 613 AGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 678
 QY 241 AGAGTGAAGTGAAGAGTGAAGAGTGAAGAGTGGGTTCTGCTGAGAGTCTCTCTGAGAG 286

RESULT 5
 ID US-08-053-131-61 STANDARD: DNA; UNC: 813 BP.

AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 61, Application US/08053131.
 CC Sequence 61, Application US/08053131.
 CC Patent No. 5661016
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic Non-Human Animals for
 CC PRODUCTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 197
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: One Market Plaza, Stewart Tower, Suite 200
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/053,131
 CC FILING DATE: 26-APR-1993
 CC CLASSIFICATION: 800
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/990,860
 CC FILING DATE: 16-DEC-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/810,279
 CC FILING DATE: 17-DEC-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/853,408
 CC FILING DATE: 18-MAR-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 61:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 813 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 241..285
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 373..678
 CC Sequence 813 BP: 204 A; 189 C; 223 G; 197 T; 0 other;

Query Match 56.9%; Score 210; DB 7; Length 813;
 Best Local Similarity 86.7%; Pred. No. 2.96e-152;
 Matches 248; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Db 394 CTGGTGCAGTCTGGGCTGAGTGAAGAGCGCTGGGCTGCTGGTGAAGTCTCTCTCAAG 453
 QY 1 CTCGAGCAGTCTGGGCTGAGGTGAAGAGCGCTGGGCTGCTGGTGAAGTCTCTCTCAAG 60
 Db 454 GCTTCTGGAGGACCTTCAGCAGGTATGCTATCATCTGCTGGTGGGAGCGCCCTGGACAA 513
 QY 61 GTTTTTCGAGACACCTTCAGCAGGTATGCTATCATCTGCTGGTGGGAGCGCCCTGGACAA 120
 Db 514 GGGCTTGGTGGTGGGAGGAGTATCTCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 573
 QY 121 GGGCTTGGTGGTGGGAGGAGTATCTCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
 Db 574 TTCCAGGCGAGTCTGAGGATACCGGCGACAAATCCAGCAGCAGCAGCAGCAGCAGCAGCAG 633
 QY 181 TTTCAGGCGAGTCTGAGGATACCGGCGAGGATTCAGCAGCAGCAGCAGCAGCAGCAGCAG 740
 Db 634 AGCAGCCTGAGTCTGAGGAGCAGCGCGGTGTATTAATTAATTAATTAATTAATTAATTAAT 679
 QY 241 ACTAGCCTCAGATCTGAGGAGCAGCGCGGTGTATTAATTAATTAATTAATTAATTAATTAAT 286

RESULT 6
 ID PCT-US94-01258-1 STANDARD: DNA; UNC: 687 BP
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application PC/TUS9401258.
 CC Sequence 1, Application PC/TUS9401258
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
 CC TITLE OF INVENTION: USING UNIVERSAL OF RANDOMIZED IMMUNOGLOBULIN LIGHT
 CC CHAINS
 CC NUMBER OF SEQUENCES: 61

CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/01258
 CC FILING DATE: 02-FEB-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/012,566
 CC FILING DATE: 02-FEB-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/174,674
 CC FILING DATE: 28-DEC-1993
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 687 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC Sequence 687 BP: 155 A; 211 C; 195 G; 126 T; 0 other;

Query Match 52.6%; Score 194; DB 12; Length 687;
 Best Local Similarity 83.4%; Pred. No. 8.57e-139;
 Matches 240; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 1 CTCGAGCAGTCTGGGCTGAGGTGAAGAGCGCTGGGCTGCTGGTGAAGTCTCTCTCAAG 50
 QY 1 CTCGAGCAGTCTGGGCTGAGGTGAAGAGCGCTGGGCTGCTGGTGAAGTCTCTCTCAAG 60
 Db 61 GCTTCTGGAGGACCTTCAGCAGGTATGCTATCATCTGCTGGTGGGAGCGCCCTGGACAA 120
 QY 61 GTTTTTCGAGACACCTTCAGCAGGTATGCTATCATCTGCTGGTGGGAGCGCCCTGGACAA 120
 Db 121 GGGCTTGGTGGTGGGAGGAGTATCTCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
 QY 121 GGGCTTGGTGGTGGGAGGAGTATCTCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
 Db 181 TTTCAGGCGAGTCTGAGGATACCGGCGAGGATTCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
 QY 181 TTTCAGGCGAGTCTGAGGATACCGGCGAGGATTCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
 Db 241 AGCAGCCTGAGTCTGAGGAGCAGCGCGGTGTATTAATTAATTAATTAATTAATTAATTAAT 286
 QY 241 AGTACCTCAGATCTGAGGAGCAGCGCGGTGTATTAATTAATTAATTAATTAATTAATTAAT 286

RESULT 7
 ID US-08-300-386A-1 STANDARD: DNA; UNC: 687 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application US/08300386A.
 CC Sequence 1, Application US/08300386A
 CC Patent No. 5667988
 CC GENERAL INFORMATION:
 CC APPLICANT: Barbas, Carlos F, III
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
 CC TITLE OF INVENTION: USING UNIVERSAL OF RANDOMIZED IMMUNOGLOBULIN LIGHT
 CC CHAINS
 CC NUMBER OF SEQUENCES: 70
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute
 CC STREET: 10666 No. 5667988th Torrey Pines Road, TPC8
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:

QY 241 ACTAGCTCAGATCTGAGGACACGGCCCTCTATTCTCTGGGAGAG 286

RESULT 9

ID US-08-217-918-3 STANDARD; DNA: UNC; 441 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 3, Application US/08217918.
CC Sequence 3, Application US/08217918
CC Patent No. 5506132
CC GENERAL INFORMATION:
CC APPLICANT: LAKE, PHILIP
CC APPLICANT: GTEBPS, LAPS
CC TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
CC TITLE OF INVENTION: VAPICELLA-20STEP VIRUS
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/217,918
CC FILING DATE: 24-MAR-1994
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO. 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 441 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHEetical: NO
CC ANTI-SENSE: NO
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..441
CC Sequence 441 BP; 89 A; 125 C; 135 G; 92 T; 0 other;

Query Match 52.0%, Score 192; DB 6, Length 441;
Best Local Similarity 82.9%; Pred. No. 4,10e-137;
Matches 242; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 72 GCAGTCTGGGGCTGAGGTCGAAGAAGCCCTGGCTCTGGTGAAGGCTCTCTCTCAAGGGCTTC 131
QY 6 GCAGCTGGGGCTGAGGTGAAGAAGCCCTGGCTCTGGTGAAGGCTCTCTCTCAAGGGCTTC 65
Db 132 TGGAGGCACTCTCAGCAACTTTGGCTATCAGCTGGGTGGGACAGGCCCCCTGGACAGGGCT 191
QY 66 TGGAGACACCTCTCAGCAGATACACTATTTCAGTGGTGGGACAGGCCCCCTGGACAGGGCC 125
Db 192 TGAGTGGTGGGGGCAATCATCA 251
QY 126 TGAGTGGTGGGAAATATCATCA 185
Db 252 GGGCAGAGTCACTGATTGAGGAGAGCCCTCTCTACGAGCAGAGCTTACATGAGAGCTGAGAG 311
QY 186 GGGCAGAGCTCTGATACACCGCCGACCATTCACGAGCAGAGCTTACATGAGAGCTGAGTAG 245
Db 312 CCTGAGATCTGAGCAGACAGGCCCATGTAATTACTGTGGGAGAGACATAAGAGTA 363

QY 246 CCTCAGATCTGAGGACACGGCCCTCTATTCTCTGGGAGAGTGTAAATATCA 297

RESULT 10

ID US-08-264-093-1 STANDARD; DNA: UNC; 363 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08264093.
CC Sequence 1, Application US/08264093
CC Patent No. 5639863
CC GENERAL INFORMATION:
CC APPLICANT: Michael D. Dan
CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CC TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
CC TITLE OF INVENTION: ANTIGEN
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ridout & Maybee
CC STREET: 2300 Richmond-Adelaide Centre
CC STREET: 101 Richmond Street West
CC CITY: Toronto
CC STATE: Ontario
CC COUNTRY: Canada
CC ZIP: M5H 2J7
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: MS-DOS 6.00
CC SOFTWARE: ASCII Editor
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/264,093
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA: No 5639863 applicable
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lake, James P
CC REGISTRATION NUMBER: 31081
CC REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (416) 868-1482
CC TELEFAX: (416) 362-0823
CC INFORMATION FOR SEQ ID NO. 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 363 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: linear
CC Sequence 363 BP; 84 A; 97 C; 108 G; 74 T; 0 other;

Query Match 47.4%, Score 175; DB 7, Length 363;
Best Local Similarity 80.3%; Pred. No. 7,28e-123;
Matches 232; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 10 CTGGTGCTAGTCTGAGCTGAGCTGAAGAAGCCCTGGCTCTGGTGAAGGCTCTCTCTCAAG 69
QY 1 CTGAGAGCACTCTGAGGCTTGAGGCTGAAGAAGCCCTGGCTCTGGTGAAGGCTCTCTCTCAAG 60
Db 70 GCTTCTGCTTACACTTTCACCACTATGCTCTCAGTGGGTGGGACAGGCTCTCTGACAA 129
QY 61 GTTTTGGGAGACACCTTCAGGATACACTATTTCAGTGGGTGGGACAGGCTCTCTGACAA 120
Db 130 GGGCTTGAGTGGATGGGATGATCAGCGGCTCACAATGCTAACACAACTCTGACAGAG 189
QY 121 GGGCTTGAGTGGGAAATATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 190 TTCCAGGCGAGAGTCTCATGACACAGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
QY 181 TTTCAGGCGAGAGTCTCATGACACAGAGATTCACAGAGAGAGATTCACAGAGAGTCT 240
Db 250 AGGAGGCTCAGATCTGAGCAGACAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 298
QY 241 AGTAGGCTCAGATCTGAGGAGACAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 289

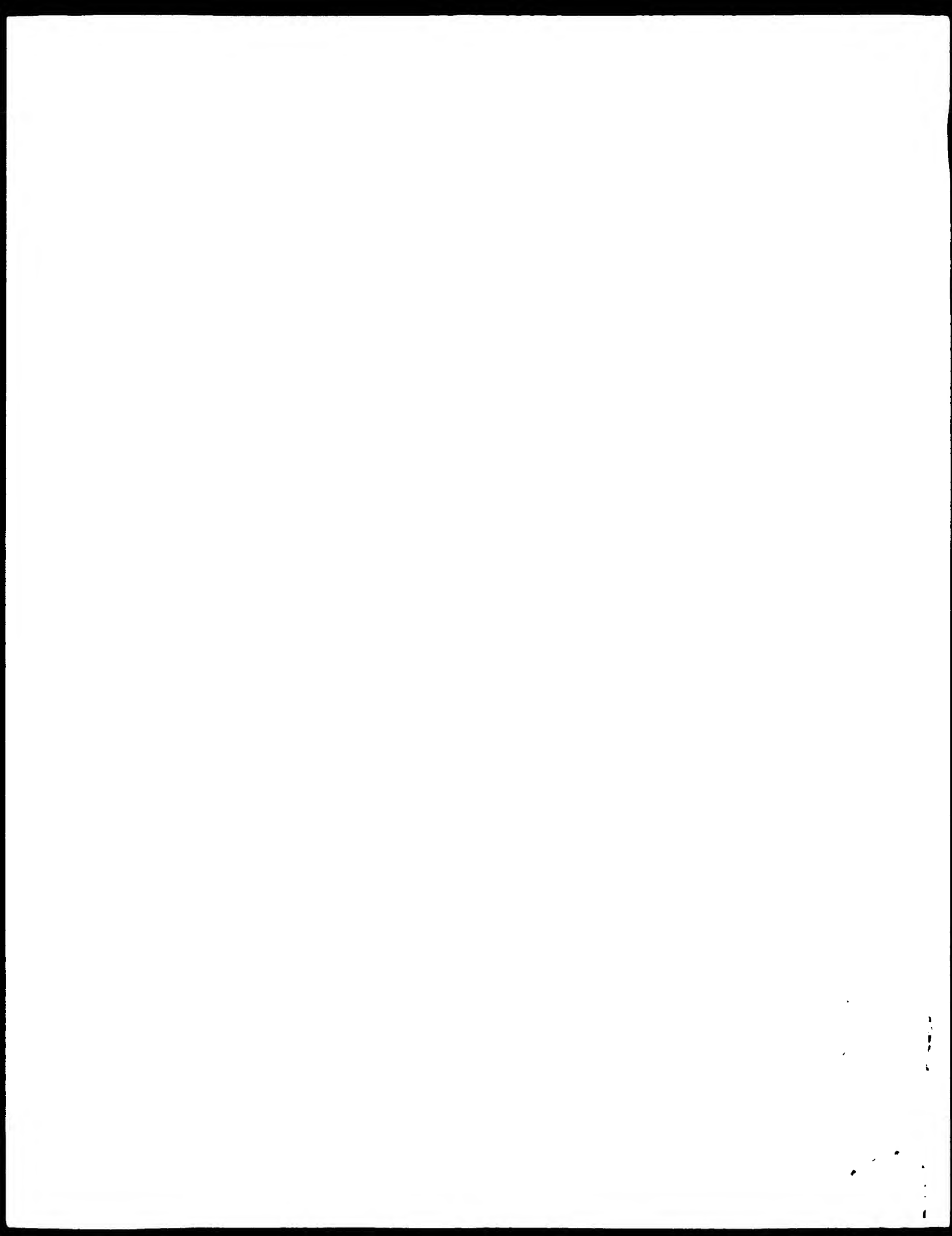
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop 1008
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCP1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 154:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3282 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 15 452
CC Sequence 3282 BP: 710 A, 1109 C, 864 G, 599 T, 0 other,
Query Match 37.1%; Score 137; DB 7; Length 3282;
Best Local Similarity 74.4%; Pred. No. 3.03e-91;
Matches 209; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
Db 87 CAGTCGGGGCTCAGGTGAAGAGCTGGGGCTCAGTGAAGTTCTTGTCAGGTTCT 146
Cc 7 CAGTCGGGGCTCAGGTGAAGAGCTGGGGCTCAGTGAAGTTCTTGTCAGGTTCT 66
Db 147 GGATACAGATTCACTAATCTTATTCATTCGGTGGCCAGGCCCCCGGACAGAGTTT 206
Cc 67 GGAGACACTTTCAGCAGATACACTATTCAGTGTGGCAGAGGCGCTTGGACAGGCGCT 126
Db 207 CAGTCGATGGATGATCAATCTTACACAGCAAAACAAAGAAATTTTACAGCAAGTTCCAG 266
Cc 127 GAGTGATGGAAATATCATCTCTCTATATACCAACTAGCGGCAGAAATTTTCAG 186
Db 267 GACAGACTACCTTTACCGCGGACACATCCGGACACAGGCTCATGAGTTGAGGAGC 326
Cc 187 GGCAGACTCTTGATACCCCGGACGATTCAGCAGCAGACAGGCTACATGAACTGATGAGC 246
Db 327 CTGAGTGTGACACAGGCTGTTTATTATTCGTGCGAGGT 367
Cc 247 CTCGATCTGAGGACAGCGCGCTGCTATTTCTGTGGAGGT 287

RESULT 14
ID PCT-US95-08743-169 STANDARD; DNA: UNC: 3282 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 169, Application PC/TUS9508743.
CC Sequence 169, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 169:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3282 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 3282 BP: 599 A, 864 C, 1109 G, 710 T, 0 other;
Query Match 37.1%; Score 137; DB 13; Length 3282;
Best Local Similarity 74.4%; Pred. No. 3.03e-91;
Matches 209; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
Db 2916 ACTCTCGCACAAATAAACAAGCGGTCTGCGACAGCTGAGGCTCTCTCACTCCATGTA 2975
Cc 297 ACTCTCGCACAAATAAACAAGCGGTCTGCGACAGCTGAGGCTCTCTCACTCCATGTA 298
Db 2976 GCTGTGTCGGGGATGTGTCGGGGTAAAGTGACTCTGCTCTGGGAACITTCGTGAAAAT 3035
Cc 227 GGTGTGTCGGGGATGTGTCGGGGTAAAGTGACTCTGCTCTGGGAACITTCGTGAAAAT 168
Db 3036 TCTTTGTTCCGTTGTAGAGGATTCATCCATCCATCCATCCATCCATCCATCCATCCAT 3095
Cc 167 TTTGTTGTTATATAGACAGGAGTATATTTCCATCCATCCATCCATCCATCCATCCATCC 108
Db 3096 TGGCGCACCCCAATGAATAACAAGTTACTGAATCTGTATCCAGAAGCTGACACAGAAATC 3155
Cc 107 TGTCCGACCACTCAATAGTGTATCTGCTGAAGGTGTCTCCAAAACCTGACAGGAGACC 48
Db 3156 TTCCTGAGGCGCCAGGCTTCTTCCACTCAGCCCGGAGCTG 3196
Cc 47 TTCACGAGGAGCCAGGCTTCTTCCACTCAGCCCGGAGCTG 7
RESULT 15
ID US-08-276-852-169 STANDARD; DNA: UNC: 3282 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 159, Application US/08276852.
CC Sequence 169, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10556 No. 169th Ave. Torrey Pines Road, Suite 220,
CC STREET: Mail Drop IPCB
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 169:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3282 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 3282 BP: 599 A; 864 C; 1109 G; 710 T; 0 other;

Query Match 37.1%; Score 137; DB 7; Length 3282;
Rest Local Similarity 74.4%; Pred. No. 3.03e-91;
Matches 209; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
Db 2916 ACTCTGACACATAATAACAGGCGTGTCTGACAGCTGAGGTCTGTTCACTGATGTATG 2975
||||| ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 287 ACTCTGACACATAATAACAGGCGTGTCTGACAGCTGAGGTCTGTTCACTGATGTATG 228
Db 2976 GCTGTGTCGGGGAATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3035
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Cp 227 GCTGTGTCGGGGAATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 168
Db 3036 TCTTGTTCGGGGAATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3095
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Cp 167 TTTGGTGATTATAGACAGGCGATATATTTTCACTGATGTATGATGAGGCGGCGGCGG 108
Db 3096 TGGGCGACCCCAATGATTAACAAAGTTACTGATGATGATGATGATGATGATGATGATGAT 3155
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Cp 107 TGTCTAAACCACTGAAATAGTGTATCTGTTGAAAGTGTGTTGAAAGTGTGTTGAAAGT 48
Db 3156 TTCACTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3196
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Cp 47 TTCACTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7

Search completed: Tue Feb 24 15:17:42 1998
Job time : 40 secs.



Query Match 58.88; Score 217; DB 28; Length 2287,

RESULT

RESUL 3
ID Q89327 standard; DNA; 294 BP.

Q89327:	AC	26-SEP-1995 (first entry)	Graves' ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity; ss.	97 G:	57 T:
DP10 VH gene.	DE			73 C:	
Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity; ss.	KW			67 A:	
Homo sapiens.	KW			294 BP:	
OS	PN	WO9508336-A.			
PD	PD	30-MAR-1995.			
FF	FF	22-SEP-1994; U10756.			
PP	PP	22-SEP-1993; US-124469.			
PA	PA	(NICH-) NICHOLS INST DIAGNOSTICS.			
PI	PI	McLachlan SM, Rapoport B;			
DR	DR	WPI: 95-139383/18.			
P-PSDB: R72068	DR				
Graves' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR	PPT				
FS Disclosure, Page 67; 94pp; English.	FS				
L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoantibody-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (IgH1) genes showed homology to the closest germ-line genes. D10 (Q89327) hvi263 (Q89328). The DNA (Q89329) and corresp. amino acid (P72070) sequences of the VH region of a representative clone OF7H1.2, are provided.	CC				
Sequence	CC				

```
Query Match      57.7%; Score 213; DB 14; Length 294;
Best Local Similarity 87.4%; Pred No 1.25e-140;
Matches 249; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
```

10	ctgggtcgagctctgggctgaagtgaagaagcctgggtcctcgtggaagatctctctcgaag	59
1	ctcagcagctcgtgagcctcagctctgaggaagagctctgctctctgctggaagctctcag	60
70	gctctctggagcacccttcagcagcctatgctatcagctcgggtggcagcagcgcctcgaaca	129
61	gttttttggacacacaccttcagcagcagctatctcagctgcttggctgctcagcagcctcgaaca	120

QY 246 CCTCAGATCTGAGGACACGGCGCTCTATTTCTGTGGGAGAG-TGTAATACCAATGCAG 304
 Db 406 ttttaccggccgggtggtgctgacccctggcgccagggcaccctggtcaccgt 465
 QY 305 TCCGGCACACGAT-GGGATAT-TACTTTGACTACTGGGCGCCAGGAACCTGTGTACCGT 362
 Db 456 ctctctca 472
 QY 363 CTCCTCA 369

RESULT 10

ID T15202 standard; cDNA; 687 BP.
 AC T15202:
 DT 23-OCT-1996 (first entry)
 DE pC3AP313 anti-tetanus toxoid Ig heavy chain variable domain cDNA.
 KW Mutagenesis: Ig; immunoglobulin; FR; framework region; variable; CDR;
 KW complementarity determining region; light; heavy chain; PCR;
 KW polymerase chain reaction; antibody library; diversity; affinity;
 KW immunospecificity; ss.
 OS Synthetic.
 PN WO9607754-Al.
 PD 14-MAR-1996.
 PF 01-SEP-1995; U11235.
 PR 02-SEP-1994; US-300386.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-171625/17.
 PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
 PT gene CDR - useful for prodn. of Ig heavy and light chain
 PT combinatorial antibody libraries
 PS Example 1: Page 83: 125pp; English.
 CC T15202 and T15203 are the heavy and light chain variable domains of
 CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Pcomb3
 CC based expression vector. The heavy and light chain variable domains
 CC are used in an example to demonstrate the prodn. of antibodies for
 CC an antibody library using mutagenic primers. Mutagenic primers of the
 CC invention have sequences at their 3' and 5' ends both capable of
 CC binding different framework regions linked by a sequence 6 to 50
 CC nucleotides long. Different immunoglobulins produced using the
 CC primers may be used to produce antibody libraries having diverse and
 CC novel immunospecificities and affinities. By using mutagenic ONS an
 CC extremely large population of different randomised binding sites can
 CC be created and use of the universal light chain increases the number
 CC of combinations which yield functional heterodimeric antibodies.
 CC sequence 687 BP; 155 A; 211 C; 195 G; 126 T;

Query Match 52.6%; Score 194; DB 22; Length 687;
 Best Local Similarity 83.9%; Pred No. 5.60e-126;
 Matches 240; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 1 ctccagcagctctgggctgaggtgaagaagcctgggtcctcgtgaggtcctcctgcagg 60
 QY 1 CTCGAGCAGTCTGGGCTGAGTGAGTGAGAAAGCTGGGTCTCGGTGAGGTCTCTGTGAG 60
 Db 61 gctctggagcacccttcaacaattatgccatcagctgggtgcgacagccctcgacaa 120
 QY 61 GTTTTGGAGACACCTTCAGCAGATACACTATTTCAGTGTGTCGACAGGCCCTGGACAA 120
 Db 121 gggcttgagtggagggatctcccttccgtaataacacaaagtacgacaac 180
 QY 121 GGGCTTGAGTGGAGGAATATCATCTCTGTCTAATAACCAACATACGCGCAGAG 180
 Db 181 ttccagggcagagtcaccattaccggcggaatccacggcgacacccctacatggagctg 240
 QY 181 TTTCAGGCGACACTCTCGATAACCGCGAGGATTCACAGGACACGCCCTACATGGAAGTG 240
 Db 241 agcagcctttagatctggagacacggccatattattgttcgagag 286
 QY 241 AGTAGCCTCAGATCTGAGGACACGGCGCTCTATTCTGTGCGAGAG 286

RESULT 11

ID Q92546 standard; DNA; 4691 BP.
 AC Q92546;
 DT 11-MAR-1996 (first entry)
 DE pComb3 expression vector.
 KW Gene III; filamentous phage; minor phage coat protein; cpIII; cp3;
 KW bacterial membrane, periplasm, E. coli, human, Fab, HIV, gp120;
 KW recombinatorial Fab library; cassette; fd/cp3; lacZ promoter/operator;
 KW ribosome binding site; RBS; PelB leader; spacer; tether sequence;
 KW M14; pM14-3; antibody; ss; cyclic.
 OS Synthetic.
 PN WO9511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994; U11907.
 PR 19-OCT-1993; US-139409.
 PR 26-APR-1994; US-233619.
 PR 19-SEP-1994; US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of
 PT HIV-induced disease
 PS Example 1: Page 185-188: 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
 CC the 406 residue minor phage coat protein, cpIII (cp3), which is expressed
 CC prior to extrusion in the phage assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector was designed for the cloning
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, fd/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a
 CC PelB leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a PelB leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the M14 Fab display phagemid expression vector, pM14-3 (see also
 CC Q92540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 CC Sequence 4691 BP; 1170 A; 1171 C; 1232 G; 1118 T;

Query Match 52.6%; Score 194; DB 16; Length 4691;
 Best Local Similarity 83.9%; Pred. No. 5.60e-126;
 Matches 240; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 3424 ctccagcagctctgggctgaggtgaagaagcctgggtcctcgtgaggtcctcctgcagg 3483
 QY 1 CTCGAGCAGTCTGGGCTGAGGTGAGGAAGCCTGGGTCTCGGTGAGGTCTCTGTGAG 60
 Db 3484 gctctggagcacccttcaacaattatgccatcagctgggtgcgacagccctcgacaa 3543
 QY 61 GTTTTGGAGACACCTTCAGCAGATACACTATTTCAGTGTGTCGACAGGCCCTGGACAA 120
 Db 3544 gggcttgagtggagggaggtctcccttccgttaataacagaaagtcacgacaagac 3603
 QY 121 GGGCTTGAGTGGAGGAATATCATCTCTGTCTAATAACCAACATACGCGCAGAG 180
 Db 3604 ttccagggcagagtcaccattaccggcggaatccacggcgacacccctacatgagctg 3663
 QY 181 TTTTCAGGCGAGACTCTCGATACAGCGCGAGATTTTCAGCAGCAGCTTACAGAACTG 240
 Db 3664 agcagcctgagatcttgagacacggccatattattgtgcgagag 3709

QY 241 ACTAGCTCAGATCTGAGAGACAGGCGGCTGCTATCTCTGTCGAGAG 286

RESULT 12
ID Q92547 standard: DNA: 6166 BP.
AC Q92547:
DT 11-MAR-1996 (first entry)
DE Expression vector, pPho-IT.
KW Human: Fab; variable chain: heavy; light: region; VH; VL; HIV: gp120;
KW 3b1, 3b3, 3b4, 3b9, M74. Humanised, monoclonal antibody, MAB,
KW immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;
KW alkaline phosphatase; phoA; ss; cyclic.
OS Synthetic.
PN W09511317-A1.
PD 27-APR-1995.
PF 19-OCT-1994: U11907.
PF 19-OCT-1993: US-139409.
PR 26-APR-1994: US-233619.
PR 19-SEP-1994: US-308841.
PA (SCEI) SCRIPPS PES INST.
PI Barbas CF, Burton DR, Lerner RA:
DR WPI: 95-170235/22.
PT Synthetic human neutralising monoclonal antibodies to human
PT Immunodeficiency virus - used for diagnosis and immuno:therapy of
PT HIV-induced disease
PS Example 2, Page 193-197, 219pp, English.
CC This sequence represents the expression vector, pPho-IT which is a
CC modified version of the phagemid expression vector, pComb3 given in
CC Q92546. pPho-IT provides for the expression of soluble Fabs which are
CC secreted into the periplasmic space which is regulated from the alkaline
CC phosphatase (phoA) promoter. This plasmid was used within the scope of
CC the invention to express various mutagenised human Fab's which comprise
CC heavy and light variable regions which bind to HIV gp120. pPho-IT
CC consists of a DNA molecule having two cassettes to express two soluble
CC proteins a heavy chain and a light chain. The vector comprises,
CC operatively linked 5' to 3', a first cassette consisting of the phoA
CC promoter/operator sequences, an EcoRI restriction site, a ribosome
CC binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer
CC region, a cloning region bordered by 5' sacI and 3' XbaI restriction
CC sites, an NcoI restriction site between the two cassettes, and a second
CC cassette consisting of an expression control RBS, a PelB leader, a human
CC consensus amino terminus spacer region comprising the sequence EVQLLE,
CC a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
CC followed by a SfiI site, expression control stop sequences and a NotI
CC restriction site. The pPho-IT expression vector contains a light
CC chain stuffer that is 1200 bp in length and a heavy chain stuffer that
CC is 300 bp in length. The nucleotide sequences of the heavy and light
CC chain stuffer encode the heavy and light chain variable domains of a
CC tetanus toxin-specific Fab.
SQ Sequence 6166 BP: 1416 A: 1706 C: 1629 G: 1415 T:

Query Match 52.6% Score 194: DB 16: Length 6166:
Best Local Similarity 83.9% Pred. No. 5,60e-12:
Matches 240: Conservative 0: Mismatches 46: Indels 0: Gaps 0:
Db 5354 ctctgaacagctcgggctgagatgaaagcctggctcctcgatggaagctcctgcagg 5413
QY 1 CTCGACGATCTGCGGCTCAGTGAAGAAAGCTTGGCTCTTGGTGAAGAGTCTGTCAG 60
Db 5414 qctctggagagagacattcaacattatattccatcagctctgggtgggacagggccctgggaca 5473
QY 61 GTTTTGGAGAGACCTTCAGAGATACATATTCAGTGGTTCGATCAAGAGAGGAGGAGAA 120
Db 5474 ggccttgatgagatggaagagatctctctcctgataatagacaaagatgagcaaacac 5533
QY 121 GGCCCTGATGATGAGGAAATATCATCCCTGCTATATACAAATACAGCCGACAG 180
Db 5534 ttccagggcagagatcacattacccggagacaaatccacgggacacagcctacatgagctg 5593
QY 181 TTTCAGGCGAGACTCTCGATATACCGCGACGATTCACAGAGACAGCTACATGGAACIG 240
Db 5594 agcaacctgagatctgagagacacggccatattatttgaggagag 5639

QY 241 ACTAGCTCAGATCTGAGAGACAGGCGGCTGCTATCTCTGTCGAGAG 286

RESULT 13
ID Q82750 standard: cDNA: 441 BP.
AC Q82750:
DT 02-OCT-1995 (first entry)
DE 93KA9 anti-Varicella zoster virus antibody heavy chain variable.
DE region cDNA.
KW Varicella zoster virus, VZV, anti-VZV monoclonal antibody: 93KA9;
KW glycoprotein II subunit; vaccine; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..441
FT /*tag= a
PN W09504080-A.
PD 09-FEB-1995.
PF 22-JUL-1994: U08241.
PR 28-JUL-1993: US-098479.
PR 24-MAR-1994: US-217918.
PA (SANG) SANDOZ PHARM CORP.
PI Lake P, Ostberg L:
DR WPI: 95-090612/12.
PT Human monoclonal antibodies specific for the glycoprotein II
PT subunit of varicella zoster virus - used in a therapy and
PT prophylaxis of infection
PS Claim 14: Fig 48: 9pp: English
CC A human anti-Varicella zoster virus monoclonal antibody was prepd.
CC using the trioma method of Ostberg et al. (1983) Hybridoma 2:561-567.
CC One resultant trioma neutralised VZV in the absence of complement.
CC This cell line, designated cell line Trq3KA9, produced an antibody
CC designated 93KA9. cDNA for the light and heavy chain variable region
CC genes of the 93KA9 antibody were cloned using PCR. At least two
CC heavy chain (gamma-1) and two light chain (kappa) specific clones
CC were sequenced (see Q82749 & Q82750 respectively).
SQ Sequence 441 BP: 89 A: 125 C: 135 G: 92 T:

Query Match 52.0% Score 192: DB 14: Length 441:
Best Local Similarity 82.9% Pred. No. 1.94e-124:
Matches 242: Conservative 0: Mismatches 50: Indels 0: Gaps 0:
Db 72 gcagctggggctgaggtgaaagagcctgggtcctcgtgtaaggtctcctggaagcttc 141
QY 6 GCACTCTGGGCTCAGATGAGAGAAAGCTTGGCTCTTGGTGAAGAGTCTGACAGTCTT 65
Db 132 tggagggaccttcagcaacttggctatcagctgggtgcagcagggccctggacaaggct 191
QY 66 TGGAGACACCTTCAGCAGATACATATTCAGTGGTTCGACAGGCGCTGACAAAGGCC 125
Db 192 tgaatggatggggcgcatcatcctctcttggtagctccacctacacacaaagttcca 251
QY 126 TAGATGATGAGGAAATATCATCCCTGCTATATACAGCAAACTACGCTACGAASITCA 195
Db 252 gggcagagctcagattagcgggagcctctacagacagcctacatgaggtgagcaq 311
QY 186 GGGCAGATCTCGATAAAGCGCGAGATTCACAGAGACAGCTACATGGAACIGAGTAS 245
Db 312 cctgagagctcagcagcagcagcagctgattattctgagcagagagacataaacagca 353
QY 245 CCTCAGATCAGGAGACAGGCGGCTCTATTCTCTGCGAGAGTGTGTAATACCA 297

RESULT 14
ID Q29767 standard: cDNA: 325 BP.
AC Q29767:
DT 18-MAR-1993 (first entry)
DE Gene for H₁ region of human rheumatoid factor antibody.
KW Heavy chain; variable region: YES8C; arthritis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 20..325


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FH Key Location/Qualifiers
FH source
FH 1..266
FH /organism="Homo sapiens"
FH /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
FH modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
FH strand cDNA was primed with a Not I - oligo(dT) primer [5'
FH TGTTACCAATCTGAAGTGGGAGCGCGGCTTTTITTTTITTTT 3'],
FH double-stranded cDNA was size selected, ligated to Eco RI
FH adapters (Pharmacia), digested with Not I and cloned into
FH the Not I and Eco RI sites of a modified pT7T3 vector
FH (Pharmacia). Library constructed by Bento Soares and
FH M. Fatima Bonaldo."
FH /clone="741181"
FH /clone_lib="Soares ovary tumor NBH0T"
FH /sex="Female"
FH /tissue_type="ovarian tumor"
FH /lab_host="DH10B (ampicillin resistant)"
FH mpna <1..266
FH Sequence 266 BP; 54 A; 90 C; 70 G; 52 T; 0 other;

Query Match 20.3%; Score 75; DB 54; Length 266;
Best Local Similarity 80.5%; Pred. No. 8.43e-107;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Db 17 caaggtacacagaagttccaggcagagtcacccctgaccagcagcagcagcagca 75
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 164 CAACCTACATGCAATCTCAGTACCTCAGTACCTCAGTACCTCAGTACCTCAG 223
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 cactctacatgggtgagcagcctgagatctgagcagcagcctgattactgtgcga 136
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 224 CAGCCTACATGCAATCTCAGTACCTCAGTACCTCAGTACCTCAGTACCTCAG 283
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 137 gag 139
|||
QY 284 GAG 286

RESULT 2
ID HS1227079 standard; RNA; EST: 230 BP.
AC AA428970:
NI 92110596
DT 25-MAY-1997 (Rel. 52, Created)
DT 25-MAY-1997 (Rel. 52, Last updated, Version 1)
DE zV49b02 r1 Soares ovary tumor NBH0T Homo sapiens cDNA clone 756600
DE 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-230
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellberg K., Steptoe M., Tan F., Theising R.,
RA White Y., Wylie T., Waterston P., Wilson P.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilson PK WashU-Merck EST Project Washington University
CC School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel. 314 286 1800 Fax 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC CC LNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 ET from Amersham.
FH Key Location/Qualifiers
FH source
FH 1..230
FH /organism="Homo sapiens"
FH /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
FH modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
FH strand cDNA was primed with a Not I - oligo(dT) primer [5'
FH TGTTACCAATCTGAAGTGGGAGCGCGGCTTTTITTTTITTTT 3'],
FH double-stranded cDNA was size selected, ligated to Eco RI

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FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT7T3 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M. Fatima Bonaldo."
FT /clone="756439"
FT /clone_lib="Soares ovary tumor NBH0T"
FT /sex="Female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT mpna <1..230
FT Sequence 230 BP; 40 A; 84 C; 70 G; 36 T; 0 other;

Query Match 9.8%; Score 36; DB 57; Length 230;
Best Local Similarity 92.9%; Pred. No. 3.24e-29;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 119 ttgcacccctggggcagggagccctggtcacccgtctctcca 160
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 328 TTTCAGTACTGGGGCCAGGGAAGCTTGGTACCGCTCTCTCA 369
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
ID HS1300461 standard; RNA; EST: 238 BP.
AC AA505044:
NI 92241204
DT 04-JUL-1997 (Rel. 52, Created)
DT 04-JUL-1997 (Rel. 52, Last updated, Version 1)
DE aa33901 r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 825648 5' similar
DE to SW-HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominoidea;
OC Homo.
RN [1]
RP 1-238
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
RT Tumor Gene Index";
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert_Strausberg@nih.gov Tissue Procurement: Louis M. Staudt,
CC M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library
CC Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA
CC Library Arrayed by: Greg Lennon, Ph.D. RNA Sequencing by:
CC Washington University Genome Sequencing Center Clone distribution:
CC NCI-CGAP clone distribution information can be found through the
CC I.M.A.G.E. Consortium/LLNL at:
CC www-bio.llnl.gov/bbrp/image/image.html Trace considered overall
CC poor quality Possible reversed clone: similarity on wrong strand
CC Seq primer: -28ml3 rev1 ET from Amersham High quality sequence
CC stop: 1.
FH Key Location/Qualifiers
FH source
FH 1..238
FH /organism="Homo sapiens"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FH was prepared from human tonsillar cells enriched for
FH germinal center B cells by flow sorting (CD20+, IgD-),
FH provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
FH (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
FH primed with a Not I - oligo(dT) primer
FH [5'-TGTTACCAATCTGAAGTGGGAGCGCGGCTTTTITTTTITTTT-
FH 3']. Double-stranded cDNA was ligated to Eco RI adaptors (
FH Pharmacia), digested with Not I and cloned into the Not I
FH and Eco RI sites of the modified pT7T3 vector. Library was
FH through one round of normalization, and was constructed by
FH Bento Soares and M. Fatima Bonaldo."
FH /clone="825648"
FH /clone_lib="NCI_CGAP_GCB1"
FH /tissue_type="germinal center B cell"

```

```
FT mRNA /lab_host="DH10B"
SQ Sequence 238 BP: 57 A: 69 C: 66 G: 46 T: 0 other:
<1..>238

Query Match 9.8% Score 46: DP 69: Length 238:
Best Local Similarity 64.3% Pred No 3.24e-29:
Matches 81: Conservative 0: Mismatches 45: Indels 0: Gaps 0:

Db 8 gaggttaaaacacccggagctctctgagatctctctgagattctctgagattctgatacagcttt 67
   ||||| || || || || || || || || || || || || || || || || || || || || ||
QY 19 GAGGTGAAGACGCTGGGTCCTCGTGAGGCTCTCTGTCAGGTTTTTGGAGACACCTTC 78
   ||||| || || || || || || || || || || || || || || || || || || || || ||

Db 68 accagcagctgattccactggtgcgcagatgccgggaagaactctagtgtatagg 127
   ||||| || || || || || || || || || || || || || || || || || || || || ||
QY 79 ACAGATACACTATTCAGTGGTGGACAGGCCCCCTGGACAGGCGCTGAGTGGATGGGA 138
   ||||| || || || || || || || || || || || || || || || || || || || || ||

Db 128 agcatc 133
   |||||
QY 139 AATATC 144
   |||||

RESULT 4
LOCUS AA0505044 238 bp mRNA EST 02-JUL-1997
DEFINITION aa63q01.r1 NCI-CGAP_GCB1 Homo sapiens cDNA clone 825648 5' similar
to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
ACCESSION AA0505044
NID 92241204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae: Mitochondrial eukaryotes; Metazoa: Chordata:
Vertebrata: Mammalia: Euthera: Primates: Catarrhini: Hominoidea:
Homo.
REFERENCE 1 (bases 1 to 238)
AUTHORS NCI-CGAP. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 Et from Amersham
High quality sequence stop. 1.
Location/Qualifiers
1..238
/organism="Homo sapiens"
/clone="825648"
/clone_lib="Soares ovary tumor NCI-CGAP"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>511

FEATURES
source
```

```
/clone_lib="NCI-CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
<1..>238

BASE COUNT 57 a 69 c 66 g 46 t
ORIGIN

Query Match 9.8% Score 36: DB 35: Length 238:
Best Local Similarity 64.3% Pred. No. 3.24e-29:
Matches 81: Conservative 0: Mismatches 45: Indels 0: Gaps 0:

Db 8 gaggttaaaacacccggagctctctgagatctctctgagattctctgagattctgatacagcttt 67
   ||||| || || || || || || || || || || || || || || || || || || || || ||
QY 19 GAGGTGAAGACGCTGGGTCCTCGTGAGGCTCTCTGTCAGGTTTTTGGAGACACCTTC 78
   ||||| || || || || || || || || || || || || || || || || || || || || ||

Db 68 accagcagctgattccactggtgcgcagatgccgggaagaactctagtgtatagg 127
   ||||| || || || || || || || || || || || || || || || || || || || || ||
QY 79 ACAGATACACTATTCAGTGGTGGACAGGCCCCCTGGACAGGCGCTGAGTGGATGGGA 138
   ||||| || || || || || || || || || || || || || || || || || || || || ||

Db 128 agcatc 133
   |||||
QY 139 AATATC 144
   |||||

RESULT 5
ID HS1258634 standard: RNA: EST: 511 BP.
AC AA646794;
NI Q2189678;
DT 13-JUN-1997 (Rel. 52, Created)
DT 13-JUN-1997 (Rel. 52, Last updated, Version 1)
DE z83h07.r1 Soares ovary tumor NBOT Homo sapiens cDNA clone R10397
DE 5' similar to gb:L21964 IG HEAVY CHAIN V-II REGION (HUMAN).
KW EST.
OS Homo sapiens (human)
OC Eukaryotae: Mitochondrial eukaryotes; Metazoa: Chordata:
OC Vertebrata: Euthera: Primates: Catarrhini: Hominoidea: Homo.
NC [1]
RP 1-511
PA Hillier L., Allen M., Bowles L., Dubuque J., Geisel G., Jost S.,
PA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
PA Moore B., Scheinberg K., Steptoe M., Tan F., Theising B.,
PA White F., Wyllie T., Waterston R., Wilson R.;
PT "Washington University EST Project 1997";
RL Unpublished.
CC Contact: Wilson R. Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC estw@wustl.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 Et from Amersham High
CC quality sequence stop: 414.
FH Key
EH Location/Qualifiers
FT source
FT 1..511
/organism="Homo sapiens"
/clone="810397"
/clone_lib="Soares ovary tumor NBOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>511

Query Match 8.1% Score 30: DB 63: Length 511:
SQ Sequence 511 BP: 105 A: 169 C: 124 G: 112 T: 0 other:
MPSA
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ID MM1263658 standard. RNA. EST. 597 BP.
AC AA4720084
NT Q2200084
DT 21-JUN-1997 (Rel. 52, Created)
DE vhl0a05.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone
DE 875024 5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);
DE gb:L36038 Mus musculus germline immunoglobulin gamma constant
DE region (MOUSE);
KW EST.
OS Mus musculus (house mouse)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
PN 11-597
PP Marra M., Hillier L., Allen M., Bowles L., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.
RT "The WashU-HMMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HMMI Mouse EST Project
CC Washington University School of Medicine 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@watson.wustl.edu This clone is available
CC royalty-free through LNL: contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. M01-514504 Seq
CC primer: -28ml3 rev2 ET from Amersham High quality sequence stop
CC 440.
FH Location/Qualifiers
FT 1..597
FT /organism="Mus musculus"
FT /strain="C57BL/6J"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
FT was primed with a Not I - oligo (dT) primer [5',
FT TGTACCAATCTGAAGTGGGAGCGGCGGCAATCGTGTGTGTGTGTGTGTGTGTGT
FT T 3']; double-stranded cDNA was ligated to Eco RI adaptors
FT (Pharmacia), digested with Not I and cloned into the Not I
FT and Eco RI sites of the modified pT73 vector. RNA provide
FT by Dr. Minoru Ko, Wayne State Univ. Library constructed an
FT normalized by Bento Soares and M. Fatima Bonaldo."
FT /clone="875024"
FT /clone_lib="Soares mouse mammary gland NbMMG"
FT /sex="male"
FT /dev_stage="4 weeks"
FT /lab_host="DH10B"
FT mRNA
FT <1..>597
SQ Sequence 597 BP, 155 A, 132 C, 153 G, 156 T, 1 other.

Query Match 7.9%, Score 29, DB 83, Length 597.
Best Local Similarity 61.1%; Pred No 3,06e-17.
Matches 80; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 280 attatcaacatactactactgaattgtggaagggaaggaattccacatctcaagagatatt 339
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 155 ATAAATACCAACATACGCGGAGAAAGTTCAGGCGACAGCTCTGCAATACCGCGACGAGT 214
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 ccaaaaatagtgctacgtcgaatgaacaccttaagtcttgaaagacacccggctattt 399
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 215 CCACGAGCACACGCTACATGACTGACTAGTCAATCTAGTCAATCTAGTCAATCTAGT 274
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 actatctactaga 410
||||| |||||
QY 275 TCTGTCCGAGA 285
||||| |||||

RESULT 9

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LOCUS AA488043 279 bp mRNA EST 24 JUN 1997
DEFINITION ab12f07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840613
5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);
ACCESSION AA488043
NID Q2215474
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
1 (bases 1 to 259)
Hillier L., Allen M., Bowles L., Dubuque T., Geisel S., Jost S.,
Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
Theising B., White Y., Wylie T., Waterston R. and Wilson R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson R.K.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham.
FEATURES
Location/Qualifiers
1..259
/organism="Homo sapiens"
/note="Organ: lung; Vector: pBluescript SK-; Site 1:
EcoPI; Site 2: XbaI; Cloned unidirectionally. Primer:
Oligo dT, normal lung. Average insert size: 1.0 kb.
uni-ZAP XP Vector: -5'; adaptor sequence: 5' GAATTCGCGACGAG
3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGTGTGT 3'."
/clone="840613"
/clone_lib="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLP cells (kanamycin resistant)"
<1..>259
BASE COUNT 51 a 99 c 71 g 38 t
ORIGIN

Query Match 6.2%; Score 23; DB 30; Length 259.
Best Local Similarity 96.0%; Pred No 4,90e-08;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 ggggaacgtgtgtacccgtctctcca 25
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 345 GCGAACCTGTGTGTCACGCTCTCTCTCA 369

RESULT 10
ID HS128117 standard. RNA. EST. 279 BP.
AC AA488043;
NI Q2215474
DT 27-JUN-1997 (Rel. 52, Created)
DT 27-JUN-1997 (Rel. 52, Last updated, Version 1)
DE ab12f07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840613
DE 5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
OC Homo.
PN 11-259
PP Hillier L., Allen M., Bowles L., Dubuque T., Geisel S., Jost S.,
RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
RA Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
RA Theising B., White Y., Wylie T., Waterston R., Wilson R.,

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RT      "WashU-NCI human EST Project";
RL      Unpublished.
CC      Contact: Wilson KK Washington University School of Medicine 4444
CC      Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
CC      1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is
CC      available royalty-free through LLNL; contact the IMAGE Consortium
CC      (info@image.llnl.gov) for further information. Seq primer: -28ml3
CC      rev1 ET from Amersham.
FH      Key
FH      Location/Qualifiers
FH      source
FH      1..259
FH      /organism="Homo sapiens"
FH      /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
FH      ;
FH      Site_2: XhoI; Cloned unidirectionally. Primer: oligo dt.
FH      normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
FH      Vector: -5' adaptor sequence: 5' GAATTCGACGAG 3' -3',
FH      adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'
FH      /clone="840613"
FH      /clone_lib="Stratagene lung (#937210)"
FH      /sex="male"
FH      /dev_stage="72 years"
FH      /lab_host="SOLR cells (kanamycin resistant)"
FH      <1..>259
FH      mrna
FH      Sequence 259 BP; 51 A; 99 C; 71 G; 38 T; 0 other;
FH      SQ
FH      Query Match
FH      Best Local Similarity 6.2%; Score 23; DB 66; Length 259;
FH      Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
FH      Db 1 gggaaagctggtcaccgctctccta 25
FH      QY 345 GGGAAACCTTGTACCGTCTCTCA 369
FH      RESULT 11
FH      LOCUS
FH      DEFINITION
FH      D. melanogaster STS determined from European Mapping Project
FH      cosmid.
FH      ACCESSION
FH      NID
FH      91263839
FH      KEYWORDS
FH      sequence tagged site.
FH      SOURCE
FH      fruit fly.
FH      ORGANISM
FH      Drosophila melanogaster
FH      Eukaryote; mitochondrial eukaryotes; Metazoa; Arthropoda;
FH      Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
FH      Ephydroidea; Drosophilidae; Drosophila.
FH      1 (bases 1 to 314)
FH      European Drosophila Mapping Consortium.
FH      Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,
FH      Downing St., Cambridge CB2 3EH, England
FH      STS_name = Dm78C5T
FH      clone_name = 78C5
FH      STS_from_promoter = T7
FH      vector_class = cosmid, Loris 6
FH      origin_of_clone = Oregon-R
FH      in_situ_site_primary = 37E
FH      BLAST_program = BLASTN
FH      database_searched = EMBL
FH      database_version = 45.0 and updates till date_of_search
FH      date_of_search = 08-01-1996
FH      BLAST_program = BLASTX
FH      database_searched = SWISSPROT
FH      database_version = 32.0
FH      date_of_search = 15-12-1995.
FH      Location/Qualifiers
FH      1..314
FH      /organism="Drosophila melanogaster"
FH      /strain="Oregon-R"
FH      /clone="78C5"
FH      BASE COUNT
FH      66 a 88 c 104 g 55 t 1 others
FH      ORIGIN

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Query Match
Best Local Similarity 84.4%; Score 22; DB 1; Length 314;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 158 cgaggagatttcggcggtgatcgagagatttgc 189
Cp 219 CGTGAATCTCGCGGCTTATCGAGAGTCTGC 188
RESULT 12
ID HSA07475 standard; RNA; EST; 435 BP.
AC AA507475;
NI 92243914
DT 05-JUL-1997 (Rel. 52, Created)
DT 16-JUL-1997 (Rel. 52, Last updated, Version 2)
DE nh76c05.s1 NCI_CGAP_Br.1.1 Homo sapiens cDNA clone 964424 similar to
DE gb:X14584 IG HEAVY CHAIN PPECUPSOR V-TII REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
OC Homo.
RN 1
RP 1-435
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
RT Tumor Gene Index";
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email.
CC Robert.Strausberg@nih.gov Tissue Procurement: Christopher Moskaluk,
CC M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library
CC Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg
CC Lennon, Ph.D. DNA Sequencing by: Washington University Genome
CC Sequencing Center Clone distribution: NCI-CGAP clone distribution
CC information can be found through the I.M.A.G.E. Consortium/LLNL at:
CC www-bio.llnl.gov/bbrp/image/image.html Insert Length: 558 Std
CC Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality
CC sequence stop: 131.
FH Key
FH Location/Qualifiers
FH source
FH 1..435
FH /organism="Homo sapiens"
FH /note="Vector: pT73D-pac (Pharmacia) with a modified
FH polylinker; 1st strand cDNA was prepared from pooled bulk
FH breast tumor tissue, and was then primed with a Not I -
FH oligo(dT) primer. Double-stranded cDNA was ligated to Eco
FH RI adaptors (Pharmacia), digested with Not I and cloned
FH into the Not I and Eco RI sites of the modified pT7T3
FH vector. Library is not normalized. (The normalized version
FH of this library is NCI_CGAP.Br.2.) Library was constructed
FH by Bento Soares and M. Fatima Bonaldo."
FH /clone="964424"
FH /clone_lib="NCI_CGAP_Br.1.1"
FH /sex="female, pooled"
FH /tissue_type="breast"
FH /lab_host="DH10B"
FH mrna
FH <1..>435
FH Sequence 435 BP, 94 A, 128 C, 112 G; 101 T, 0 other.
FH SQ
FH Query Match
FH Best Local Similarity 64.5%; Score 22; DB 80; Length 435;
FH Matches 49; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
FH Db 264 ctgctaaaggtgaatccagagggtgcacagagagagctctcaggagccccccagagctgacc 323
FH Cp 83 CTGCTGAAGGTGCTCCAAAACCTCAGAGGAGCTTTTACCGAGAGCCAGGCTTTTTC 24
FH Db 324 aagcctccccccagact 339
FH Cp 23 ACCTCAGCCCCCAGACT 8

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RESULT 13
 LOCUS A507475 435 bp mRNA EST 15-JUL-1997
 DEFINITION gb:U4584 s1 NCI-CGAP_R11 Homo sapiens cDNA clone 364424 similar to
 ACCESSION A507475
 NID Q2243914
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Primates; Catarrhini; Hominoidea;
 Homo.
 REFERENCE 1 (bases 1 to 435)
 AUTHORS NCI-CGAP.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Tumor Gene Index.
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 558 Std Error: 0.00
 Seq primer: -40ml3 fwd FT from Amersham
 High quality sequence stop: 131.

FEATURES

Location/Qualifiers
 1 435

/organism="Homo sapiens"
 /note="Vector: pT73B-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is not normalized. (The normalized
 version of this library is NCI-CGAP_R2.) Library was
 constructed by Bento Soares and M. Fatima Honald.
 /clone="964424"
 /sex="female, pooled"
 /tissue="breast"
 /lab="host="DH10R"
 <1..>435

mRNA
 BASE COUNT 94 a 129 c 112 g 101 t

Query Match 6.0% Score 22; DR 40; Length 435;
 Best Local Similarity 64.5% Pred. No. 1:24e-06;
 Matches 49; Conservative 0; Mismatches 27; Indels 0; Gaps 0.

Db 264 ctcttaaaagtgtaacccagagaggtccaggaacccccccaggtgtacc 323
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 83 CTCTGAAGGTGTTCTCAAAACCTTACAGTATCTTCTAGAGTACAGTCTTCTC 24
 Db 324 aaactccccagact 339
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 23 ACCTCAGCCACAGACT 8

RESULT 14
 LOCUS DM36D7S 156 bp DNA STS
 DEFINITION D. melanogaster STS determined from European Mapping Project
 cosmid.
 ACCESSION Z70880
 NID Q1263754

KEYWORDS

sequence tagged site.

SOURCE

fruit fly
 Drosophila melanogaster
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;
 Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 156)
 European Drosophila Mapping Consortium.
 Direct Submission

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,
 Downing St., Cambridge CB2 3EH, England
 STS_name = Dm36D7S
 clone_name = 36D7
 STS_from_promoter = SP6
 vector_class = cosmid, Loris 6
 origin_of_clone = Oregon-R
 in_situ_site_primary = 98C
 BLAST_program = BLASTN
 database_version = EMBL
 date_of_search = 08-01-1996
 BLAST_program = BLASTX
 database_searched = SWISSPROT
 database_version = 32.0
 date_of_search = 15-12-1995.

FEATURES

source

1..156
 /organism="Drosophila melanogaster"
 /strain="Oregon-R"
 /clone="36D7"

BASE COUNT 28 a 37 c 30 g 27 t 34 others
 ORIGIN

Query Match 5.7% Score 21; DR 1; Length 156;
 Best Local Similarity 25.5% Pred. No. 2:8e-05;
 Matches 12; Conservative 22; Mismatches 13; Indels 0; Gaps 0.

Db 10 rttgtagtgagkssrrgrgrrgkrrgagksksrrgkrrkskr 56
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 91 ATTTCAGTGGTTCGACAGAGCCCTCTGACAAAGGCTCAGTGATGG 137

RESULT 15
 LOCUS AAS15152 420 bp mRNA EST 14-JUL-1997
 DEFINITION gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN).

ACCESSION AAS15152
 NID Q2254752
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.

REFERENCE 1 (bases 1 to 420)
 AUTHORS NCI-CGAP.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Tumor Gene Index.
 COMMENT Unpublished (1997)

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 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. EI from Amersham

